

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
11 January 2001 (11.01.2001)

PCT

(10) International Publication Number
WO 01/02568 A2

(51) International Patent Classification⁷: C12N 15/12,
15/55, 15/54, 15/61, C07K 14/47, C12N 9/64, 9/12, 9/90,
C12Q 1/68, C12N 15/11, C07K 16/18, 16/40, G01N
33/566, A61K 38/00

(21) International Application Number: PCT/US00/18374

(22) International Filing Date: 30 June 2000 (30.06.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/142,310 2 July 1999 (02.07.1999) US
60/142,311 2 July 1999 (02.07.1999) US

(71) Applicants: CHIRON CORPORATION [US/US]; 4560
Horton Street, Emeryville, CA 94608 (US). HYSEQ,
INC. [US/US]; 675 Almanor Avenue, Sunnyvale, CA
94086 (US).

(72) Inventors: WILLIAMS, Lewis, T.; Chiron Corporation,
P.O. Box 8097, Emeryville, CA 94662-8097 (US). ES-
COBEDO, Jaime; Chiron Corporation, P.O. Box 8097,
Emeryville, CA 94662-8097 (US). INNIS, Michael, A.;
Chiron Corporation, P.O. Box 8097, Emeryville, CA
94662-8097 (US). GARCIA, Pablo, Dominguez; Chiron
Corporation, P.O. Box 8097, Emeryville, CA 94662-8097
(US). KLINGER, Julie; Chiron Corporation, P.O. Box
8097, Emeryville, CA 94662-8097 (US). KASSAM,
Altaf; Chiron Corporation, P.O. Box 8097, Emeryville,
CA 94662-8097 (US). REINHARD, Christoph; Chiron
Corporation, P.O. Box 8097, Emeryville, CA 94662-8097
(US). RANDAZZO, Filippo; Chiron Corporation,
P.O. Box 8097, Emeryville, CA 94662-8097 (US).
KENNEDY, Guilina, C.; Chiron Corporation, P.O. Box
8097, Emeryville, CA 94662-8097 (US). POT, David;
Chiron Corporation, P.O. Box 8097, Emeryville, CA
94662-8097 (US). LAMSON, George; Chiron Corpora-
tion, P.O. Box 8097, Emeryville, CA 94662-8097 (US).

DRMANAC, Radoje; 675 Almanor Avenue, Sunnyvale,
CA 94086 (US). CRKENJAKOV, Radomir; 675 Al-
manor Avenue, Sunnyvale, CA 94086 (US). DRMANAC,
Snezana; 675 Almanor Avenue, Sunnyvale, CA 94086
(US). DICKSON, Mark; 675 Almanor Avenue, Sun-
nyvale, CA 94086 (US). LABAT, Ivan; 675 Almanor
Avenue, Sunnyvale, CA 94086 (US). LESHKOWITZ,
Dena; 675 Almanor Avenue, Sunnyvale, CA 94086 (US).
KITA, David; 675 Almanor Avenue, Sunnyvale, CA
94086 (US). GARCIA, Veronica; 675 Almanor Avenue,
Sunnyvale, CA 94086 (US). JONES, Lee, William; 675
Almanor Avenue, Sunnyvale, CA 94086 (US). STRA-
CHE-CRAIN, Birgit; 675 Almanor Avenue, Sunnyvale,
CA 94086 (US).

(74) Agents: BLACKBURN, Robert, P.; Chiron Corporation,
4560 Horton Street, Emeryville, CA 94608-2916 et al.
(US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian
patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European
patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,
IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— Without international search report and to be republished
upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.

(54) Title: NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS

(57) Abstract: The invention provides novel polynucleotides. The invention further provides novel members of protein families, and polynucleotides that are differentially expressed in cancer cells relative to normal cells, and in metastatic cancer cells relative to normal cells or non-metastatic cancer cells.



WO 01/02568 A2

NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS

FIELD OF THE INVENTION

The present invention relates to novel polynucleotides of human origin and the encoded gene products.

5 BACKGROUND OF THE INVENTION

Identification of novel polynucleotides, particularly those that encode an expressed gene product, is important in the advancement of drug discovery, diagnostic technologies, and the understanding of the progression and nature of complex diseases such as cancer. Identification of genes expressed in different cell types isolated from
10 sources that differ in disease state or stage, developmental stage, exposure to various environmental factors, the tissue of origin, the species from which the tissue was isolated, and the like is key to identifying the genetic factors that are responsible for the phenotypes associated with these various differences.

This invention provides novel human polynucleotides, the polypeptides
15 encoded by these polynucleotides, and the genes and proteins corresponding to these novel polynucleotides.

SUMMARY OF THE INVENTION

This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these
20 polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a polynucleotide comprising the sequence information of at least one of SEQ ID NOs: 1-3351.

25 Various aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA genomic sequences, and genes

corresponding to these sequences and degenerate variants thereof, and to polypeptides encoded by the polynucleotides of the invention and polypeptide variants.

Polypeptide variants differ from wild type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild type protein.

Six of the polypeptides disclosed herein encode new members of the MKK kinase family; the coding region is found within the nucleotide region in parentheses: SEQ ID NO:29 (nucleotides 295-421); SEQ ID NO:31 (298-397); SEQ ID NO:196 (37-322); SEQ ID NO:3175 (nucleotides 14-164); SEQ ID NO:3190 (229-390); and SEQ ID NO:3281 (15-182). Twenty-four of the polypeptides encode new members of the family of transcription factor proteins having a basic region plus leucine zipper: SEQ ID NO:410 (42-191); SEQ ID NO:552 (116-288); SEQ ID NO:768 (116-288); SEQ ID NO:822 (108-262); SEQ ID NO:836 (158-353); SEQ ID NO:1288 (73-234); SEQ ID NO:1365 (69-257); SEQ ID NO:1540 (289-471); SEQ ID NO:1549 (200-391); SEQ ID NO:1556 (163-354); SEQ ID NO:1557 (207-398); SEQ ID NO:1563 (107-298); SEQ ID NO:1622 (180-365); SEQ ID NO:1630 (100-291); SEQ ID NO:1704 (184-372); SEQ ID NO:1808 (36-161); SEQ ID NO:1454 (49-209); SEQ ID NO:2363 (48-211); SEQ ID NO:2424 (43-194); SEQ ID NO:3147 (190-369); SEQ ID NO:3152 (129-320); SEQ ID NO:3158 (167-334); and SEQ ID NO:3208 (34-256).

SEQ ID NOs:186 (175-395); 2591 (60-165); 3307 (43-321); and 3339 (94-342) encode polypeptides having an SH2 domain, and SEQ ID NOs:234 (23-121), 1832 (18-173), and 1835 (57-206) encode polypeptides having an SH3 domain. Nine polypeptides encode new members of the family of proteins having Ank repeat regions: SEQ ID NO:187 (358-432); SEQ ID NO:1268 (238-315); SEQ ID NO:1804 (301-378); SEQ ID NO:1819 (278-355); SEQ ID NO:1839 (224-307); SEQ ID NO:1830 (184-267); SEQ ID NO:2562 (18-101); SEQ ID NO:3015 (131-214); and SEQ ID NO:3267 (97-180).

The following eleven polynucleotides encode polypeptides having a C2H2 type zinc finger: SEQ ID NOs:308 (110-172); 807 (339-392); 1324 (294-356); 1503 (154-216); 1527 (156-212); 1674 (196-258); 1779 (64-126); 1801 (295-351); 3081 (190-252); 3193 (293-355); and 3306 (161-223). Eight polynucleotides encode polypeptides of the family of ATPases: SEQ ID NOs:431 (71-428); 639 (157-561); 2135 (2-401); 2684 (9-461); 2859 (100-320); 3178 (45-386); 3197 (281-343) and 3266 (8-139). Polypeptides having a fibronectin type III domain are encoded by SEQ ID NO:746 (209-427) and 1192 (186-416). Polypeptides having an EF-hand domain are encoded by SEQ ID NO:820 (341-

406); 1755 (281-367) and 3285(16-102). Six polypeptides of the protein kinase family are encoded by SEQ ID NOs:1157 (41-444); 1478 (54-437), 1496 (241-520); 2286 (12-182); 2969 (5-387); and 3190 (118-390).

LIM domain-containing polypeptides are encoded by SEQ ID NO:1269
 5 (79-240); 1309 (248-404); 1360 (222-377); and 1386 (243-398). Two polypeptides of the family having a C2 domain (protein kinase C-like) are encoded by SEQ ID NO:1325 (1-234) and 2282(183-353). Polypeptides having a WD domain, G-beta repeat motif are encoded by SEQ ID NOs:1336 (66-164); 1380 (42-140); 1711 (263-361); 1762 (236-334); 1909 (160-258); 2218 (127-225); 3047 (191-292); 3108 (275-367) and 3292 (208-300).
 10 SEQ ID NO:1410 (222-350) encodes a member of the trypsin family. SEQ ID NOs:1417 (8-354); 2281 (20-387) and 2310 (20-371) encode members of the protein tyrosine phosphatase family. SEQ ID NOs:1464 (4-180) and 1514 (2-252) encode members of the family having an RNA recognition motif (also known as RRM, RBD, or RNP domain). SEQ ID NOs:1496 (241-520) and 3297(7-153) encode helicases having a
 15 conserved C-terminal domain. SEQ ID NO:1538 (9-635) encodes a member of the wnt family of developmental signaling proteins.

Three polynucleotides encode polypeptides having a homeobox domain: SEQ ID NOs:1676 (9-86); 1820 (123-299); and 1821 (127-303). A novel thioredoxin is encoded by SEQ ID NO:1677 (316-369). Two novel members of the ras family are
 20 encoded by SEQ ID NO:1688(109-410) and 3258(138-394). A novel polypeptide having a phosphatidylinositol-specific phospholipase C Y-domain is encoded by SEQ ID NO:1707 (92-439). A novel serine carboxypeptidase is encoded by SEQ ID NO:1744 (238-433). A novel polypeptide having N-terminal homology in the Ets domain is encoded by SEQ ID NO:1811 (184-315). A novel polypeptide having a bromodomain is encoded by SEQ ID
 25 NO:1814 (127-294). A novel polypeptide having a double-stranded RNA binding motif is encoded by SEQ ID NO:1818 (9-146). A novel polypeptide having a G-protein alpha subunit is encoded by SEQ ID NO:1846 (12-398).

SEQ ID NOs:1911 (35-151) and 1980 (60-197) encode polypeptides having a C3HC4 type zinc finger domain (RING finger). SEQ ID NO:2065 (253-306)
 30 encodes a polypeptide having a CCHC zinc finger domain. SEQ ID NO:2216 (90-179) encodes a polypeptide having a WW/rsp5/WWP domain. SEQ ID NO:2428 (25-350) encodes a polypeptide member of the dual specificity phosphatase family, having a catalytic domain.

SEQ ID NOs:2577 (0-311); 3183 (14-215); and 3195 (0-215) encode
 35 members of the 4 transmembrane segment integral membrane protein family. SEQ ID

NOs:2826 (116-400) and 2871 (198-392) encode polypeptides of the DEAD and DEAH box helicase family. SEQ ID NO:2944 (18-281) encodes a polypeptide having a calpain large subunit, domain III.

5 SEQ ID NO:3274 (11-187) encodes a eukaryotic transcription factor with a fork head domain. SEQ ID NO:3345 (65-271) encodes a polypeptide having a PDZ domain, and SEQ ID NO:3351 (124-270) encodes a polypeptide in the family of phorbol esters/glycerol binding proteins.

Described below are polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene
10 product, expression of these polynucleotides and genes, identification of structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides
15 and their encoded gene products for therapeutic and diagnostic purposes.

Polynucleotide Compositions

The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID NOs:1-3351; polynucleotides obtained from the biological materials
20 described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a
25 gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here.
30 "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the length or structure of the nucleic acid unless specifically indicated.

The invention features polynucleotides that are expressed in human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid

compositions of the invention comprise a sequence set forth in any one of SEQ ID NOs:1-3351 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely identifies a polynucleotide sequence, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOs:1-3351.

The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, U.S. Patent No. 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.*, allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences (SEQ ID NOs:1-3351) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, *e.g.*, primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

Preferably, hybridization is performed using at least 15 contiguous nucleotides (nt) of at least one of SEQ ID NOs:1-3351. That is, when at least 15 contiguous nt of one of the disclosed SEQ ID NOs. is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nt can be used, *e.g.*, probes of from about 18 nt to about 100 nt, but 15 nt represents sufficient sequence for unique identification.

The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants).

5 Variants of the polynucleotides of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

10 The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOs:1-3351, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.* Between mammalian species, *e.g.*, human and mouse, homologs generally have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul et al., *J. Mol. Biol.* (1990) 215:403-10.

25 In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90%, 91%, 92%, 93%, 94%, 95%, or 96%, most preferably 97%, 98% or 99%. For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

30 The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence

elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

5 A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as
10 promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences
15 required for proper tissue, stage-specific, or disease-state specific expression.

 The nucleic acid compositions of the subject invention can encode all or a part of the subject polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.*
20 Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nt selected from the polynucleotide sequences as shown in SEQ ID NOs:1-3351. The fragments also include those of lengths intermediate to the specifically mentioned lengths, such as 35,
25 36, 37, 38, 39, *etc.*; 150, 151, 152, 153, 154, *etc.* For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least 12 nt selected from the group consisting of the polynucleotides shown in SEQ ID NOs:1-3351.

30 Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOs:1-3351. The probes are preferably at least about a 12, 15, 16, 18, 20, 22, 24, or 25 nt fragment of a corresponding contiguous sequence of SEQ ID NOs:1-3351, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be
35 generated from longer polynucleotides using restriction enzymes. The probes can be

labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOs:1-3351. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following
5 application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in
10 substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring
15 chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory
20 sequences known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium
25 phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (*e.g.*, extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single
30 stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the polynucleotide sequences as shown in SEQ ID NOs:1-3351 or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA, Gene, and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOs:1-3351, or a portion thereof comprising at least 12, 15, 18, or 20 nt, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in U.S. Patent No. 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. As described in the Examples, cDNA of the invention was isolated from specific cell or tissue types, and such cells and tissues are preferable for obtaining related nucleic acids.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from SEQ ID NOs:1-3351. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences

5' to the end of a partial cDNA, 5' RACE (*PCR Protocols: A Guide to Methods and Applications*, (1990) Academic Press, Inc.) can be performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to the isolation of full-length cDNAs. Briefly, the provided
5 polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1
10 or YAC, as described in detail in Sambrook et al., 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook et al., such that adjacent and overlapping fragments of genomic DNA are
15 isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed
20 on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook et al., *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be
25 produced using the instant sequences as primers.

PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods as described in Gruber et al., WO
30 95/04745 and Gruber et al., U.S. Patent No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) 15:890-893; Edwards et al., *Nuc. Acids Res.* (1991)
35 19:5227-5232). When a single gene-specific RACE primer is paired with the common

primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

5 The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the "TATA" box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is
10 highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook et al., 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure
15 herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses
20 nucleic acid molecules ranging in length from 15 nt (corresponding to at least 15 contiguous nt of one of SEQ ID NOs:1-3351) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOs:1-3351; (b) the nucleic
25 acid of (a) also comprising at least one additional polynucleotide or gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b) ; and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

30 The sequence of a nucleic acid comprising at least 15 contiguous nt of at least any one of SEQ ID NOs:1-3351, preferably the entire sequence of at least any one of SEQ ID NOs:1-3351, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function
35 and can be dictated by coding regions desired, the intron-like regions desired, and the

regulatory regions desired. Where the entire sequence of any one of SEQ ID NOs:1-3351 is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOs:1-3351.

Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

5 The provided polynucleotides (*e.g.*, a polynucleotide having a sequence of one of SEQ ID NOs:1-3351), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product. Constructs of polynucleotides having sequences of SEQ ID NOs:1-3351 can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of
10 oligodeoxyribonucleotides is described by, *e.g.*, Stemmer et al., *Gene (Amsterdam)* (1995) 164(1):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build
15 increasingly longer DNA fragments during the assembly process.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS,
20 National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Vectors, host cells and methods for obtaining expression in same are well known in the art. Suitable vectors and host cells are described in U.S. Patent
25 No. 5,654,173.

Polynucleotide molecules comprising a polynucleotide sequence provided herein are generally propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain
30 vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are

available commercially. Methods for preparation of vectors comprising a desired sequence are well known in the art.

The polynucleotides set forth in SEQ ID NOs:1-3351 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any appropriate host cells or organisms are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670.

Identification of Functional and Structural Motifs of Novel Genes

Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. Also, sequences exhibiting similarity with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides.

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed

herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient. These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular
5 Sequence Analysis" *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST, available over the world
10 wide web at <http://www.ncbi.nlm.nih.gov/BLAST>. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, *supra*. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The
15 Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* (1997) 70: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer.
20 This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases.

High Similarity. In general, in alignment results considered to be of high
25 similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the
30 region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity
35 is found, the query sequence is considered to have high similarity with a profile

sequence when the p value is less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} ; even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more typically; no more than or equal to about 10^{-10} ; even more typically; no more than or equal to about 10^{-15} for the query sequence
5 to be considered high similarity.

Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence
10 if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More
15 typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define
20 either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (*e.g.*, polypeptides) encoded by the provided polynucleotides or corresponding
25 cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described,
30 for example, in Birney et al., *Nucl. Acid Res.* (1996) 24(14): 2730-2739. MSAs of some protein families and motifs are publicly available. MSAs are described also in Sonnhammer et al., *Proteins* (1997) 28: 405-420. A brief description of MSAs is reported in Pascarella et al., *Prot. Eng.* (1996) 9(3):249-251. Techniques for building profiles from MSAs are described in Sonnhammer et al., *supra*; Birney et al., *supra*;

and "Computer Methods for Macromolecular Sequence Analysis," *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning
5 the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile (see Birney et al., *supra*). Other techniques to compare the sequence and profile are described in Sonnhammer et al., *supra* and Doolittle, *supra*.

10 Next, methods described by Feng et al., *J. Mol. Evol.* (1987) 25:351 and Higgins et al., *CABIOS* (1989) 5:151 can be used align the query sequence with the members of a family or motif, also known as a MSA. Sequence alignments can be generated using any of a variety of software tools. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng et al., *J. Mol. Evol.*
15 (1987) 25:351. Another method, GAP, uses the alignment method of Needleman et al., *J. Mol. Biol.* (1970) 48:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith et al., *Adv. Appl. Math.* (1981) 2:482. In general, the following factors are used to determine if a similarity between a query
20 sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce
25 the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer
30 frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or

some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically; at least about 55%.

Identification of Secreted and Membrane-Bound Polypeptides

Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, plasma, serum, and other body fluids such as urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) 78:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) 157: 105-132; and RAOAR algorithm, Degli Esposti et al., *Eur. J. Biochem.* (1990) 190: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine

Identification of the Function of an Expression Product of a Full-Length Gene

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. The phosphoramidite method of oligonucleotide synthesis can be used to construct antisense molecules and ribozymes. See Beaucage et al., *Tet. Lett.* (1981) 22:1859 and U.S. Patent No. 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA, phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA.

Oligonucleotides of up to 200 nt can be synthesized, more typically, 100 nt, more typically 50 nt; even more typically 30 to 40 nt. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook et al., *supra*. Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an *in vitro* or *in vivo* context, by detecting the phenotypic effect.

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot," testing the polynucleotide as an antisense compound in the corresponding cancer cells is warranted.

Dominant negative mutations also are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic

domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, *e.g.*, Herskowitz, *Nature* (1987) 329:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

Polypeptides and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOs:1-3351 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.*, other animal or plant species, where such homologs, usually mammalian species, *e.g.*, rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By "homolog" is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST algorithm, with the parameters described above.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.*, are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide
5 is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of
10 polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not
15 necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/ hydrophilicity, and/or steric bulk of the amino acid substituted. Variants can be designed so as to retain biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). Selection
20 of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (see, *e.g.*, Go et al., *Int. J. Peptide Protein Res.* (1980) 15:211), the thermostability of the variant polypeptide (see, *e.g.*, Querol et al., *Prot. Eng.* (1996) 9:265), desired glycosylation sites (see, *e.g.*, Olsen and Thomsen, *J. Gen. Microbiol.* (1991) 137:579), desired disulfide bridges (see, *e.g.*, Clarke et al.,
25 *Biochemistry* (1993) 32:4322; and Wakarchuk et al., *Protein Eng.* (1994) 7:1379), desired metal binding sites (see, *e.g.*, Toma et al., *Biochemistry* (1991) 30:97, and Haezebrouck et al., *Protein Eng.* (1993) 6:643), and desired substitutions with in proline loops (see, *e.g.*, Masul et al., *Appl. Env. Microbiol.* (1994) 60:3579). Cysteine-depleted muteins can be produced as disclosed in U.S. Patent No. 4,959,314.

30 Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will
35 have a stretch of amino acids that is identical to a polypeptide encoded by a

polynucleotide having a sequence of any SEQ ID NOs:1-3351, or a homolog thereof. The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

5 Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have

the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

The polynucleotide libraries of the subject invention generally comprise sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOs:1-3351. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOs:1-3351. The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, *etc.*

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.*, the nucleic acid sequences of any of the polynucleotides of SEQ ID NOs:1-3351, can be recorded on computer readable media, *e.g.*, any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.*, word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (*e.g.*, searchable files, executable files, *etc.*, including, but not limited to, for example, search program software, *etc.*).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the BLAST (Altschul et al.,

supra.) and BLAZE (Brutlag et al. *Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information. Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.*, MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt. A variety of comparing means can be used to accomplish comparison of sequence information from a sample (*e.g.*, to analyze target sequences, target motifs, or relative expression levels) with the data storage means. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention to accomplish comparison of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are

not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks the relative expression levels of different polynucleotides. Such presentation provides a skilled artisan with a ranking of relative expression levels to determine a gene expression profile.

As discussed above, the "library" of the invention also encompasses biochemical libraries of the polynucleotides of SEQ ID NOs:1-3351, *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOs:1-3351 is represented on the array. By array is meant an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOs:1-3351.

Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

Polynucleotide probes, generally comprising at least 12 contiguous nt of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Detection of Expression Levels. Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots,

mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for *in situ* hybridization to cells to detect expression. Probes
5 can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and U.S. Patent No. 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means
10 for detecting small amounts of target nucleic acids (see, *e.g.*, Mullis et al., *Meth. Enzymol.* (1987) 155:335; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202). Two primer polynucleotides nucleotides that hybridize with the target nucleic acids are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and
15 5' to these polynucleotides, they need not hybridize to them or the complements. After amplification of the target with a thermostable polymerase, the amplified target nucleic acids can be detected by methods known in the art, *e.g.*, Southern blot. mRNA or cDNA can also be detected by traditional blotting techniques (*e.g.*, Southern blot, Northern blot, *etc.*) described in Sambrook et al., "Molecular Cloning: A Laboratory
20 Manual" (New York, Cold Spring Harbor Laboratory, 1989) (*e.g.*, without PCR amplification). In general, mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis, and transferred to a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe, washed to remove any unhybridized probe, and duplexes containing the labeled probe
25 are detected.

Mapping. Polynucleotides of the present invention can be used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-
30 related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in U.S. Patent No. 5,783,387. An exemplary mapping method is fluorescence *in situ* hybridization (FISH), which facilitates comparative genomic hybridization to allow total genome assessment of changes in
35 relative copy number of DNA sequences (see, *e.g.*, Valdes et al., *Methods in Molecular*

Biology (1997) 68:1). Polynucleotides can also be mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach et al., *Advances in Genetics*, (1995) 33:63-99; Walter et al., *Nature Genetics* (1994) 7:22; Walter and Goodfellow, *Trends in Genetics* (1992) 9:352. Panels for radiation
5 hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web at <http://www.sph.umich.edu/group/statgen/software>. In addition, commercial programs are available for identifying
10 regions of chromosomes commonly associated with disease, such as cancer.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR,
15 branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

Tissue typing can be used to identify the developmental organ or tissue source of a metastatic lesion by identifying the expression of a particular marker of that
20 organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified. Expression of a particular polynucleotide can be assayed by detection of either the corresponding mRNA or the protein product.

Use of Polymorphisms. A polynucleotide of the invention can be used in
25 forensics, genetic analysis, mapping, and diagnostic applications where the corresponding region of a gene is polymorphic in the human population. Any means for detecting a polymorphism in a gene can be used, including, but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

30 Antibody Production

Expression products of a polynucleotide of the invention, as well as the corresponding mRNA, cDNA, or complete gene, can be prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional

method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an *in vitro* expression system.

Methods for production of monoclonal and polyclonal antibodies that specifically bind a selected antigen are well known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. Epitopes that involve non-contiguous amino acids may require a longer polypeptide, *e.g.*, at least 15, 25, or 50 amino acids. Antibodies that specifically bind to human polypeptides encoded by the provided polynucleotides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically polypeptides of the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

The invention also contemplates naturally occurring antibodies specific for a polypeptide of the invention. For example, serum antibodies to a polypeptide of the invention in a human population can be purified by methods well known in the art, *e.g.*, by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, the invention also contemplates genetically engineered antibodies, antibody derivatives (*e.g.*, single chain antibodies, antibody fragments (*e.g.*, Fab, *etc.*)), according to methods well known in the art.

Other embodiments of the present invention include humanized monoclonal antibodies capable of binding to the polypeptides of the invention. The phrase "humanized antibody" refers to an antibody derived from a non-human antibody - typically a mouse monoclonal antibody. Alternatively, a humanized antibody may be derived from a chimeric antibody that retains or substantially retains the antigen-binding properties of the parental, non-human, antibody but which exhibits diminished immunogenicity as compared to the parental antibody when administered to humans. The phrase "chimeric antibody," as used herein, refers to an antibody containing

sequence derived from two different antibodies (*see, e.g.*, U.S. Patent No. 4,816,567) which typically originate from different species. Most typically, chimeric antibodies comprise human and murine antibody fragments, generally human constant and mouse variable regions.

5 Because humanized antibodies are far less immunogenic in humans than the parental mouse monoclonal antibodies, they can be used for the treatment of humans with far less risk of anaphylaxis. Thus, these antibodies may be preferred in therapeutic applications that involve *in vivo* administration to a human such as, *e.g.*, use as radiation sensitizers for the treatment of neoplastic disease or use in methods to reduce the side
10 effects of, *e.g.*, cancer therapy.

Humanized antibodies may be achieved by a variety of methods including, for example: (1) grafting the non-human complementarity determining regions (CDRs) onto a human framework and constant region (a process referred to in the art as “humanizing”), or, alternatively, (2) transplanting the entire non-human
15 variable domains, but “cloaking” them with a human-like surface by replacement of surface residues (a process referred to in the art as “veneering”). In the present invention, humanized antibodies will include both “humanized” and “veneered” antibodies. These methods are disclosed in, *e.g.*, Jones et al., *Nature* 321:522-525 (1986); Morrison et al., *Proc. Natl. Acad. Sci., U.S.A.*, 81:6851-6855 (1984); Morrison and Oi, *Adv. Immunol.*, 44:65-92 (1988); Verhoeyer et al., *Science* 239:1534-1536
20 (1988); Padlan, *Molec. Immunol.* 28:489-498 (1991); Padlan, *Molec. Immunol.* 31(3):169-217 (1994); and Kettleborough, C.A. et al., *Protein Eng.* 4(7):773-83 (1991) each of which is incorporated herein by reference.

The phrase “complementarity determining region” refers to amino acid
25 sequences which together define the binding affinity and specificity of the natural Fv region of a native immunoglobulin binding site. *See, e.g.*, Chothia et al., *J. Mol. Biol.* 196:901-917 (1987); Kabat et al., U.S. Dept. of Health and Human Services NIH Publication No. 91-3242 (1991). The phrase “constant region” refers to the portion of the antibody molecule that confers effector functions. In the present invention, mouse
30 constant regions are substituted by human constant regions. The constant regions of the subject humanized antibodies are derived from human immunoglobulins. The heavy chain constant region can be selected from any of the five isotypes: alpha, delta, epsilon, gamma or mu.

One method of humanizing antibodies comprises aligning the non-
35 human heavy and light chain sequences to human heavy and light chain sequences,

selecting and replacing the non-human framework with a human framework based on such alignment, molecular modeling to predict the conformation of the humanized sequence and comparing to the conformation of the parent antibody. This process is followed by repeated back mutation of residues in the CDR region which disturb the structure of the CDRs until the predicted conformation of the humanized sequence model closely approximates the conformation of the non-human CDRs of the parent non-human antibody. Such humanized antibodies may be further derivatized to facilitate uptake and clearance, *e.g.*, via Ashwell receptors. *See, e.g.*, U.S. Patent Nos. 5,530,101 and 5,585,089 which patents are incorporated herein by reference.

Humanized antibodies can also be produced using transgenic animals that are engineered to contain human immunoglobulin loci. For example, WO 98/24893 discloses transgenic animals having a human Ig locus wherein the animals do not produce functional endogenous immunoglobulins due to the inactivation of endogenous heavy and light chain loci. WO 91/10741 also discloses transgenic non-primate mammalian hosts capable of mounting an immune response to an immunogen, wherein the antibodies have primate constant and/or variable regions, and wherein the endogenous immunoglobulin-encoding loci are substituted or inactivated. WO 96/30498 discloses the use of the Cre/Lox system to modify the immunoglobulin locus in a mammal, such as to replace all or a portion of the constant or variable region to form a modified antibody molecule. WO 94/02602 discloses non-human mammalian hosts having inactivated endogenous Ig loci and functional human Ig loci. U.S. Patent No. 5,939,598 discloses methods of making transgenic mice in which the mice lack endogenous heavy chains, and express an exogenous immunoglobulin locus comprising one or more xenogeneic constant regions.

Using a transgenic animal described above, an immune response can be produced to a selected antigenic molecule, and antibody-producing cells can be removed from the animal and used to produce hybridomas that secrete human monoclonal antibodies. Immunization protocols, adjuvants, and the like are known in the art, and are used in immunization of, for example, a transgenic mouse as described in WO 96/33735. This publication discloses monoclonal antibodies against a variety of antigenic molecules including IL-6, IL-8, TNF, human CD4, L-selectin, gp39, and tetanus toxin. The monoclonal antibodies can be tested for the ability to inhibit or neutralize the biological activity or physiological effect of the corresponding protein. WO 96/33735 discloses that monoclonal antibodies against IL-8, derived from immune cells of transgenic mice immunized with IL-8, blocked IL-8-induced functions of

neutrophils. Human monoclonal antibodies with specificity for the antigen used to immunize transgenic animals are also disclosed in WO 96/34096.

Polynucleotides or Arrays for Diagnostics

5 Polynucleotide arrays are created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocellulose, *etc.*) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then
10 hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed away. Techniques for constructing arrays and methods of using these arrays are described in EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; U.S. Patent No. 5,593,839; U.S. Patent No.
15 5,578,832; EP 728 520; U.S. Patent No. 5,599,695; EP 721 016; U.S. Patent No. 5,556,752; WO 95/22058; and U.S. Patent No. 5,631,734. Arrays can be used to, for example, examine differential expression of genes and can be used to determine gene function. For example, arrays can be used to detect differential expression of a polynucleotide between a test cell and control cell (*e.g.*, cancer cells and normal cells).
20 For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific gene product. Exemplary uses of arrays are further described in, for example, Pappalarado et al., *Sem. Radiation Oncol.* (1998) 8:217; and Ramsay, *Nature Biotechnol.* (1998) 16:40.

Differential Expression in Diagnosis

25 The polynucleotides of the invention can also be used to detect differences in expression levels between two cells, *e.g.*, as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific
30 polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the

same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (*e.g.*, brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in U.S. Patent Nos. 5,688,641 and 5,677,125.

A genetic predisposition to disease in a human can also be detected by comparing expression levels of an mRNA or protein corresponding to a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an *in vitro*-fertilized embryo. The comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. In general, diagnostic, prognostic, and other methods of the invention based on differential expression involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (*e.g.*, breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (*e.g.*, cells substantially unaffected by cancer) and/or other control cells (*e.g.*, to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease. It should be noted that use of the term "diagnostic" herein is not necessarily meant to exclude "prognostic" or "prognosis," but rather is used as a matter of convenience.

The term "differentially expressed gene" is generally intended to encompass a polynucleotide that can, for example, include an open reading frame

encoding a gene product (*e.g.*, a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, *i.e.*, a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a difference in expression level associated with an increase in expression of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1 ½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, *i.e.*, an overexpressed or up-regulated gene.

“Differentially expressed polynucleotide” as used herein means a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially expressed gene in a sample. “Differentially expressed polynucleotides” is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

“Diagnosis” as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly encompasses diagnosis of subjects in the context of breast cancer (*e.g.*, carcinoma *in situ* (*e.g.*, ductal carcinoma *in situ*), estrogen receptor (ER)-positive breast cancer, ER-negative breast cancer, or other forms and/or stages of breast cancer), lung cancer (*e.g.*, small cell carcinoma, non-small cell carcinoma, mesothelioma, and

other forms and/or stages of lung cancer), and colon cancer (*e.g.*, adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

“Sample” or “biological sample” as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (*e.g.*, ductal adenocarcinoma), and the like. “Samples” is also meant to encompass derivatives and fractions of such samples (*e.g.*, cell lysates). Where the sample is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for determining the nucleic acid abundance in a sample are known to those of skill in the art (see, *e.g.*, WO 97/27317). In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (*e.g.*, mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOs:1-3351. The patient from whom the sample is obtained can be apparently healthy, susceptible to disease (*e.g.*, as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

Diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least two or more, at least

3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOs:1-3351, and can involve detection of expression of genes corresponding to all of SEQ ID NOs:1-3351 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is
5 designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. Examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided
10 herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes, (*e.g.*, fluorescein isothiocyanate (FITC), rhodamine,
15 Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (*e.g.*, ³²P, ³⁵S, ³H, *etc.*), and the like. The detectable label can involve a two stage systems (*e.g.*,
20 biotin-avidin, hapten-anti-hapten antibody, *etc.*)

Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to
25 detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

Polypeptide detection in diagnosis. In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be
30 accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically
35 bind a differentially expressed polypeptide of the invention are added to a sample, and

incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (*e.g.*, using radioisotopes, enzymes, fluorescers, chemilumescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (*e.g.*,
5 biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, *e.g.*, fluorescein, rhodamine, Texas red, *etc.*). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, *etc.* Any suitable alternative methods can of qualitative or quantitative detection of levels or
10 amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, *etc.*

mRNA detection. The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or
15 quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, *in situ* hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A⁺ mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. mRNA expression levels in a
20 sample can also be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) *Science* 252:1651). Enumeration of the relative representation of ESTs within the library can be used to approximate the relative representation of the gene transcript within the starting sample. The results of EST
25 analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein. Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (*e.g.*, Velculescu et al.,
30 *Science* (1995) 270:484) or differential display (DD) methodology (see, *e.g.*, U.S. Patent NOs. 5,776,683 and 5,807,680).

Alternatively, gene expression can be analyzed using hybridization analysis. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized
35 to a known capture sequence determined qualitatively or quantitatively, to provide

information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including
5 filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (*e.g.*, mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene.
10 For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (*e.g.*, a polymorphism in an coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, *etc.*

15 A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, *e.g.*, a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of
20 mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (*e.g.*, using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. Alternatively, various
25 methods are also known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, see *e.g.*, Riley et al., *Nucl. Acids Res.* (1990) 18:2887; and Delahunty et al., *Am. J. Hum. Genet.* (1996) 58:1239.

The amplified or cloned sample nucleic acid can be analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or
30 other methods, and the sequence of bases compared to a selected sequence, *e.g.*, to a wild-type sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (*e.g.*, by Southern blot, dot blot, *etc.*). The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in U.S.
35 Patent No. 5,445,934, or in WO 95/35505, can also be used as a means of identifying

polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility.

5 Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

10 Screening for mutations in a gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein
15 assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

Pattern matching in diagnosis using arrays. In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP).
20 The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (*e.g.*, a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of SEQ ID NOs:1-3351. Of particular interest is a selected set of genes that includes genes
25 differentially expressed in the disease for which the test sample is to be screened.

“Reference sequences” or “reference polynucleotides” as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference
30 sequences, preferably comprising positive and negative control sequences, can be included as reference sequences. Additional suitable reference sequences are found in Genbank, Unigene, and other nucleotide sequence databases (including, *e.g.*, expressed sequence tag (EST), partial, and full-length sequences).

“Reference array” means an array having reference sequences for use in
35 hybridization with a sample, where the reference sequences include all, at least one of,

or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (*e.g.*, cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more. Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. Patent NOs. 5,134,854 and 5,445,934 using light-directed synthesis techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers. Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published application no. WO 95/35505.

A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is associated with a selected cell type, *e.g.*, a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (*e.g.*, a cell of unknown or suspected disease state, from which mRNA is isolated).

REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, *e.g.*, by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The sequence information can then be stored in a format (*e.g.*, a computer-readable format) that allows for ready comparison of the REP with a TEP. The REP can be

normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (*e.g.*, some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

5 TEPs can be generated in a manner similar to REPs, *e.g.*, by hybridizing a test sample to an array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously,
10 or the TEP can be compared to previously generated and stored REPs.

 In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed
15 polynucleotides described herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated using an array having the same or similar selected set of differentially expressed polynucleotides. Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples
20 relative to the other.

 Methods for collection of data from hybridization of samples with a reference arrays are well known in the art. For example, the polynucleotides of the reference and test samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the
25 microarrays for the presence of the detectable label using, for example, a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in U.S. Patent No. 5,631,734. A scanning laser microscope is described in Shalon et al.,
30 *Genome Res.* (1996) 6:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from one sample (*e.g.*, a test sample) is compared to the fluorescent signal from another sample (*e.g.*, a reference sample), and the relative signal intensity
35 determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, *i.e.*, data
5 deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

In general, the test sample is classified as having a gene expression
10 profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (*e.g.*, from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, *etc.*). The criteria for a match or a substantial match between a TEP and a REP include
15 expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (*e.g.*, no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference sequence. In general, a
20 pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (*e.g.*, arrays),
25 design of oligonucleotides for use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. Patent No. 5,800,992.

Diagnosis, Prognosis and Management of Cancer

30 The polynucleotides of the invention and their gene products are of particular interest as genetic or biochemical markers (*e.g.*, in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive interventions. For example, the level of expression of certain polynucleotides can be indicative of a poorer prognosis, and

therefore warrant more aggressive chemo- or radio-therapy for a patient or vice versa. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients can define prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include
5 antibody targeting and gene therapy. Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as polynucleotide expression, can also be used
10 to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

The polynucleotides of the invention can be useful to monitor patients
15 having or susceptible to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. Furthermore, a polynucleotide of the invention identified as important for one type of cancer can also have implications for development or risk of development of other types of cancer, *e.g.*, where a polynucleotide is differentially expressed across various cancer types. Thus,
20 for example, expression of a polynucleotide that has clinical implications for metastatic colon cancer can also have clinical implications for stomach cancer or endometrial cancer.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Generally, if a cancer is only detectable in
25 the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

30 The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggressivity of a cancer, *e.g.*, the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive

therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identify tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors being more aggressive than well differentiated or low-grade tumors. The following guidelines are generally used for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressivity of a tumor, such as metastatic potential.

Detection of lung cancer. The polynucleotides of the invention can be used to detect lung cancer in a subject. Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma) usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

The polynucleotides of the invention, *e.g.*, polynucleotides differentially expressed in normal cells versus cancerous lung cells (*e.g.*, tumor cells of high or low metastatic potential) or between types of cancerous lung cells (*e.g.*, high metastatic versus low metastatic), can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer and selecting an appropriate

therapy. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Detection of breast cancer. The majority of breast cancers are adenocarcinomas subtypes, which can be summarized as follows: 1) ductal carcinoma *in situ* (DCIS), including comedocarcinoma; 2) infiltrating (or invasive) ductal carcinoma (IDC); 3) lobular carcinoma *in situ* (LCIS); 4) infiltrating (or invasive) lobular carcinoma (ILC); 5) inflammatory breast cancer; 6) medullary carcinoma; 7) mucinous carcinoma; 8) Paget's disease of the nipple; 9) Phyllodes tumor; and 10) tubular carcinoma.

The expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer, as well as to distinguish between types of breast cancer. Detection of breast cancer can be determined using expression levels of any of the appropriate polynucleotides of the invention, either alone or in combination. Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, *e.g.*, ER expression. In addition, development of breast cancer can be detected by examining the ratio of expression of a differentially expressed polynucleotide to the levels of steroid hormones (*e.g.*, testosterone or estrogen) or to other hormones (*e.g.*, growth hormone, insulin). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, *etc.*

Detection of colon cancer. The polynucleotides of the invention exhibiting the appropriate expression pattern can be used to detect colon cancer in a subject. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. Multiple familial colorectal cancer disorders have

been identified, which are summarized as follows: 1) Familial adenomatous polyposis (FAP); 2) Gardner's syndrome; 3) Hereditary nonpolyposis colon cancer (HNPCC); and 4) Familial colorectal cancer in Ashkenazi Jews. The expression of appropriate polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. Detection of colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression. Determination of the aggressive nature and/or the metastatic potential of a colon cancer can be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.*, expression of p53, DCC ras, or FAP (see, *e.g.*, Fearon ER, et al., *Cell* (1990) 61(5):759; Hamilton SR et al., *Cancer* (1993) 72:957; Bodmer W, et al., *Nat Genet.* (1994) 4(3):217; Fearon ER, *Ann N Y Acad Sci.* (1995) 768:101). For example, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (*e.g.*, ras) or tumor suppressor genes (*e.g.*, FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous colon tissue, to discriminate between colon cancers with different cells of origin, to discriminate between colon cancers with different potential metastatic rates, *etc.*

Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (see, *e.g.*, U.S. Patent No. 5,010,175, and WO 91/17823). Agonists or antagonists of the polypeptides of the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, *etc.* The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

Such screening and experimentation can lead to identification of a novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

10 Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions of the invention can comprise polypeptides, antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The term “therapeutically effective amount” as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term “pharmaceutically acceptable carrier” refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity. Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers,

and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present
5 in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical
10 composition, *e.g.*, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., New Jersey, 1991).

15 Delivery Methods. Once formulated, the compositions of the invention can be (1) administered directly to the subject (*e.g.*, as polynucleotide or polypeptides); or (2) delivered *ex vivo*, to cells derived from the subject (*e.g.*, as in *ex vivo* gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, *e.g.*, subcutaneously, intraperitoneally, intravenously or
20 intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hypodermic sprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells
25 into a subject are known in the art and described in *e.g.*, International Publication No. WO 93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by, for example, dextran-mediated transfection,
30 calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and
35 hyperplasia, the disorder can be amenable to treatment by administration of a

therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (*e.g.*, antisense, ribozyme, *etc.*).

The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. For example, administration of polynucleotide therapeutic compositions agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. Preferably, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide disclosed herein. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis et al., *Trends Biotechnol.* (1993) 11:202; Chiou et al., *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu et al., *J. Biol. Chem.* (1988) 263:621; Wu et al., *J. Biol. Chem.* (1994) 269:542; Zenke et al., *Proc. Natl. Acad. Sci. (USA)* (1990) 87:3655; Wu et al., *J. Biol. Chem.* (1991) 266:338. Therapeutic compositions containing a polynucleotide are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 mg to about 2 mg, about 5 mg to about 500 mg, and about 20 mg to about 100 mg of DNA can also be used during a gene therapy protocol. Factors such as method of action (*e.g.*, for enhancing or inhibiting levels of the encoded gene product) and efficacy of transformation and expression are considerations which will

affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide-related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in U.S. Patent No. 5,654,173.

The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) 1:51; Kimura, *Human Gene Therapy* (1994) 5:845; Connelly, *Human Gene Therapy* (1995) 1:185; and Kaplitt, *Nature Genetics* (1994) 6:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5, 219,740; WO 93/11230; WO 93/10218; U.S. Patent No. 4,777,127; GB Patent No. 2,200,651; EP 0 345 242; and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) 3:147 can also be employed.

Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, *Hum. Gene Ther.* (1992) 3:147); ligand-linked DNA (see, e.g., Wu, *J. Biol. Chem.* 264:16985 (1989)); eukaryotic cell delivery vehicles (see, e.g., U.S. Patent No. 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction

methods are described in WO 90/11092 and U.S. Patent No. 5,580,859. Liposomes that can act as gene delivery vehicles are described in U.S. Patent No. 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, *Mol. Cell Biol.* 14:2411 (1994), and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) 91:1581.

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin et al., *Proc. Natl. Acad. Sci. USA* 91(24):11581 (1994). Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, e.g., U.S. Patent No. 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, e.g., U.S. Patent No. 5,149,655); use of ionizing radiation for activating transferred gene (see, e.g., U.S. Patent No. 5,206,152 and WO 92/11033).

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

EXAMPLES

EXAMPLE 1

SOURCE OF BIOLOGICAL MATERIALS AND OVERVIEW OF NOVEL POLYNUCLEOTIDES EXPRESSED BY THE BIOLOGICAL MATERIALS

5

Cell lines and human normal and tumor tissue were used to construct cDNA libraries from mRNA isolated from the cells and tissues. Most sequences were about 275-300 nucleotides in length. The cells lines include Km12L4-A cell line, a high metastatic colon cancer cell line (Morika, W. A. K. et al., *Cancer Research* (1988) 48:6863). The KM12L4-A cell line is derived from the KM12C cell line. The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B2 surgical specimen (Morikawa et al. *Cancer Res.* (1988) 48:6863). The KML4-A is a highly metastatic subline derived from KM12C (Yeatman et al. *Nucl. Acids. Res.* (1995) 23:4007; Bao-Ling et al. *Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-A, etc.) are well-recognized in the art as model cell lines for the study of colon cancer (see, e.g., Moriakawa et al., *supra*; Radinsky et al. *Clin. Cancer Res.* (1995) 1:19; Yeatman et al., (1995) *supra*; Yeatman et al., *Clin. Exp. Metastasis* (1996) 14:246). These and other cell lines and tissue are described in Table 6.

20

The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams et al., eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie et al. *Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. The sequences remaining after masking were then used in a BLASTN vs. Genbank search; sequences that exhibited greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40} were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

30

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the Genbank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high
5 similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on
10 these sequences. First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} were discarded. Sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded. Second, a
15 BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1×10^{-40} , and greater than 99% overlap were discarded.

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final
20 result provided the 3351 sequences listed in the accompanying Sequence Listing. Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Polynucleotides that were determined to be novel were assigned a sequence identification number.

The novel polynucleotides were assigned sequence identification numbers
25 SEQ ID NOs:1-3351. The first 1847 DNA sequences corresponding to the novel polynucleotides are provided in the Sequence Listing in Table 1. DNA sequences corresponding to the novel polynucleotides of SEQ ID NOs:1848-3351 are provided in the Sequence Listing in Table 2. The DNA sequences of Table 2, while numbered SEQ ID 1-1504, correspond to SEQ ID NOs:1848-3351 in the Sequence Listing, *e.g.*, Table 2 SEQ ID
30 1 is SEQ ID NO:1848, Table 2 SEQ ID 2 is SEQ ID NO:1849, *etc.* Each DNA sequence in Table 4 is uniquely identified by a number that is 1847 less than its SEQ ID NO in the Sequence Listing. Tables 1 and 2 provide: 1) the SEQ ID NO assigned to each sequence for use in the present specification or a corresponding number; 2) the sequence name used as an internal identifier of the sequence; 3) the name assigned to the clone from which the

sequence was isolated; and 4) the number of the cluster to which the sequence is assigned (Cluster ID; where the cluster ID is 0, the sequence was not assigned to any cluster).

Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different
5 regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOs: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

EXAMPLE 2

RESULTS OF PUBLIC DATABASE SEARCH TO IDENTIFY FUNCTION OF GENE PRODUCTS

10

SEQ ID NOs:1-3351 were translated in all three reading frames to determine the best alignment with the individual sequences. These amino acid sequences and nucleotide sequences are referred to, generally, as query sequences, which are aligned with the individual sequences. Query and individual sequences were
15 aligned using the BLAST programs, available over the world wide web at <http://www.ncbi.nlm.nih.gov/BLAST/>. Again the sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Tables 3 and 4 (inserted before the claims) show the results of the
20 alignments. Table 3 contains alignment information for SEQ ID NOs:1-1847 and Table 4 contains alignment information for SEQ ID NOs:1848-3351. The DNA sequences of Table 4, while numbered SEQ ID 1-1504, correspond to SEQ ID NOs:1848-3351. Each DNA sequence in Table 4 is uniquely identified by a number that is 1847 less than its SEQ ID NO. Tables 3 and 4 refer to each sequence by its SEQ ID NO or a corresponding number,
25 the accession numbers and descriptions of nearest neighbors from the Genbank and Non-Redundant Protein searches, and the p values of the search results.

For each of SEQ ID NOs:1-1847, the best alignment to a protein or DNA sequence is included in Table 3, and the best alignment for each of SEQ ID NOs:1848-3351 is included in Table 4. The activity of the polypeptide encoded by SEQ ID
30 NOs:1-3351 is the same or similar to the nearest neighbor reported in Table 3 or 4. The accession number of the nearest neighbor is reported, providing a reference to the activities exhibited by the nearest neighbor. The search program and database used for the alignment also are indicated as well as a calculation of the p value.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of SEQ ID NOs:1-3351. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of SEQ ID
5 NOs:1-3351.

EXAMPLE 3 MEMBERS OF PROTEIN FAMILIES

The sequences (SEQ ID NOs:1-3351) were used to conduct a profile
10 search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 5). "Start" and "stop" in Table 3 indicate the position within the individual sequences that align with
15 the query sequence having the indicated SEQ ID NO. The direction indicates the orientation of the query sequence with respect to the individual sequence, where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence
20 Listing.

Some polynucleotides exhibited multiple profile hits because, for example, the particular sequence contains overlapping profile regions, and/or the sequence contains two different functional domains. These profile hits are described in more detail below.

25 Ank Repeats (ANK). SEQ ID NOs:187, 1268, 1804, 1819, 1830, 1839, 2652, 3015 and 3267 represent polynucleotides encoding an Ank repeat-containing protein. The ankyrin motif is a 33 amino acid sequence named for the protein ankyrin which has 24 tandem 33-amino-acid motifs. Ank repeats were originally identified in the cell-cycle-control protein cdc10 (Breedon et al., *Nature* (1987) 329:651). Proteins
30 containing ankyrin repeats include ankyrin, myotropin, I-kappaB proteins, cell cycle protein cdc10, the Notch receptor (Matsuno et al., *Development* (1997) 124(21):4265); G9a (or BAT8) of the class III region of the major histocompatibility complex (*Biochem J.* 290:811-818, 1993), FABP, GABP, 53BP2, Lin12, glp-1, SW14, and SW16. The functions of the ankyrin repeats are compatible with a role in protein-

protein interactions (Bork, *Proteins* (1993) 17(4):363; Lambert and Bennet, *Eur. J. Biochem.* (1993) 211:1; Kerr et al., *Current Op. Cell Biol.* (1992) 4:496; Bennet et al., *J. Biol. Chem.* (1980) 255:6424).

ATPases Associated with Various Cellular Activities (ATPases).

5 Sequences within SEQ ID NOs:431, 639, 2135, 2684, 2859, 3197 and 3266 correspond to a sequence that encodes a novel member of the "ATPases Associated with diverse cellular Activities" (AAA) protein family. The AAA protein family is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich et al., *J. Cell Biol.* (1991) 114:443; Erdmann et al., *Cell* (1991) 64:499; Peters et al., *EMBO J.* (1990) 9:1757; Kunau et al., *Biochimie* 10 (1993) 75:209-224; Confalonieri et al., *BioEssays* (1995) 17:639; <http://yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.html>). The proteins that belong to this family either contain one or two AAA domains. In general, the AAA domains in these proteins act as ATP-dependent protein clamps (Confalonieri et al. 15 (1995) *BioEssays* 17:639). In addition to the ATP-binding 'A' and 'B' motifs, which are located in the N-terminal half of this domain, there is a highly conserved region located in the central part of the domain which was used in the development of the signature pattern. The consensus pattern is: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]-D-x-A-[LIFA]-x-R.

20 Bromodomain (bromodomain). SEQ ID NO:1814 represents a polynucleotide encoding a polypeptide having a bromodomain region (Haynes et al., 1992, *Nucleic Acids Res.* 20:2693-2603, Tamkun et al., 1992, *Cell* 68:561-572, and Tamkun, 1995, *Curr. Opin. Genet. Dev.* 5:473-477), which is a conserved region of about 70 amino acids. The bromodomain is thought to be involved in protein-protein 25 interactions and may be important for the assembly or activity of multicomponent complexes involved in transcriptional activation. The consensus pattern, which spans a major part of the bromodomain, is: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)-[LIVMFY]-x(3)-[LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-[FY].

30 Basic Region Plus Leucine Zipper Transcription Factors (BZIP). SEQ ID NOs:410, 552, 768, 822, 836, 1288, 1365, 1454, 1540, 1549, 1556, 1557, 1563, 1622, 1630, 1704, 1808, 2363, 2424, 3147, 3152, 3158 and 3208 represent polynucleotides encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) 2:105; 35 and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) 4:12) of eukaryotic DNA-binding

transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

5 EF Hand (EFhand). SEQ ID NOs:820, 1755 and 3285 correspond to polynucleotides encoding a novel protein in the family of EF-hand proteins. Many calcium-binding proteins belong to the same evolutionary family and share a type of calcium-binding domain known as the EF-hand (Kawasaki et al., *Protein. Prof.* (1995) 2:305-490). This type of domain consists of a twelve residue loop flanked on both sides
10 by a twelve residue alpha-helical domain. In an EF-hand loop the calcium ion is coordinated in a pentagonal bipyramidal configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12; these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position 12 provides two oxygens for liganding Ca (bidentate ligand). The consensus pattern includes the complete EF-hand loop as
15 as well as the first residue which follows the loop and which seem to always be hydrophobic: D-x-[DNS]-{ILVFYW}-[DENSTG]-[DNQGHRK]-{GP}-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW].

Ets Domain (Ets Nterm). SEQ ID NO:1811 represents a polynucleotide encoding a polypeptide with N-terminal homology in ETS domain. Proteins of this
20 family contain a conserved domain, the "ETS-domain," that is involved in DNA binding. The domain appears to recognize purine-rich sequences; it is about 85 to 90 amino acids in length, and is rich in aromatic and positively charged residues (Wasylyk, et al., *Eur. J. Biochem.* (1993) 211:718). The *ets* gene family encodes a novel class of DNA-binding proteins, each of which binds a specific DNA sequence and comprises an
25 *ets* domain that specifically interacts with sequences containing the common core trinucleotide sequence GGA. In addition to an *ets* domain, native *ets* proteins comprise other sequences which can modulate the biological specificity of the protein. *Ets* genes and proteins are involved in a variety of essential biological processes including cell growth, differentiation and development, and three members are implicated in
30 oncogenic process.

G-Protein Alpha Subunit (G-alpha). SEQ ID NO:1846 represents a polynucleotide encoding a novel polypeptide of the G-protein alpha subunit family. Guanine nucleotide binding proteins (G-proteins) are a family of membrane-associated proteins that couple extracellularly-activated integral-membrane receptors to
35 intracellular effectors, such as ion channels and enzymes that vary the concentration of

second messenger molecules. G-proteins are composed of 3 subunits (alpha, beta and gamma) which, in the resting state, associate as a trimer at the inner face of the plasma membrane. The alpha subunit binds GTP and exhibits GTPase activity. G-protein alpha subunits are 350-400 amino acids in length and have molecular weights in the range 40-45 kDa. Seventeen distinct types of alpha subunit have been identified in mammals, and fall into 4 main groups on the basis of both sequence similarity and function: alpha-s, alpha-q, alpha-i and alpha-12 (Simon et al., *Science* (1993) 252:802). They are often N-terminally acylated, usually with myristate and/or palmitoylate, and these fatty acid modifications can be important for membrane association and high-affinity interactions with other proteins.

Helicases conserved C-terminal domain (helicase C). SEQ ID NOs:1496, 2826 and 2871 represent polynucleotides encoding novel members of the DEAD/H helicase family. A number of eukaryotic and prokaryotic proteins have been characterized (Schmid S.R., et al., *Mol. Microbiol.* (1992) 6:283; Linder P., et al., *Nature* (1989) 337:121; Wassarman D.A., et al., *Nature* (1991) 349:463) on the basis of their structural similarity. All are involved in ATP-dependent, nucleic-acid unwinding. All DEAD box family members of the above proteins share a number of conserved sequence motifs, some of which are specific to the DEAD family while others are shared by other ATP-binding proteins or by proteins belonging to the helicases 'superfamily' (Hodgman T.C., *Nature* (1988) 333:22 and *Nature* (1988) 333:578 (Errata). One of these motifs, called the "D-E-A-D-box", represents a special version of the B motif of ATP-binding proteins. Some other proteins belong to a subfamily which have His instead of the second Asp and are thus said to be "D-E-A-H-box" proteins (Wassarman D.A., et al., *Nature* (1991) 349:463; Harosh I., et al., *Nucleic Acids Res.* (1991) 19:6331; Koonin E.V. et al., *J. Gen. Virol.* (1992) 73:989. The following signature patterns are used to identify members of both subfamilies: 1) [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN]; and 2) [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].

Homeobox domain (homeobox). SEQ ID NOs:1676, 1820 and 1821 represent polynucleotides encoding proteins having a homeobox domain. The homeobox is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp. 1-10, Oxford University Press, Oxford, (1994); Buerklin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring, *Trends Biochem. Sci.* (1992) 17:277-280; Gehring et al., *Annu. Rev. Genet.* (1986) 20:147-173; Schofield, *Trends Neurosci.* (1987) 10:3-6) first

identified in a number of *Drosophila* homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below.

The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

```

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXHHHHHHHHtttHHHHHHHHXXXXXXXXXXXX
1                                                                                     60

```

The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain. The consensus pattern is as follows: [LIVMFYGG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

MAP kinase kinase (mkk). SEQ ID NOs:29, 31, 196, 3175, 3190 and 3281 represent novel members of the MAP kinase kinase family. MAP kinases (MAPK) are involved in signal transduction, and are important in cell cycle and cell growth controls. The MAP kinase kinases (MAPKK) are dual-specificity protein kinases which phosphorylate and activate MAP kinases. MAPKK homologues have been found in yeast, invertebrates, amphibians, and mammals. Moreover, the MAPKK/MAPK phosphorylation switch constitutes a basic module activated in distinct pathways in yeast and in vertebrates. MAPKKs are essential transducers through which signals must pass before reaching the nucleus. For review, see, *e.g.*, Biologique *Biol Cell* (1993) 79:193-207; Nishida et al., *Trends Biochem Sci* (1993) 18:128-31; Ruderman, *Curr Opin Cell Biol* (1993) 5:207-13; Dhanasekaran et al., *Oncogene* (1998) 17:1447-55; Kiefer et al., *Biochem Soc Trans* (1997) 25:491-8; and Hill, *Cell Signal* (1996) 8:533-44.

Protein Kinase (protkinase). SEQ ID NOs:1157, 1478, 1496, 2286, 2969 and 3190 represent polynucleotides encoding protein kinases. Protein kinases catalyze phosphorylation of proteins in a variety of pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks S.K., et al., *FASEB J.* (1995) 9:576; Hunter T., *Meth. Enzymol.* (1991) 200:3; Hanks S.K., et al., *Meth. Enzymol.* (1991) 200:38; Hanks S.K.,

Curr. Opin. Struct. Biol. (1991) 1:369; Hanks S.K. et al., *Science* (1988) 241:42) are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein kinases. There are a number of conserved regions in the catalytic domain of protein kinases. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme (Knighton D.R. et al., *Science* (1991) 253:407). The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is based on the alignment in (Hanks S.K. et al., *FASEB J.* (1995) 9:576) and covers the entire catalytic domain.

The consensus patterns are as follows: 1) [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-[LIVCAT]-{PD}-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-[LIVMFAGCKR]-K, where K binds ATP; 2) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-[LIVMFYCT](3), where D is an active site residue; and 3) [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue.

If a protein analyzed includes two of the above protein kinase signatures, the probability of it being a protein kinase is close to 100%.

Ras family proteins (ras). SEQ ID NOs:1688 and 3258 represent polynucleotides encoding novel members of the ras family of small GTP/GDP-binding proteins (Valencia et al., 1991, *Biochemistry* 30:4637-4648). Ras family members generally require a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase activity. Among ras-related proteins, the highest degree of sequence conservation is found in four regions that are directly involved in guanine nucleotide binding. The first two constitute most of the phosphate and Mg²⁺ binding site (PM site) and are located in the first half of the G-domain. The other two regions are involved in guanosine binding and are located in the C-terminal half of the molecule. Motifs and conserved structural features of the ras-related proteins are described in Valencia et al., 1991, *Biochemistry* 30:4637-4648. A major consensus pattern of ras proteins is: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y.

Thioredoxin family active site (Thioredox). SEQ ID NO:1677 represents a polynucleotide encoding a protein having a thioredoxin family active site. Thioredoxins (Holmgren A., *Annu. Rev. Biochem.* (1985) 54:237; Gleason F.K. et al., *FEMS Microbiol. Rev.* (1988) 54:271; Holmgren, A. *J. Biol. Chem.* (1989) 264:13963; 5 Eklund H. et al., *Proteins* (1991) 11:13) are small proteins of approximately one hundred amino- acid residues which participate in various redox reactions via the reversible oxidation of an active center disulfide bond. They exist in either a reduced form or an oxidized form where the two cysteine residues are linked in an intramolecular disulfide bond. Thioredoxin is present in prokaryotes and eukaryotes 10 and the sequence around the redox-active disulfide bond is well conserved. All PDI contains two or three (ERp72) copies of the thioredoxin domain. The consensus pattern is: [LIVMF]-[LIVMSTA]-x-[LIVMFYC]-[FYWSTHE]-x(2)-[FYWGTN]-C-[GATPLVE]-[PHYWSTA]-C-x(6)-[LIVMFYWT] (where the two C's form the redox-active bond).

15 Trypsin (trypsin). SEQ ID NO:1410 corresponds to a novel serine protease of the trypsin family. The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well 20 conserved in this family of proteases (Brenner S., *Nature* (1988) 334:528). The consensus patterns for this trypsin protein family are: 1) [LIVM]-[ST]-A-[STAG]-H-C, where H is the active site residue; and 2) [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]-[LIVMFYSTANQH], where S is the active site residue. All sequences known to belong to this family are detected by the above 25 consensus sequences, except for 18 different proteases which have lost the first conserved glycine. If a protein includes both the serine and the histidine active site signatures, the probability of it being a trypsin family serine protease is 100%.

WD Domain, G-Beta Repeats (WD domain). SEQ ID NOs:1336, 1380, 1711, 1762, 1909, 2218, 3047, 3108 and 3292 represent novel members of the WD 30 domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) 56:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but 35 they seem to be required for the replacement of GDP by GTP as well as for membrane

anchoring and receptor recognition. In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). The consensus pattern for the WD domain/G-Beta repeat family is:
 5 [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

wnt Family of Developmental Signaling Proteins (Wnt_dev_sign). SEQ ID NO:1538 corresponds to a novel member of the wnt family of developmental signaling proteins. Wnt-1 (previously known as int-1), the seminal member of this family, (Nusse R., *Trends Genet.* (1988) 4:291) is thought to play a role in intercellular communication and seems to be a signalling molecule important in the development of the central nervous system (CNS). All wnt family proteins share the following features characteristics of secretory proteins: a signal peptide, several potential N-glycosylation sites and 22 conserved cysteines that are probably involved in disulfide bonds. The Wnt proteins seem to adhere to the plasma membrane of the secreting cells and are therefore likely to signal over only few cell diameters. The consensus pattern, which is based upon a highly conserved region including three cysteines, is as follows: C-K-C-H-G-[LIVMT]-S-G-x-C.
 15

Protein Tyrosine Phosphatase (Y_phosphatase). SEQ ID NO:1417 represents a polynucleotide encoding a protein tyrosine kinase. Tyrosine specific protein phosphatases (EC 3.1.3.48) (PTPase) (Fischer et al., *Science* (1991) 253:401; Charbonneau et al., *Annu. Rev. Cell Biol.* (1992) 8:463; Trowbridge, *J. Biol. Chem.* (1991) 266:23517; Tonks et al., *Trends Biochem. Sci.* (1989) 14:497; and Hunter, *Cell* (1989) 58:1013) catalyze the removal of a phosphate group attached to a tyrosine residue. These enzymes are very important in the control of cell growth, proliferation, differentiation and transformation. Multiple forms of PTPase have been characterized and can be classified into two categories: soluble PTPases and transmembrane receptor proteins that contain PTPase domain(s). Structurally, all known receptor PTPases are made up of a variable length extracellular domain, followed by a transmembrane region and a C-terminal catalytic cytoplasmic domain. PTPase domains consist of about 300 amino acids. The search of two conserved cysteines has been shown to be absolutely required for activity. Furthermore, a number of conserved residues in its immediate vicinity have also been shown to be important. The consensus pattern for PTPases is:
 20 [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY]; C is the active site residue.
 25
 30
 35

Zinc Finger, C2H2 Type (Zincfing C2H2). SEQ ID NOs:308, 807, 1324, 1503, 1527, 3081, 3193 and 3306 correspond to polynucleotides encoding novel members of the of the C2H2 type zinc finger protein family. Zinc finger domains (Klug et al., *Trends Biochem. Sci.* (1987) 12:464; Evans et al., *Cell* (1988) 52:1; Payre et al., 5 *FEBS Lett.* (1988) 234:245; Miller et al., *EMBO J.* (1985) 4:1609; and Berg, *Proc. Natl. Acad. Sci. USA* (1988) 85:99) are nucleic acid-binding protein structures. In addition to the conserved zinc ligand residues, it has been shown that a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld et al., 10 *J. Biomol. Struct. Dyn.* (1993) 11:557) The best conserved position is found four residues after the second cysteine; it is generally an aromatic or aliphatic residue. The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.

Src homology 2. SEQ ID NOs:186, 2591, 3307 and 3339 represent polynucleotides encoding novel members of the family of Src homology 2 (SH2) 15 proteins. The Src homology 2 (SH2) domain is a protein domain of about 100 amino acid residues first identified as a conserved sequence region between the oncoproteins Src and Fps (Sadowski I. et al., *Mol. Cell. Biol.* 6:4396-4408 (1986)). Similar sequences are found in many other intracellular signal-transducing proteins (Russel R.B. et al., *FEBS Lett.* 304:15-20 (1992)). SH2 domains function as regulatory modules of 20 intracellular signalling cascades by interacting with high affinity to phosphotyrosine-containing target peptides in a sequence-specific and phosphorylation-dependent manner (Marangere L.E.M., Pawson T., *J. Cell Sci. Suppl.* 18:97-104 (1994); Pawson T., Schlessinger J., *Curr. Biol.* 3:434-442 (1993); Mayer B.J., Baltimore D., *Trends Cell. Biol.* 3:8-13 (1993); Pawson T., *Nature* 373:573-580 (1995)).

25 The SH2 domain has a conserved 3D structure consisting of two alpha helices and six to seven beta-strands. The core of the domain is formed by a continuous beta-meander composed of two connected beta-sheets (Kuriyan J., Cowburn D., *Curr. Opin. Struct. Biol.* 3:828-837(1993)). The profile to detect SH2 domains is based on a structural alignment consisting of 8 gap-free blocks and 7 linker regions totaling 92 30 match positions.

Src homology 3. SEQ ID NO:234, 1832, and 1835 represent polynucleotides encoding novel members of the family of Src homology 3 (SH3) proteins. The Src homology 3 (SH3) domain is a small protein domain of about 60 amino acid residues first identified as a conserved sequence in the non-catalytic part of 35 several cytoplasmic protein tyrosine kinases (e.g., Src, Abl, Lck) (Mayer B.J. et al.,

Nature 332:272-275 (1988)). Since then, it has been found in a great variety of other intracellular or membrane-associated proteins (Musacchio A. et al., *FEBS Lett.* 307:55-61 (1992); Pawson T., Schlessinger J., *Curr. Biol.* 3:434-442 (1993); Mayer B.J., Baltimore D., *Trends Cell Biol.* 3:8-13 (1993); Pawson T., *Nature* 373:573-580 (1995)).

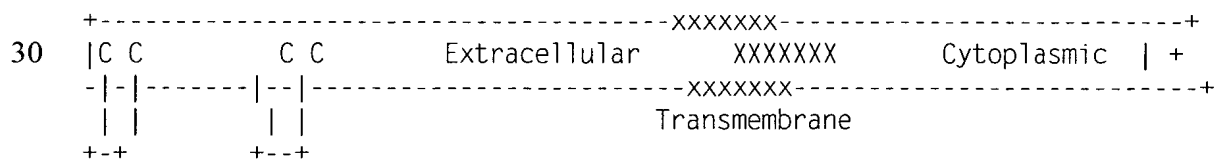
5 The SH3 domain has a characteristic fold which consists of five or six beta strands arranged as two tightly packed anti-parallel beta sheets. The linker regions may contain short helices (Kuriyan J., Cowburn D., *Curr. Opin. Struct. Biol.* 3:828-837 (1993)).

The function of the SH3 domain may be to mediate assembly of specific
10 protein complexes via binding to proline-rich peptides (Morton C.J., Campbell I.D., *Curr. Biol.* 4:615-617 (1994)).

In general SH3 domains are found as single copies in a given protein, but there are a significant number of proteins with two SH3 domains and a few with 3 or 4 copies.

15 Fibronectin type III. SEQ ID NOs:746 and 1192 represent polynucleotides encoding novel members of the family of fibronectin type III proteins. A number of receptors for lymphokines, hematopoietic growth factors and growth hormone-related molecules have been found to share a common binding domain. (Bazan J.F., *Biochem. Biophys. Res. Commun.* 164:788-795 (1989); Bazan J.F., *Proc.*
20 *Natl. Acad. Sci. U.S.A.* 87:6934-6938 (1990); Cosman D. et al., *Trends Biochem. Sci.* 15:265-270 (1990); d'Andrea A.D., Fasman G.D., Lodish H.F., *Cell* 58:1023-1024 (1989); d'Andrea A.D., Fasman G.D., Lodish H.F., *Curr. Opin. Cell Biol.* 2:648-651 (1990)).

The conserved region constitutes all or part of the extracellular ligand-
25 binding region and is about 200 amino acid residues long. In the N-terminal of this domain there are two pairs of cysteines known, in the growth hormone receptor, to be involved in disulfide bonds.



35 Two patterns detect this family of receptors. The first one is derived from the first N-terminal disulfide loop, the second is a tryptophan-rich pattern located at the C-terminal extremity of the extracellular region.

A consensus for this protein family is: C-[LVFYR]-x(7,8)-[STIVDN]-C-x-W (The two C's are linked by a disulfide bond]. A second consensus for this protein family is: [STGL]-x-W-[SG]-x-W-S.

LIM domain containing proteins. SEQ ID NOs:1269, 1309, 1360, and 5 1386 represent polynucleotides encoding novel members of the family of LIM domain containing proteins. A number of proteins contain a conserved cysteine-rich domain of about 60 amino-acid residues. (Freyd G. et al., *Nature* 344:876-879 (1990); Baltz R. et al., *Plant Cell* 4:1465-1466 (1992); Sanchez-Garcia I., Rabbitts T.H., *Trends Genet.* 10:315-320 (1994)).

10 In the LIM domain, there are seven conserved cysteine residues and a histidine. The arrangement followed by these conserved residues is C-x(2)-C-x(16,23)-H-x(2)-[CH]-x(2)-C-x(2)-C-x(16,21)-C-x(2,3)-[CHD]. The LIM domain binds two zinc ions (Michelsen J.W. et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:4404-4408 (1993)). LIM does not bind DNA, rather it seems to act as interface for protein-protein interaction. 15 The consensus for this protein family is: C-x(2)-C-x(15,21)-[FYWH]-H-x(2)-[CH]-x(2)-C-x(2)-C-x(3)-[LIVMF]. The 5 C's and the H bind zinc.

C2 domain (protein kinase C like). SEQ ID NOs:1325 and 2282 represent polynucleotides encoding novel members of the family of C2 domain containing proteins. Some isozymes of protein kinase C (PKC) contain a domain, 20 known as C2, of about 116 amino-acid residues, which is located between the two copies of the C1 domain (that bind phorbol esters and diacylglycerol) and the protein kinase catalytic domain. (Azzi A. et al., *Eur. J. Biochem.* 208:547-557 (1992); Stabel S., *Semin. Cancer Biol.* 5:277-284 (1994)).

The C2 domain is involved in calcium-dependent phospholipid binding 25 (Davletov B.A., Suedhof T.C., *J. Biol. Chem.* 268:26386-26390 (1993)). Since domains related to the C2 domain are also found in proteins that do not bind calcium, other putative functions for the C2 domain include binding to inositol-1,3,5-tetrphosphate. (Fukuda M., et al., *J. Biol. Chem.* 269:29206-29211 (1994).)

The consensus pattern for the C2 domain is located in a conserved part 30 of that domain, the connecting loop between beta strands 2 and 3. The profile for the C2 domain covers the total domain. The consensus for this protein family is:: [ACG]-x(2)-L-x(2,3)-D-x(1,2)-[NGSTLIF]-[GTMR]-x-[STAP]-D-[PA]-[FY]

Serine proteases, trypsin family, active sites. SEQ ID NO:1410 represents a polynucleotide encoding a novel member of the family of serine protease, 35 trypsin proteins. The catalytic activity of the serine proteases from the trypsin family is

provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., *Nature* 334:528-530 (1988)).

5 A consensus for this protein family is: [LIVM]-[ST]-A-[STAG]-H-C [H is the active site residue]. A second consensus for this protein family is: [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]- [LIVMFYWH]-[LIVMFYSTANQH] [S is the active site residue].

RNA Recognition Motif Domain (RRM, RBD, or RNP). SEQ ID NOs:
10 1464 and 1514 represent polynucleotides encoding novel members of the family of RNA recognition motif domain proteins (Bandziulis R.J. et al., *Genes Dev.* 3:431-437 (1989); Dreyfuss G. et al., *Trends Biochem. Sci.* 13:86-91 (1988)).

Inside the putative RNA-binding domain there are two regions which are highly conserved. The first one is a hydrophobic segment of six residues (which is
15 called the RNP-2 motif); the second one is an octapeptide motif (which is called RNP-1 or RNP-CS). The position of both motifs in the domain is shown in the following schematic representation:

20 xxxxxxxx#####xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx#####xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
RNP-2 RNP-1

As a consensus pattern for this type of domain the RNP-1 motif was used. The consensus for this protein family is: [RK]-G-{EDRKHPCG}-[AGSCI]-[FY]-[LIVA]-x-[FYLM]

25 Phosphatidylinositol-specific phospholipase C, Y Domain. SEQ ID NO: 1707 represents a polynucleotide encoding a novel member of the phosphatidylinositol-specific phospholipase C, Y domain family of proteins. Phosphatidylinositol-specific phospholipase C (EC3.1.4.11), a eukaryotic intracellular enzyme, plays an important role in signal transduction processes (Meldrum E. et al., *Biochim. Biophys. Acta*
30 1092:49-71 (1991)). It catalyzes the hydrolysis of 1-phosphatidyl-D-myo-inositol-3,4,5- triphosphate into the second messenger molecules diacylglycerol and inositol-1,4,5-triphosphate. This catalytic process is tightly regulated by reversible phosphorylation and binding of regulatory proteins (Rhee S.G., Choi K.D., *Adv. Second Messenger Phosphoprotein Res.* 26:35-61 (1992); Rhee S.G., Choi K.D., *J. Biol. Chem.*
35 267:12393-12396 (1992); Sternweis P.C., Smrcka A.V., *Trends Biochem. Sci.* 17:502-506 (1992)).

All eukaryotic PI-PLCs contain two regions of homology, referred to as "X-box" and "Y-box". The order of these two regions is the same (NH₂-X-Y-COOH), but the spacing is variable. In most isoforms, the distance between these two regions is only 50-100 residues but in the gamma isoforms one PH domain, two SH2 domains, and one SH3 domain are inserted between the two PLC-specific domains. The two conserved regions have been shown to be important for the catalytic activity. At the C-terminal of the Y-box, there is a C2 domain possibly involved in Ca-dependent membrane attachment.

Serine Carboxypeptidases. SEQ ID NO:1744 represents a polynucleotide encoding a novel member of the serine carboxypeptidases family of proteins. Carboxypeptidases may be either metallo carboxypeptidases or serine carboxypeptidases (EC 3.4.16.5 and EC 3.4.16.6). The catalytic activity of the serine carboxypeptidases, like that of the trypsin family serine proteases, is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which is itself hydrogen-bonded to a serine (Liao D.I., Remington S.J., *J. Biol. Chem.* 265:6528-6531 (1990)).

The sequences surrounding the active site serine and histidine residues are highly conserved in all these serine carboxypeptidases. A consensus for this protein family is: [LIVM]-x-[GTA]-E-S-Y-[AG]-[GS] [S is the active site residue]. A second consensus for this protein family is: [LIVF]-x(2)-[LIVSTA]-x-[IVPST]-x-[GSDNQL]-[SAGV]-[SG]-H-x- [IVAQ]-P-x(3)-[PSA] [H is the active site residue].

dsrcm Double-Stranded RNA Binding Motif. SEQ ID NO:1818 represents a polynucleotide encoding a novel member of the dsrcm double-stranded RNA binding motif proteins. In eukaryotic cells, a multitude of RNA-binding proteins play key roles in the posttranscriptional regulation of gene expression. Characterization of these proteins has led to the identification of several RNA-binding motifs. Several human and other vertebrate genetic disorders are caused by aberrant expression of RNA-binding proteins. (C. G. Burd & G. Dreyfuss, *Science* 265: 615-621 (1994)).

Proteins containing double stranded RNA binding motifs bind to specific RNA targets. Double stranded RNA binding motifs are exemplified by interferon-induced protein kinase in humans, which is part of the cellular response to dsRNA.

SEQ ID NOs:2577, 3183 and 3195 encode members of the 4 transmembrane integral membrane protein family. This family consists of type III proteins, which are integral membrane proteins that contain a N-terminal membrane-anchoring domain that is not cleaved during biosynthesis, and which functions as a translocation

signal and a membrane anchor. The proteins also have three additional transmembrane regions. The consensus pattern is: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF] (2)-G-C-x-[GA]-[STA]-x(20-[eG]-x(20-[CwN]-[LIVM](2).

SEQ ID NO:2944 encodes a polypeptide having a calpain large subunit, domain III. Calpains are a family of intracellular proteases that play a variety of biological roles. Calpain 3, also known as p94, is predominantly expressed in skeletal muscle and plays a role in limb-girdle muscular dystrophy type 2A. (Sorimachi, H. et al., Biochem. J. 328:721-732, 1997).

SEQ ID NOS:1911 and 1980 encode polypeptides having a C3HC4 type zinc finger domain (RING finger), which is a cysteine-rich domain of 40 to 60 residues that binds two atoms of zinc, and is believed to be involved in mediating protein-protein interactions. Mammalian proteins of this family include V(D)J recombination activating protein, which activates the rearrangement of immunoglobulin and T-cell receptor genes; breast cancer type 1 susceptibility protein (BRCA1); bmi-1 proto-oncogene; cbl proto-oncogene; and mel-18 protein, which is expressed in a variety of tumor cells and is a transcriptional repressor that recognizes and binds a specific DNA sequence. The consensus pattern is: C-x-H-x-[LIVMFY]-C-x(2)-C-[LIVMYA].

SEQ ID NO:3274 encodes a eukaryotic transcription factor with a fork head domain, of about 100 amino acid residues. Proteins of this group are transcription factors, including mammalian transcription factors HNF-3-alpha, -beta, and -gamma; interleukin-enhancer binding factor; and HTLF, which binds to a region of human T-cell leukemia virus long terminal repeat. The consensus pattern is [KR]-P-[PTQ]-[FYLVQH]-S-[FY]x(2)-[LIVM]-X(3,4)-[AC]-[LIM].

SEQ ID NO:3345 encodes a polypeptide having a PDZ domain. Several dozen signaling proteins belong to this group of proteins that have 80-100 residue repeats known as PDZ domains. Several of the proteins interact with the C-terminal tetrapeptide motifs X-Ser/Thr/X-Val-COO- of ion channels and/or receptors. (Ponting, C. P., Protein Sci. 6:464-468, 1997.)

SEQ ID NO:3351 encodes a polypeptide in the family of phorbol esters/glycerol binding proteins. Phorbol esters (PE) are analogues of diacylglycerol (DAG) and potent tumor promoters. DAG activates a family of serine-threonine protein kinases, known as protein kinase C. The N-terminal region of protein kinase C binds PE and DAG, and contains one or two copies of a cysteine-rich domain of about 50 amino acid residues. Other proteins having this domain include diacylglycerol kinase; the vav oncogene; and N-chimaerin, a brain-specific protein. The DAG/PE binding

domain binds two zinc ions through the six cysteines and two histidines that are conserved in the domain. The consensus pattern is: H-x-[LIVMFYW]-x(8, 11)-C-x(2)-C-x(3)-[LIVMFC]-x(5, 10)-C-x(2)-C-x(4)-[HD]-x(2)-C-x(5, 9)-C.

5 SEQ ID NO:2216 encodes a polypeptide having a WW/rsp5/WWP domain. The protein is named for the presence of conserved aromatic positions, generally tryptophan, as well as a conserved proline. Proteins having the domain include dystrophin, vertebrate YAP protein, and IQGAP, a human GTPase activating protein which acts on ras. The consensus pattern is: W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE]-[GSTQCR]-[FYW]-x(2)-P.

10 SEQ ID NO:2428 encodes a member of the dual specificity phosphatase family, having a catalytic domain, and SEQ IDS NOs:2281 and 2310 encode members of the protein tyrosine phosphatase family. These families are related and classified as tyrosine specific protein phosphatases. The enzymes catalyze the removal of a phosphate group from a tyrosine residue, and are important in the control of cell growth,
15 proliferation, differentiation, and transformation. The consensus pattern is [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY].

Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1	377044	RTA00002676F.p.11.2.P.Seq	F	M00039329A:C01	CH09LNL
2	377708	RTA00002683F.m.01.2.P.Seq	F	M00040089A:G08	CH09LNL
3	427782	RTA00002666F.l.06.1.P.Seq	F	M00032638D:A06	CH08LNL
4	29372	RTA00002712F.a.06.1.P.Seq	F	M00023282A:C02	CH04MAL
5	455003	RTA00002694F.b.02.1.P.Seq	F	M00043419D:A10	CH20COHLV
6	380625	RTA00002684F.d.03.2.P.Seq	F	M00040118D:G10	CH09LNL
7	450959	RTA00002691F.b.05.3.P.Seq	F	M00043306D:B07	CH17COHLV
8	397851	RTA00002680F.b.04.1.P.Seq	F	M00039775A:A09	CH09LNL
9	20652	RTA00002710F.k.01.1.P.Seq	F	M00022440B:E01	CH03MAH
10	97830	RTA00002663F.k.18.1.P.Seq	F	M00022767B:G11	CH03MAH
11	373071	RTA00002670F.j.23.1.P.Seq	F	M00033442A:D06	CH09LNL
12	162369	RTA00002713F.e.01.1.P.Seq	F	M00027292D:F10	CH04MAL
13	401247	RTA00002685F.f.15.2.P.Seq	F	M00039508A:C12	CH12EDT
14	430738	RTA00002669F.l.15.3.P.Seq	F	M00033231D:B09	CH08LNL
15	46779	RTA00002711F.c.14.1.P.Seq	F	M00022860C:G04	CH03MAH
16	375772	RTA00002681F.p.01.2.P.Seq	F	M00039909C:G05	CH09LNL
17	430689	RTA00002669F.j.01.3.P.Seq	F	M00033243B:A05	CH08LNL
18	376546	RTA00002677F.d.07.2.P.Seq	F	M00039345C:C12	CH09LNL
19	430041	RTA00002667F.f.17.1.P.Seq	F	M00032790B:A07	CH08LNL
20	431643	RTA00002669F.l.16.1.P.Seq	F	M00033276D:H09	CH08LNL
21	19422	RTA00002709F.c.02.1.P.Seq	F	M00005449B:B10	CH02COH
22	376802	RTA00002677F.c.18.2.P.Seq	F	M00039544B:G07	CH09LNL
23	376814	RTA00002674F.h.02.1.P.Seq	F	M00039139C:G12	CH09LNL
24	375492	RTA00002677F.m.19.2.P.Seq	F	M00039418B:D08	CH09LNL
25	379114	RTA00002681F.n.24.2.P.Seq	F	M00039903C:F03	CH09LNL
26	380668	RTA00002670F.p.11.1.P.Seq	F	M00033581C:H10	CH09LNL
27	213817	RTA00002664F.l.19.2.P.Seq	F	M00027634A:D11	CH04MAL
28	375749	RTA00002680F.f.23.1.P.Seq	F	M00039795D:G06	CH09LNL
29	430896	RTA00002669F.b.20.4.P.Seq	F	M00033185C:D01	CH08LNL
30	380462	RTA00002670F.o.01.1.P.Seq	F	M00033570B:E06	CH09LNL
31	430896	RTA00002669F.b.20.3.P.Seq	F	M00033185C:D01	CH08LNL
32	376996	RTA00002676F.p.13.2.P.Seq	F	M00039329C:B10	CH09LNL
33	374846	RTA00002677F.k.19.2.P.Seq	F	M00039412D:G06	CH09LNL
34	379075	RTA00002672F.n.13.2.P.Seq	F	M00039039B:E03	CH09LNL
35	374172	RTA00002673F.k.16.2.P.Seq	F	M00039097D:D06	CH09LNL
36	373104	RTA00002683F.o.15.2.P.Seq	F	M00040098D:G12	CH09LNL
37	186302	RTA00002713F.m.21.1.P.Seq	F	M00027591B:C04	CH04MAL
38	427947	RTA00002665F.o.01.1.P.Seq	F	M00032495B:D02	CH08LNL
39	375180	RTA00002673F.d.17.1.P.Seq	F	M00039064D:H09	CH09LNL
40	377584	RTA00002683F.l.22.2.P.Seq	F	M00040088C:E10	CH09LNL
41	377364	RTA00002678F.a.15.2.P.Seq	F	M00039432C:A01	CH09LNL
42	376347	RTA00002675F.l.08.1.P.Seq	F	M00039249C:G11	CH09LNL
43	446747	RTA00002689F.d.16.2.P.Seq	F	M00042740A:E09	CH15CON
44	28092	RTA00002711F.g.12.1.P.Seq	F	M00023032A:B05	CH03MAH
45	378206	RTA00002671F.a.20.3.P.Seq	F	M00033588C:G04	CH09LNL
46	378206	RTA00002671F.a.20.2.P.Seq	F	M00033588C:G04	CH09LNL
47	14940	RTA00002709F.d.11.1.P.Seq	F	M00005623A:G02	CH02COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
48	378411	RTA00002672F.g.13.2.P.Seq	F	M00039004B:A06	CH09LNL
49	38120	RTA00002712F.i.14.1.P.Seq	F	M00026927D:F02	CH04MAL
50	375730	RTA00002678F.i.13.2.P.Seq	F	M00039612B:G05	CH09LNL
51	428959	RTA00002667F.h.15.1.P.Seq	F	M00032811B:D02	CH08LNH
52	376851	RTA00002677F.c.03.2.P.Seq	F	M00039341C:H11	CH09LNL
53	373808	RTA00002671F.d.14.2.P.Seq	F	M00038272A:G01	CH09LNL
54	376168	RTA00002675F.n.17.1.P.Seq	F	M00039258B:E06	CH09LNL
55	18653	RTA00002712F.o.08.1.P.Seq	F	M00027135A:B11	CH04MAL
56	187632	RTA00002664F.i.15.1.P.Seq	F	M00027617B:C12	CH04MAL
57	374122	RTA00002673F.i.22.1.P.Seq	F	M00039104D:C09	CH09LNL
58	374946	RTA00002673F.j.24.1.P.Seq	F	M00039096A:E07	CH09LNL
59	375666	RTA00002677F.n.16.2.P.Seq	F	M00039422D:F04	CH09LNL
60	162369	RTA00002713F.d.24.1.P.Seq	F	M00027292D:F10	CH04MAL
61	21480	RTA00002709F.c.18.2.P.Seq	F	M00005531D:F06	CH02COH
62	18560	RTA00002711F.e.20.1.P.Seq	F	M00022938B:F07	CH03MAH
63	96575	RTA00002663F.j.08.1.P.Seq	F	M00022641C:H05	CH03MAH
64	377576	RTA00002682F.f.18.1.P.Seq	F	M00039975C:C11	CH09LNL
65	446747	RTA00002689F.d.16.3.P.Seq	F	M00042740A:E09	CH15CON
66	379311	RTA00002682F.g.01.1.P.Seq	F	M00039976D:A12	CH09LNL
67	379311	RTA00002682F.f.24.1.P.Seq	F	M00039976D:A12	CH09LNL
68	124549	RTA00002713F.c.07.1.P.Seq	F	M00027237C:B08	CH04MAL
69	449785	RTA00002691F.c.07.3.P.Seq	F	M00043345C:A06	CH17COHLV
70	375134	RTA00002673F.k.22.2.P.Seq	F	M00039099A:H08	CH09LNL
71	186593	RTA00002713F.n.15.1.P.Seq	F	M00027620D:F11	CH04MAL
72	449831	RTA00002691F.a.17.3.P.Seq	F	M00042518D:A06	CH17COHLV
73	379678	RTA00002676F.b.06.1.P.Seq	F	M00039274B:G07	CH09LNL
74	20599	RTA00002708F.h.06.1.P.Seq	F	M00004264B:A05	CH01COH
75	41115	RTA00002713F.o.11.1.P.Seq	F	M00027632B:F11	CH04MAL
76	21109	RTA00002708F.h.12.1.P.Seq	F	M00004278A:F09	CH01COH
77	455702	RTA00002694F.b.11.1.P.Seq	F	M00043433C:G07	CH20COHLV
78	380643	RTA00002683F.p.09.2.P.Seq	F	M00040103B:H10	CH09LNL
79	374413	RTA00002672F.i.15.2.P.Seq	F	M00039015B:G10	CH09LNL
80	378891	RTA00002672F.i.18.2.P.Seq	F	M00039016A:A02	CH09LNL
81	379374	RTA00002672F.k.11.2.P.Seq	F	M00039028C:B11	CH09LNL
82	17253	RTA00002709F.h.23.1.P.Seq	F	M00006866A:D07	CH02COH
83	21565	RTA00002709F.e.11.1.P.Seq	F	M00005778B:F09	CH02COH
84	373996	RTA00002673F.n.11.1.P.Seq	F	M00039108D:B06	CH09LNL
85	380437	RTA00002683F.c.09.1.P.Seq	F	M00040039D:D06	CH09LNL
86	430729	RTA00002669F.h.18.2.P.Seq	F	M00033226A:A11	CH08LNH
87	376791	RTA00002674F.l.17.1.P.Seq	F	M00039166B:G06	CH09LNL
88	373760	RTA00002672F.p.20.1.P.Seq	F	M00039049D:G07	CH09LNL
89	373837	RTA00002672F.p.22.1.P.Seq	F	M00039050A:H10	CH09LNL
90	376435	RTA00002678F.h.17.2.P.Seq	F	M00039476B:A02	CH09LNL
91	373881	RTA00002672F.b.20.1.P.Seq	F	M00038638D:H03	CH09LNL
92	377086	RTA00002676F.p.07.1.P.Seq	F	M00039328D:D07	CH09LNL
93	377889	RTA00002672F.c.08.1.P.Seq	F	M00038661A:A07	CH09LNL
94	380442	RTA00002684F.b.05.2.P.Seq	F	M00040111C:D05	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
95	374689	RTA00002676F.m.13.2.P.Seq	F	M00039318B:B09	CH09LNL
96	375339	RTA00002678F.m.23.2.P.Seq	F	M00039616A:B10	CH09LNL
97	14197	RTA00002710F.f.15.1.P.Seq	F	M00022084D:B01	CH03MAH
98	380666	RTA00002684F.c.04.2.P.Seq	F	M00040115B:H12	CH09LNL
99	377352	RTA00002677F.i.13.2.P.Seq	F	M00039404B:A05	CH09LNL
100	379188	RTA00002682F.a.03.1.P.Seq	F	M00039914D:G12	CH09LNL
101	428269	RTA00002666F.c.13.1.P.Seq	F	M00032539B:C11	CH08LNLH
102	373464	RTA00002671F.l.13.3.P.Seq	F	M00038327A:C11	CH09LNL
103	15527	RTA00002710F.p.07.1.P.Seq	F	M00022747D:E03	CH03MAH
104	377504	RTA00002671F.i.17.3.P.Seq	F	M00038303C:D02	CH09LNL
105	33508	RTA00002710F.g.17.1.P.Seq	F	M00022183B:C02	CH03MAH
106	129179	RTA00002662F.d.19.2.P.Seq	F	M00007157C:F11	CH02COH
107	377086	RTA00002676F.p.07.2.P.Seq	F	M00039328D:D07	CH09LNL
108	375872	RTA00002675F.h.15.1.P.Seq	F	M00039233A:A03	CH09LNL
109	375652	RTA00002676F.l.07.3.P.Seq	F	M00039303C:F11	CH09LNL
110	374266	RTA00002674F.i.08.2.P.Seq	F	M00039144C:E06	CH09LNL
111	378983	RTA00002682F.a.07.1.P.Seq	F	M00039915D:C11	CH09LNL
112	377343	RTA00002684F.g.04.1.P.Seq	F	M00040302C:A04	CH09LNL
113	378679	RTA00002681F.f.16.2.P.Seq	F	M00039869B:F06	CH09LNL
114	374095	RTA00002671F.p.08.2.P.Seq	F	M00038618C:C08	CH09LNL
115	375843	RTA00002671F.o.06.2.P.Seq	F	M00038614C:H11	CH09LNL
116	377788	RTA00002684F.h.01.2.P.Seq	F	M00040305C:H06	CH09LNL
117	21403	RTA00002709F.j.05.1.P.Seq	F	M00006928D:D07	CH02COH
118	23184	RTA00002709F.b.05.2.P.Seq	F	M00005358B:B06	CH02COH
119	15671	RTA00002710F.k.16.1.P.Seq	F	M00022495D:H08	CH03MAH
120	177367	RTA00002663F.m.22.1.P.Seq	F	M00022986D:H09	CH03MAH
121	377788	RTA00002684F.g.24.1.P.Seq	F	M00040305C:H06	CH09LNL
122	375058	RTA00002675F.h.02.1.P.Seq	F	M00039230D:G12	CH09LNL
123	380412	RTA00002680F.k.15.2.P.Seq	F	M00039816B:D04	CH09LNL
124	178447	RTA00002663F.n.06.1.P.Seq	F	M00023007A:H04	CH03MAH
125	376647	RTA00002674F.h.07.1.P.Seq	F	M00039140D:D09	CH09LNL
126	44679	RTA00002661F.e.19.1.P.Seq	F	M00003800A:F09	CH01COH
127	377659	RTA00002678F.a.04.2.P.Seq	F	M00039430B:F12	CH09LNL
128	379703	RTA00002682F.h.03.1.P.Seq	F	M00039982C:H04	CH09LNL
129	374673	RTA00002673F.e.08.2.P.Seq	F	M00039068B:B04	CH09LNL
130	20513	RTA00002710F.j.12.1.P.Seq	F	M00022391D:F10	CH03MAH
131	376124	RTA00002682F.n.17.1.P.Seq	F	M00040021A:F09	CH09LNL
132	374679	RTA00002676F.d.07.2.P.Seq	F	M00039281D:B04	CH09LNL
133	23184	RTA00002709F.b.05.1.P.Seq	F	M00005358B:B06	CH02COH
134	430953	RTA00002668F.i.23.1.P.Seq	F	M00033007C:E01	CH08LNLH
135	380442	RTA00002684F.b.05.1.P.Seq	F	M00040111C:D05	CH09LNL
136	12374	RTA00002709F.a.01.1.P.Seq	F	M00004825D:D05	CH02COH
137	427466	RTA00002665F.b.11.3.P.Seq	F	M00028184D:G10	CH08LNLH
138	36611	RTA00002668F.f.03.1.P.Seq	F	M00032942D:C12	CH08LNLH
139	33756	RTA00002662F.a.18.2.P.Seq	F	M00005359A:D04	CH02COH
140	456026	RTA00002694F.e.03.1.P.Seq	F	M00043616C:A05	CH02COHLV
141	15766	RTA00002710F.k.02.1.P.Seq	F	M00022444D:G01	CH03MAH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
142	24352	RTA00002709F.a.05.1.P.Seq	F	M00004839C:H02	CH02COH
143	24354	RTA00002709F.a.03.1.P.Seq	F	M00004832D:H02	CH02COH
144	379114	RTA00002681F.o.01.2.P.Seq	F	M00039903C:F03	CH09LNL
145	19609	RTA00002709F.c.05.1.P.Seq	F	M00005457C:A03	CH02COH
146	21685	RTA00002709F.e.23.1.P.Seq	F	M00006581D:F08	CH02COH
147	380085	RTA00002682F.i.10.1.P.Seq	F	M00039987A:F09	CH09LNL
148	20700	RTA00002710F.i.18.1.P.Seq	F	M00022373A:B05	CH03MAH
149	379981	RTA00002682F.i.18.1.P.Seq	F	M00039988A:E06	CH09LNL
150	376591	RTA00002675F.c.01.1.P.Seq	F	M00039213A:D01	CH09LNL
151	92058	RTA00002663F.m.04.1.P.Seq	F	M00022895A:H08	CH03MAH
152	196936	RTA00002663F.m.02.1.P.Seq	F	M00022885C:H05	CH03MAH
153	430702	RTA00002668F.h.04.1.P.Seq	F	M00032990B:A11	CH08LNH
154	378448	RTA00002680F.n.21.2.P.Seq	F	M00039832A:B12	CH09LNL
155	41606	RTA00002713F.e.10.1.P.Seq	F	M00027301A:G05	CH04MAL
156	213817	RTA00002664F.i.19.1.P.Seq	F	M00027634A:D11	CH04MAL
157	373464	RTA00002671F.l.13.1.P.Seq	F	M00038327A:C11	CH09LNL
158	379483	RTA00002679F.k.12.1.P.Seq	F	M00039700B:D02	CH09LNL
159	375796	RTA00002680F.f.17.1.P.Seq	F	M00039795B:H10	CH09LNL
160	375796	RTA00002680F.f.17.2.P.Seq	F	M00039795B:H10	CH09LNL
161	120485	RTA00002663F.b.12.1.P.Seq	F	M00021665B:F12	CH03MAH
162	374291	RTA00002673F.f.17.1.P.Seq	F	M00039072C:E02	CH09LNL
163	380513	RTA00002677F.p.15.2.P.Seq	F	M00039428C:E01	CH09LNL
164	379416	RTA00002683F.j.07.2.P.Seq	F	M00040077D:C11	CH09LNL
165	378178	RTA00002680F.l.13.1.P.Seq	F	M00039820A:F11	CH09LNL
166	427947	RTA00002665F.n.24.1.P.Seq	F	M00032495B:D02	CH08LNH
167	427269	RTA00002665F.d.03.3.P.Seq	F	M00028212C:B08	CH08LNH
168	20451	RTA00002710F.j.10.1.P.Seq	F	M00022391B:E01	CH03MAH
169	377003	RTA00002683F.g.09.2.P.Seq	F	M00040062B:B05	CH09LNL
170	427759	RTA00002665F.o.11.1.P.Seq	F	M00032499C:A01	CH08LNH
171	427549	RTA00002668F.k.13.1.P.Seq	F	M00033034C:A06	CH08LNH
172	373881	RTA00002672F.b.20.2.P.Seq	F	M00038638D:H03	CH09LNL
173	188215	RTA00002664F.f.13.2.P.Seq	F	M00027200A:F02	CH04MAL
174	379683	RTA00002681F.d.04.2.P.Seq	F	M00039857B:G10	CH09LNL
175	380652	RTA00002678F.d.12.2.P.Seq	F	M00039455D:H04	CH09LNL
176	378334	RTA00002679F.h.10.1.P.Seq	F	M00039682C:H11	CH09LNL
177	377930	RTA00002680F.g.14.1.P.Seq	F	M00039798B:B02	CH09LNL
178	378692	RTA00002680F.o.20.3.P.Seq	F	M00039835A:F07	CH09LNL
179	32279	RTA00002709F.d.23.1.P.Seq	F	M00005673B:B12	CH02COH
180	376379	RTA00002680F.c.15.1.P.Seq	F	M00039782A:H10	CH09LNL
181	375963	RTA00002675F.i.12.1.P.Seq	F	M00039238A:B12	CH09LNL
182	378683	RTA00002680F.a.14.2.P.Seq	F	M00039773D:A09	CH09LNL
183	374946	RTA00002673F.j.24.2.P.Seq	F	M00039096A:E07	CH09LNL
184	429583	RTA00002666F.g.10.1.P.Seq	F	M00032584A:H08	CH08LNH
185	28338	RTA00002711F.e.17.1.P.Seq	F	M00022930C:E02	CH03MAH
186	427970	RTA00002665F.j.13.1.P.Seq	F	M00031368A:E10	CH08LNH
187	379650	RTA00002683F.h.22.2.P.Seq	F	M00040072C:G09	CH09LNL
188	379661	RTA00002676F.c.05.2.P.Seq	F	M00039277D:G10	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
189	376182	RTA00002677F.b.17.2.P.Seq	F	M00039540B:E07	CH09LNL
190	374797	RTA00002678F.b.12.2.P.Seq	F	M00039444C:H02	CH09LNL
191	375389	RTA00002674F.a.13.1.P.Seq	F	M00039120C:C09	CH09LNL
192	397115	RTA00002683F.i.22.2.P.Seq	F	M00040076C:D06	CH09LNL
193	186655	RTA00002712F.i.21.1.P.Seq	F	M00026941D:A04	CH04MAL
194	404682	RTA00002687F.b.13.1.P.Seq	F	M00039766D:H01	CH14EDT
195	19609	RTA00002709F.c.05.2.P.Seq	F	M00005457C:A03	CH02COH
196	404682	RTA00002687F.b.13.2.P.Seq	F	M00039766D:H01	CH14EDT
197	380412	RTA00002680F.k.15.1.P.Seq	F	M00039816B:D04	CH09LNL
198	394413	RTA00002689F.d.17.3.P.Seq	F	M00042742D:D05	CH15CON
199	380086	RTA00002679F.m.16.1.P.Seq	F	M00039710C:G03	CH09LNL
200	430738	RTA00002669F.i.15.2.P.Seq	F	M00033231D:B09	CH08LNL
201	40667	RTA00002712F.g.22.1.P.Seq	F	M00026882D:G09	CH04MAL
202	397421	RTA00002681F.c.16.2.P.Seq	F	M00039854B:F09	CH09LNL
203	398775	RTA00002679F.f.11.1.P.Seq	F	M00039675D:H05	CH09LNL
204	87345	RTA00002712F.f.19.1.P.Seq	F	M00026850D:F09	CH04MAL
205	379920	RTA00002679F.b.24.2.P.Seq	F	M00039660C:C10	CH09LNL
206	380666	RTA00002684F.c.04.1.P.Seq	F	M00040115B:H12	CH09LNL
207	404340	RTA00002687F.b.05.2.P.Seq	F	M00039764C:D07	CH14EDT
208	375509	RTA00002680F.e.08.2.P.Seq	F	M00039790B:D03	CH09LNL
209	46423	RTA00002712F.i.02.1.P.Seq	F	M00026914A:H10	CH04MAL
210	401713	RTA00002685F.p.10.2.P.Seq	F	M00039647A:H11	CH12EDT
211	377003	RTA00002683F.g.09.1.P.Seq	F	M00040062B:B05	CH09LNL
212	378891	RTA00002672F.i.18.1.P.Seq	F	M00039016A:A02	CH09LNL
213	412778	RTA00002685F.l.07.2.P.Seq	F	M00039533D:F04	CH12EDT
214	373786	RTA00002679F.a.20.2.P.Seq	F	M00039655C:C07	CH09LNL
215	378692	RTA00002680F.o.20.2.P.Seq	F	M00039835A:F07	CH09LNL
216	88888	RTA00002713F.f.22.1.P.Seq	F	M00027355A:B07	CH04MAL
217	358187	RTA00002676F.b.04.2.P.Seq	F	M00039273D:B02	CH09LNL
218	377131	RTA00002682F.e.10.1.P.Seq	F	M00039938C:E11	CH09LNL
219	21488	RTA00002708F.f.17.1.P.Seq	F	M00004152A:C12	CH01COH
220	447487	RTA00002689F.e.04.3.P.Seq	F	M00042895A:D10	CH15CON
221	364	RTA00002710F.a.06.1.P.Seq	F	M00007929C:B08	CH03MAH
222	404024	RTA00002687F.e.18.2.P.Seq	F	M00039958A:A08	CH14EDT
223	152305	RTA00002712F.d.02.1.P.Seq	F	M00023376B:G04	CH04MAL
224	106050	RTA00002713F.o.17.1.P.Seq	F	M00027668C:H12	CH04MAL
225	41126	RTA00002713F.l.12.1.P.Seq	F	M00027546C:B10	CH04MAL
226	113496	RTA00002713F.n.20.1.P.Seq	F	M00027625A:H01	CH04MAL
227	447487	RTA00002689F.e.04.1.P.Seq	F	M00042895A:D10	CH15CON
228	146335	RTA00002712F.j.17.1.P.Seq	F	M00026980A:D09	CH04MAL
229	376647	RTA00002674F.h.07.2.P.Seq	F	M00039140D:D09	CH09LNL
230	376746	RTA00002674F.f.12.2.P.Seq	F	M00039133B:F08	CH09LNL
231	373523	RTA00002674F.n.21.2.P.Seq	F	M00039177B:D03	CH09LNL
232	455466	RTA00002694F.c.10.1.P.Seq	F	M00043461D:E06	CH20COHLV
233	374031	RTA00002683F.p.17.2.P.Seq	F	M00040105C:F11	CH09LNL
234	373997	RTA00002673F.m.04.2.P.Seq	F	M00039105C:B08	CH09LNL
235	455717	RTA00002694F.a.06.1.P.Seq	F	M00042593C:G06	CH20COHLV

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
236	373837	RTA00002672F.p.22.2.P.Seq	F	M00039050A:H10	CH09LNL
237	374513	RTA00002672F.i.16.2.P.Seq	F	M00039015B:H09	CH09LNL
238	375628	RTA00002672F.k.04.2.P.Seq	F	M00039026D:F05	CH09LNL
239	377732	RTA00002681F.p.09.1.P.Seq	F	M00039910C:G10	CH09LNL
240	378326	RTA00002681F.m.11.1.P.Seq	F	M00039896C:H01	CH09LNL
241	378001	RTA00002681F.m.22.1.P.Seq	F	M00039898D:C06	CH09LNL
242	378459	RTA00002681F.i.07.2.P.Seq	F	M00039879D:B11	CH09LNL
243	373862	RTA00002671F.g.01.2.P.Seq	F	M00038284B:H04	CH09LNL
244	373252	RTA00002670F.k.16.1.P.Seq	F	M00033451A:H01	CH09LNL
245	378475	RTA00002672F.g.24.1.P.Seq	F	M00039006D:B01	CH09LNL
246	379941	RTA00002682F.j.15.1.P.Seq	F	M00039990C:D10	CH09LNL
247	427703	RTA00002665F.e.11.1.P.Seq	F	M00028357A:G10	CH08LNH
248	373976	RTA00002671F.p.15.2.P.Seq	F	M00038619B:A03	CH09LNL
249	431643	RTA00002669F.l.16.3.P.Seq	F	M00033276D:H09	CH08LNH
250	383502	RTA00002670F.k.07.1.P.Seq	F	M00033446D:B02	CH09LNL
251	378764	RTA00002681F.j.04.1.P.Seq	F	M00039884A:H11	CH09LNL
252	431629	RTA00002669F.l.14.3.P.Seq	F	M00033276B:G08	CH08LNH
253	372992	RTA00002671F.b.16.2.P.Seq	F	M00033594C:B03	CH09LNL
254	431601	RTA00002669F.k.08.3.P.Seq	F	M00033263B:G04	CH08LNH
255	21059	RTA00002710F.c.05.1.P.Seq	F	M00008053A:F10	CH03MAH
256	430689	RTA00002669F.i.24.3.P.Seq	F	M00033243B:A05	CH08LNH
257	131764	RTA00002662F.c.14.1.P.Seq	F	M00006893C:E07	CH02COH
258	373300	RTA00002674F.c.21.2.P.Seq	F	M00039126D:A08	CH09LNL
259	384601	RTA00002670F.k.06.1.P.Seq	F	M00033446C:G08	CH09LNL
260	375389	RTA00002674F.a.13.2.P.Seq	F	M00039120C:C09	CH09LNL
261	15248	RTA00002710F.f.23.1.P.Seq	F	M00022127C:H03	CH03MAH
262	428134	RTA00002666F.c.15.1.P.Seq	F	M00032540A:A09	CH08LNH
263	374184	RTA00002672F.a.19.1.P.Seq	F	M00038633A:D07	CH09LNL
264	136225	RTA00002676F.n.02.2.P.Seq	F	M00039319C:A04	CH09LNL
265	401713	RTA00002685F.p.10.1.P.Seq	F	M00039647A:H11	CH12EDT
266	27104	RTA00002661F.a.09.1.P.Seq	F	M00001363D:D09	CH01COH
267	207466	RTA00002664F.j.08.2.P.Seq	F	M00027733A:A02	CH04MAL
268	143045	RTA00002663F.a.02.1.P.Seq	F	M00007941D:C09	CH03MAH
269	378830	RTA00002675F.e.07.1.P.Seq	F	M00039221A:H03	CH09LNL
270	21731	RTA00002709F.k.07.1.P.Seq	F	M00007013A:D09	CH02COH
271	428552	RTA00002666F.c.16.1.P.Seq	F	M00032541D:H08	CH08LNH
272	187632	RTA00002664F.i.15.2.P.Seq	F	M00027617B:C12	CH04MAL
273	431053	RTA00002668F.o.05.2.P.Seq	F	M00033130B:F06	CH08LNH
274	188972	RTA00002664F.d.20.1.P.Seq	F	M00027030C:H06	CH04MAL
275	430678	RTA00002668F.h.12.1.P.Seq	F	M00032994A:A08	CH08LNH
276	374042	RTA00002672F.a.08.1.P.Seq	F	M00038631C:B10	CH09LNL
277	24332	RTA00002709F.j.07.1.P.Seq	F	M00006935C:F06	CH02COH
278	376764	RTA00002674F.f.20.1.P.Seq	F	M00039135D:F05	CH09LNL
279	134338	RTA00002662F.c.15.2.P.Seq	F	M00006897A:H02	CH02COH
280	375541	RTA00002680F.d.21.2.P.Seq	F	M00039788A:E03	CH09LNL
281	228909	RTA00002664F.e.08.2.P.Seq	F	M00027085C:E11	CH04MAL
282	58063	RTA00002661F.h.18.1.P.Seq	F	M00004234A:E07	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
283	380500	RTA00002670F.p.19.2.P.Seq	F	M00033583B:E06	CH09LNL
284	34928	RTA00002710F.p.21.1.P.Seq	F	M00022795B:G06	CH03MAH
285	374028	RTA00002674F.k.03.2.P.Seq	F	M00039156A:B11	CH09LNL
286	374121	RTA00002672F.h.22.2.P.Seq	F	M00039013A:C09	CH09LNL
287	429547	RTA00002668F.c.07.1.P.Seq	F	M00032917D:G09	CH08LNL
288	380668	RTA00002670F.p.11.2.P.Seq	F	M00033581C:H10	CH09LNL
289	258704	RTA00002665F.m.06.1.P.Seq	F	M00032480B:E10	CH08LNL
290	380325	RTA00002670F.p.22.2.P.Seq	F	M00033583D:B05	CH09LNL
291	378326	RTA00002681F.m.11.2.P.Seq	F	M00039896C:H01	CH09LNL
292	375618	RTA00002675F.d.13.1.P.Seq	F	M00039218A:F03	CH09LNL
293	20999	RTA00002709F.j.16.1.P.Seq	F	M00006977C:G04	CH02COH
294	29102	RTA00002710F.p.18.1.P.Seq	F	M00022795D:B01	CH03MAH
295	379334	RTA00002680F.b.22.1.P.Seq	F	M00039778C:A04	CH09LNL
296	23943	RTA00002709F.i.12.1.P.Seq	F	M00006836D:H02	CH02COH
297	373998	RTA00002672F.a.10.2.P.Seq	F	M00038631D:B02	CH09LNL
298	373325	RTA00002672F.c.14.2.P.Seq	F	M00038662B:A12	CH09LNL
299	373818	RTA00002672F.e.15.2.P.Seq	F	M00038995C:G08	CH09LNL
300	429843	RTA00002668F.c.10.1.P.Seq	F	M00032918B:E06	CH08LNL
301	427755	RTA00002665F.d.19.3.P.Seq	F	M00028316B:H12	CH08LNL
302	189177	RTA00002664F.c.23.2.P.Seq	F	M00026922C:G03	CH04MAL
303	13294	RTA00002709F.j.15.1.P.Seq	F	M00006968A:G08	CH02COH
304	178801	RTA00002663F.n.01.1.P.Seq	F	M00022997A:F06	CH03MAH
305	230865	RTA00002664F.d.03.2.P.Seq	F	M00026928D:A03	CH04MAL
306	178801	RTA00002663F.m.24.1.P.Seq	F	M00022997A:F06	CH03MAH
307	378809	RTA00002672F.g.21.2.P.Seq	F	M00039005C:H01	CH09LNL
308	378957	RTA00002670F.d.17.2.P.Seq	F	M00033362C:C05	CH09LNL
309	373523	RTA00002674F.n.21.1.P.Seq	F	M00039177B:D03	CH09LNL
310	375458	RTA00002678F.l.06.2.P.Seq	F	M00039611D:D11	CH09LNL
311	429794	RTA00002668F.c.09.1.P.Seq	F	M00032918B:D08	CH08LNL
312	72797	RTA00002661F.e.07.1.P.Seq	F	M00003761C:F02	CH01COH
313	429992	RTA00002668F.c.21.1.P.Seq	F	M00032921B:H08	CH08LNL
314	374410	RTA00002674F.k.11.2.P.Seq	F	M00039158B:G12	CH09LNL
315	376553	RTA00002674F.g.19.1.P.Seq	F	M00039139A:C09	CH09LNL
316	429096	RTA00002666F.f.16.1.P.Seq	F	M00032578A:G06	CH08LNL
317	181948	RTA00002663F.n.05.1.P.Seq	F	M00023003C:D07	CH03MAH
318	378475	RTA00002672F.h.01.2.P.Seq	F	M00039006D:B01	CH09LNL
319	427336	RTA00002665F.c.23.1.P.Seq	F	M00028210B:D02	CH08LNL
320	374042	RTA00002672F.a.08.2.P.Seq	F	M00038631C:B10	CH09LNL
321	386543	RTA00002672F.f.13.2.P.Seq	F	M00038999B:G11	CH09LNL
322	376659	RTA00002678F.h.11.2.P.Seq	F	M00039475C:E10	CH09LNL
323	29135	RTA00002663F.c.09.1.P.Seq	F	M00021923C:D11	CH03MAH
324	377967	RTA00002681F.m.17.2.P.Seq	F	M00039897D:C10	CH09LNL
325	431330	RTA00002668F.m.16.2.P.Seq	F	M00033074A:C08	CH08LNL
326	373824	RTA00002680F.i.19.2.P.Seq	F	M00039808D:H02	CH09LNL
327	50094	RTA00002661F.j.02.2.P.Seq	F	M00004378A:B10	CH01COH
328	214272	RTA00002664F.h.03.2.P.Seq	F	M00027366A:F11	CH04MAL
329	377293	RTA00002680F.b.17.2.P.Seq	F	M00039777C:E05	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
330	195053	RTA00002663F.n.16.1.P.Seq	F	M00023044B:D02	CH03MAH
331	21274	RTA00002709F.m.09.1.P.Seq	F	M00007194A:B09	CH02COH
332	376580	RTA00002675F.b.20.1.P.Seq	F	M00039212C:C12	CH09LNL
333	374725	RTA00002673F.f.02.2.P.Seq	F	M00039070D:C02	CH09LNL
334	25238	RTA00002710F.n.08.1.P.Seq	F	M00022634D:C08	CH03MAH
335	377337	RTA00002683F.l.07.2.P.Seq	F	M00040085D:A10	CH09LNL
336	450485	RTA00002692F.a.13.2.P.Seq	F	M00042625C:B04	CH18CON
337	21989	RTA00002709F.h.22.1.P.Seq	F	M00006861B:F09	CH02COH
338	58296	RTA00002661F.i.20.2.P.Seq	F	M00004354D:E05	CH01COH
339	379144	RTA00002679F.l.14.1.P.Seq	F	M00039705D:F02	CH09LNL
340	379690	RTA00002680F.b.21.2.P.Seq	F	M00039778B:G03	CH09LNL
341	379640	RTA00002681F.d.12.2.P.Seq	F	M00039859C:G10	CH09LNL
342	373988	RTA00002673F.h.23.1.P.Seq	F	M00039079A:A05	CH09LNL
343	373988	RTA00002673F.h.23.2.P.Seq	F	M00039079A:A05	CH09LNL
344	380673	RTA00002673F.j.13.2.P.Seq	F	M00039084C:H03	CH09LNL
345	55243	RTA00002661F.i.06.2.P.Seq	F	M00004282D:C11	CH01COH
346	40557	RTA00002713F.h.21.1.P.Seq	F	M00027398C:F07	CH04MAL
347	375467	RTA00002677F.m.03.1.P.Seq	F	M00039417A:D03	CH09LNL
348	398406	RTA00002679F.j.02.1.P.Seq	F	M00039689C:E08	CH09LNL
349	430392	RTA00002668F.k.19.1.P.Seq	F	M00033037D:C11	CH08LNH
350	376746	RTA00002674F.f.12.1.P.Seq	F	M00039133B:F08	CH09LNL
351	115595	RTA00002713F.e.07.1.P.Seq	F	M00027297A:C04	CH04MAL
352	377182	RTA00002682F.l.11.1.P.Seq	F	M00040010A:F10	CH09LNL
353	380659	RTA00002684F.e.07.2.P.Seq	F	M00040124D:H01	CH09LNL
354	373862	RTA00002671F.g.01.1.P.Seq	F	M00038284B:H04	CH09LNL
355	376096	RTA00002677F.b.16.2.P.Seq	F	M00039340A:D05	CH09LNL
356	372887	RTA00002670F.d.05.2.P.Seq	F	M00033358A:H12	CH09LNL
357	378475	RTA00002672F.g.24.2.P.Seq	F	M00039006D:B01	CH09LNL
358	427336	RTA00002665F.c.23.3.P.Seq	F	M00028210B:D02	CH08LNH
359	373814	RTA00002672F.b.02.2.P.Seq	F	M00038635A:G09	CH09LNL
360	215506	RTA00002664F.h.08.2.P.Seq	F	M00027438C:G07	CH04MAL
361	374465	RTA00002673F.c.07.2.P.Seq	F	M00039058C:H02	CH09LNL
362	428784	RTA00002667F.c.18.1.P.Seq	F	M00032744B:F10	CH08LNH
363	379581	RTA00002676F.a.21.2.P.Seq	F	M00039273B:F02	CH09LNL
364	378371	RTA00002678F.f.20.2.P.Seq	F	M00039465A:A08	CH09LNL
365	375154	RTA00002676F.c.13.2.P.Seq	F	M00039279B:H02	CH09LNL
366	431214	RTA00002669F.k.04.1.P.Seq	F	M00033262D:A11	CH08LNH
367	376053	RTA00002675F.l.03.1.P.Seq	F	M00039249A:C12	CH09LNL
368	373282	RTA00002680F.j.19.2.P.Seq	F	M00039813B:D11	CH09LNL
369	33397	RTA00002661F.h.04.1.P.Seq	F	M00004168A:G11	CH01COH
370	376706	RTA00002675F.c.02.1.P.Seq	F	M00039213B:F05	CH09LNL
371	378292	RTA00002681F.i.09.2.P.Seq	F	M00039880A:H11	CH09LNL
372	431612	RTA00002669F.e.23.3.P.Seq	F	M00033202D:G06	CH08LNH
373	378471	RTA00002679F.o.17.1.P.Seq	F	M00039727C:B09	CH09LNL
374	378666	RTA00002681F.i.05.2.P.Seq	F	M00039879C:F05	CH09LNL
375	374894	RTA00002675F.f.04.1.P.Seq	F	M00039224A:E12	CH09LNL
376	430191	RTA00002667F.j.24.1.P.Seq	F	M00032829B:E06	CH08LNH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
377	428581	RTA00002667F.c.12.1.P.Seq	F	M00032739A:A06	CH08LNH
378	379598	RTA00002679F.k.03.1.P.Seq	F	M00039697B:F11	CH09LNL
379	45300	RTA00002710F.j.23.1.P.Seq	F	M00022434D:D06	CH03MAH
380	23030	RTA00002709F.b.10.1.P.Seq	F	M00005384A:C11	CH02COH
381	379928	RTA00002679F.o.06.1.P.Seq	F	M00039720D:D02	CH09LNL
382	430191	RTA00002667F.k.01.1.P.Seq	F	M00032829B:E06	CH08LNH
383	374684	RTA00002675F.g.02.1.P.Seq	F	M00039228A:B05	CH09LNL
384	375728	RTA00002676F.h.05.2.P.Seq	F	M00039299B:G12	CH09LNL
385	230237	RTA00002670F.b.08.2.P.Seq	F	M00033306D:H09	CH09LNL
386	380673	RTA00002673F.j.13.1.P.Seq	F	M00039084C:H03	CH09LNL
387	378938	RTA00002679F.k.20.1.P.Seq	F	M00039702A:B12	CH09LNL
388	375115	RTA00002673F.e.01.1.P.Seq	F	M00039066D:G08	CH09LNL
389	378673	RTA00002680F.p.21.2.P.Seq	F	M00039838A:F05	CH09LNL
390	372909	RTA00002670F.a.12.2.P.Seq	F	M00033300D:H12	CH09LNL
391	373300	RTA00002674F.c.21.1.P.Seq	F	M00039126D:A08	CH09LNL
392	379318	RTA00002683F.h.16.2.P.Seq	F	M00040071B:A10	CH09LNL
393	378319	RTA00002681F.k.07.2.P.Seq	F	M00039890A:H05	CH09LNL
394	374608	RTA00002675F.g.20.1.P.Seq	F	M00039230A:A10	CH09LNL
395	374328	RTA00002673F.c.24.2.P.Seq	F	M00039061B:F08	CH09LNL
396	374328	RTA00002673F.d.01.2.P.Seq	F	M00039061B:F08	CH09LNL
397	428401	RTA00002667F.b.07.1.P.Seq	F	M00032725C:F06	CH08LNH
398	136202	RTA00002687F.p.05.2.P.Seq	F	M00040349D:B09	CH14EDT
399	374394	RTA00002673F.c.15.1.P.Seq	F	M00039059C:G08	CH09LNL
400	37784	RTA00002708F.c.17.1.P.Seq	F	M00003816D:E11	CH01COH
401	378282	RTA00002681F.h.11.1.P.Seq	F	M00039876D:H09	CH09LNL
402	185663	RTA00002712F.p.17.2.P.Seq	F	M00027178B:G09	CH04MAL
403	14866	RTA00002709F.d.14.1.P.Seq	F	M00005623D:G12	CH02COH
404	383502	RTA00002670F.k.07.2.P.Seq	F	M00033446D:B02	CH09LNL
405	13463	RTA00002709F.f.18.1.P.Seq	F	M00006657C:G05	CH02COH
406	21274	RTA00002709F.m.09.2.P.Seq	F	M00007194A:B09	CH02COH
407	13745	RTA00002714F.b.13.1.P.Seq	F	M00027801C:C11	CH04MAL
408	23485	RTA00002714F.c.10.1.P.Seq	F	M00027836D:F12	CH04MAL
409	428364	RTA00002667F.c.09.1.P.Seq	F	M00032737B:E09	CH08LNH
410	431629	RTA00002669F.l.14.2.P.Seq	F	M00033276B:G08	CH08LNH
411	379754	RTA00002682F.h.08.1.P.Seq	F	M00039983D:A06	CH09LNL
412	431601	RTA00002669F.k.08.2.P.Seq	F	M00033263B:G04	CH08LNH
413	375749	RTA00002680F.f.23.2.P.Seq	F	M00039795D:G06	CH09LNL
414	378764	RTA00002681F.j.04.2.P.Seq	F	M00039884A:H11	CH09LNL
415	215605	RTA00002664F.i.20.1.P.Seq	F	M00027647C:D03	CH04MAL
416	376144	RTA00002675F.j.09.1.P.Seq	F	M00039241A:E11	CH09LNL
417	373071	RTA00002670F.j.23.2.P.Seq	F	M00033442A:D06	CH09LNL
418	379684	RTA00002681F.c.09.2.P.Seq	F	M00039851B:G11	CH09LNL
419	379610	RTA00002680F.k.11.2.P.Seq	F	M00039815C:F09	CH09LNL
420	22392	RTA00002708F.a.10.1.P.Seq	F	M00001395D:H02	CH01COH
421	377555	RTA00002683F.l.08.2.P.Seq	F	M00040085D:E04	CH09LNL
422	32624	RTA00002713F.f.15.1.P.Seq	F	M00027347C:G07	CH04MAL
423	375024	RTA00002675F.p.12.1.P.Seq	F	M00039266D:F12	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
424	374725	RTA00002673F.f.02.1.P.Seq	F	M00039070D:C02	CH09LNL
425	376228	RTA00002676F.f.19.2.P.Seq	F	M00039293A:H04	CH09LNL
426	375906	RTA00002675F.i.18.1.P.Seq	F	M00039238D:A08	CH09LNL
427	186190	RTA00002714F.a.04.1.P.Seq	F	M00027729D:H06	CH04MAL
428	57694	RTA00002713F.f.02.1.P.Seq	F	M00027319D:B11	CH04MAL
429	7007	RTA00002709F.d.08.1.P.Seq	F	M00005614B:B01	CH02COH
430	400084	RTA00002685F.o.19.2.P.Seq	F	M00039641C:D07	CH12EDT
431	375648	RTA00002676F.h.18.2.P.Seq	F	M00039301B:F06	CH09LNL
432	166493	RTA00002663F.h.08.1.P.Seq	F	M00022492C:A02	CH03MAH
433	379632	RTA00002682F.h.14.1.P.Seq	F	M00039984B:G12	CH09LNL
434	373234	RTA00002676F.g.15.2.P.Seq	F	M00039297C:H08	CH09LNL
435	401230	RTA00002685F.i.05.2.P.Seq	F	M00039533A:C12	CH12EDT
436	186623	RTA00002712F.f.15.1.P.Seq	F	M00026843B:D10	CH04MAL
437	127714	RTA00002712F.k.14.1.P.Seq	F	M00027018A:C09	CH04MAL
438	451857	RTA00002692F.a.01.1.P.Seq	F	M00042584B:C10	CH18CON
439	404620	RTA00002687F.c.03.2.P.Seq	F	M00039770A:G11	CH14EDT
440	186872	RTA00002663F.k.23.1.P.Seq	F	M00022797B:G08	CH03MAH
441	42729	RTA00002709F.c.06.2.P.Seq	F	M00005458A:F11	CH02COH
442	373380	RTA00002674F.b.07.1.P.Seq	F	M00039123A:B10	CH09LNL
443	374465	RTA00002673F.c.07.1.P.Seq	F	M00039058C:H02	CH09LNL
444	403557	RTA00002687F.d.10.2.P.Seq	F	M00039948A:E03	CH14EDT
445	16749	RTA00002709F.b.14.2.P.Seq	F	M00005402B:F08	CH02COH
446	375592	RTA00002680F.f.22.2.P.Seq	F	M00039795D:E10	CH09LNL
447	376103	RTA00002676F.g.06.2.P.Seq	F	M00039295B:D03	CH09LNL
448	40228	RTA00002712F.i.18.1.P.Seq	F	M00027049B:F05	CH04MAL
449	374606	RTA00002673F.j.23.1.P.Seq	F	M00039096A:A05	CH09LNL
450	378270	RTA00002680F.h.08.2.P.Seq	F	M00039801A:H11	CH09LNL
451	236321	RTA00002668F.k.14.1.P.Seq	F	M00033034C:F02	CH08LNH
452	378676	RTA00002680F.m.20.2.P.Seq	F	M00039827B:F07	CH09LNL
453	373252	RTA00002670F.k.16.2.P.Seq	F	M00033451A:H01	CH09LNL
454	384601	RTA00002670F.k.06.2.P.Seq	F	M00033446C:G08	CH09LNL
455	403772	RTA00002687F.a.03.2.P.Seq	F	M00039746C:G09	CH14EDT
456	379566	RTA00002683F.k.04.1.P.Seq	F	M00040081C:E01	CH09LNL
457	136202	RTA00002687F.p.05.1.P.Seq	F	M00040349D:B09	CH14EDT
458	14317	RTA00002713F.c.13.1.P.Seq	F	M00027248A:C02	CH04MAL
459	375349	RTA00002672F.j.11.1.P.Seq	F	M00039024B:B10	CH09LNL
460	403020	RTA00002687F.a.02.2.P.Seq	F	M00039746C:A08	CH14EDT
461	374060	RTA00002672F.i.07.1.P.Seq	F	M00039014B:C04	CH09LNL
462	183399	RTA00002712F.o.10.1.P.Seq	F	M00027136C:C09	CH04MAL
463	373789	RTA00002671F.c.20.1.P.Seq	F	M00038259B:G08	CH09LNL
464	20168	RTA00002711F.b.22.1.P.Seq	F	M00022834B:G11	CH03MAH
465	452641	RTA00002692F.d.05.2.P.Seq	F	M00043003C:D08	CH18CON
466	431370	RTA00002669F.m.04.2.P.Seq	F	M00033288B:D12	CH08LNH
467	153044	RTA00002713F.j.03.1.P.Seq	F	M00027476A:C09	CH04MAL
468	378229	RTA00002679F.c.16.2.P.Seq	F	M00039663C:G09	CH09LNL
469	374328	RTA00002673F.d.01.1.P.Seq	F	M00039061B:F08	CH09LNL
470	39606	RTA00002713F.i.20.1.P.Seq	F	M00027468A:C09	CH04MAL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
471	59077	RTA00002713F.n.01.1.P.Seq	F	M00027596C:E06	CH04MAL
472	1935	RTA00002710F.b.11.1.P.Seq	F	M00008006B:B03	CH03MAH
473	379684	RTA00002681F.c.09.1.P.Seq	F	M00039851B:G11	CH09LNL
474	451564	RTA00002691F.f.12.2.P.Seq	F	M00043411D:H06	CH17COHLV
475	7571	RTA00002710F.a.15.1.P.Seq	F	M00007943D:C09	CH03MAH
476	129323	RTA00002713F.k.21.1.P.Seq	F	M00027525B:D06	CH04MAL
477	12960	RTA00002710F.a.23.1.P.Seq	F	M00007976A:C10	CH03MAH
478	186730	RTA00002713F.o.05.1.P.Seq	F	M00027641C:A03	CH04MAL
479	59077	RTA00002713F.m.24.1.P.Seq	F	M00027596C:E06	CH04MAL
480	185884	RTA00002712F.b.06.1.P.Seq	F	M00023316C:G08	CH04MAL
481	19471	RTA00002708F.g.08.1.P.Seq	F	M00004197B:H10	CH01COH
482	45206	RTA00002710F.c.06.1.P.Seq	F	M00008063B:A06	CH03MAH
483	404257	RTA00002687F.g.06.2.P.Seq	F	M00040208A:C03	CH14EDT
484	372997	RTA00002679F.p.04.1.P.Seq	F	M00039729A:A10	CH09LNL
485	43792	RTA00002713F.k.16.1.P.Seq	F	M00027520A:C05	CH04MAL
486	400052	RTA00002687F.h.13.2.P.Seq	F	M00040291D:C05	CH14EDT
487	452194	RTA00002692F.c.14.2.P.Seq	F	M00042988A:F06	CH18CON
488	24034	RTA00002710F.b.06.1.P.Seq	F	M00007992C:F06	CH03MAH
489	447544	RTA00002689F.e.18.1.P.Seq	F	M00042905D:D02	CH15CON
490	401872	RTA00002686F.c.23.1.P.Seq	F	M00040141D:F05	CH13EDT
491	376553	RTA00002674F.g.19.2.P.Seq	F	M00039139A:C09	CH09LNL
492	455051	RTA00002694F.a.07.1.P.Seq	F	M00042595A:A11	CH20COHLV
493	16760	RTA00002708F.j.03.1.P.Seq	F	M00004393B:E07	CH01COH
494	374174	RTA00002672F.i.12.2.P.Seq	F	M00039015A:D07	CH09LNL
495	374283	RTA00002672F.k.21.2.P.Seq	F	M00039030B:E02	CH09LNL
496	375772	RTA00002681F.o.24.1.P.Seq	F	M00039909C:G05	CH09LNL
497	376417	RTA00002678F.i.03.2.P.Seq	F	M00039477D:A10	CH09LNL
498	428971	RTA00002666F.o.02.1.P.Seq	F	M00032678C:D06	CH08LNH
499	394098	RTA00002681F.j.15.1.P.Seq	F	M00039887C:E07	CH09LNL
500	379761	RTA00002670F.n.03.1.P.Seq	F	M00033561C:A02	CH09LNL
501	374266	RTA00002674F.i.08.1.P.Seq	F	M00039144C:E06	CH09LNL
502	372946	RTA00002670F.l.07.1.P.Seq	F	M00033457D:A05	CH09LNL
503	228909	RTA00002664F.e.08.1.P.Seq	F	M00027085C:E11	CH04MAL
504	427524	RTA00002665F.e.05.1.P.Seq	F	M00028354D:A03	CH08LNH
505	380413	RTA00002680F.k.19.2.P.Seq	F	M00039816C:D05	CH09LNL
506	373866	RTA00002671F.c.24.2.P.Seq	F	M00038259C:H09	CH09LNL
507	427202	RTA00002665F.g.15.1.P.Seq	F	M00028617C:A12	CH08LNH
508	373000	RTA00002670F.j.13.1.P.Seq	F	M00033437C:C03	CH09LNL
509	378838	RTA00002678F.p.11.2.P.Seq	F	M00039637C:A10	CH09LNL
510	24945	RTA00002710F.p.05.1.P.Seq	F	M00022739A:B03	CH03MAH
511	20277	RTA00002710F.e.17.1.P.Seq	F	M00021972D:C11	CH03MAH
512	20820	RTA00002710F.e.02.1.P.Seq	F	M00021919C:A10	CH03MAH
513	376791	RTA00002674F.l.17.2.P.Seq	F	M00039166B:G06	CH09LNL
514	9809	RTA00002710F.g.12.1.P.Seq	F	M00022178B:D06	CH03MAH
515	429562	RTA00002667F.m.03.1.P.Seq	F	M00032853D:G12	CH08LNH
516	12920	RTA00002710F.e.15.1.P.Seq	F	M00021964C:E10	CH03MAH
517	377565	RTA00002684F.h.19.1.P.Seq	F	M00040309A:E11	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
518	429356	RTA00002668F.d.23.1.P.Seq	F	M00032953A:C10	CH08LNH
519	427634	RTA00002665F.f.09.1.P.Seq	F	M00028369D:E08	CH08LNH
520	427713	RTA00002665F.e.23.1.P.Seq	F	M00028364C:G08	CH08LNH
521	373607	RTA00002674F.d.15.2.P.Seq	F	M00039127D:E10	CH09LNL
522	378781	RTA00002674F.o.14.1.P.Seq	F	M00039196B:H06	CH09LNL
523	429361	RTA00002666F.d.11.1.P.Seq	F	M00032550D:C02	CH08LNH
524	126754	RTA00002663F.a.16.1.P.Seq	F	M00008045A:H02	CH03MAH
525	428047	RTA00002665F.k.10.1.P.Seq	F	M00031417C:G09	CH08LNH
526	18863	RTA00002709F.d.15.1.P.Seq	F	M00005625A:C02	CH02COH
527	379761	RTA00002670F.n.03.2.P.Seq	F	M00033561C:A02	CH09LNL
528	46407	RTA00002665F.c.10.1.P.Seq	F	M00028196D:A03	CH08LNH
529	21365	RTA00002709F.k.06.1.P.Seq	F	M00007012D:H08	CH02COH
530	427466	RTA00002665F.b.11.1.P.Seq	F	M00028184D:G10	CH08LNH
531	400265	RTA00002685F.c.03.2.P.Seq	F	M00039374B:B07	CH12EDT
532	380056	RTA00002680F.a.16.2.P.Seq	F	M00039773D:F11	CH09LNL
533	375324	RTA00002678F.l.12.2.P.Seq	F	M00039612B:B10	CH09LNL
534	25165	RTA00002710F.k.17.1.P.Seq	F	M00022496B:E12	CH03MAH
535	401296	RTA00002685F.h.23.2.P.Seq	F	M00039529C:D07	CH12EDT
536	394098	RTA00002681F.j.15.2.P.Seq	F	M00039887C:E07	CH09LNL
537	17430	RTA00002710F.i.11.1.P.Seq	F	M00022365D:A03	CH03MAH
538	373820	RTA00002674F.d.06.1.P.Seq	F	M00039127A:G11	CH09LNL
539	378548	RTA00002672F.g.14.2.P.Seq	F	M00039004B:C11	CH09LNL
540	222679	RTA00002664F.f.18.2.P.Seq	F	M00027228D:A01	CH04MAL
541	376874	RTA00002670F.e.23.2.P.Seq	F	M00033375A:G04	CH09LNL
542	21329	RTA00002709F.b.08.1.P.Seq	F	M00005379A:E04	CH02COH
543	119905	RTA00002710F.p.13.1.P.Seq	F	M00022785C:G06	CH03MAH
544	377028	RTA00002678F.n.21.2.P.Seq	F	M00039631A:C10	CH09LNL
545	373351	RTA00002671F.l.18.3.P.Seq	F	M00038327D:A05	CH09LNL
546	376082	RTA00002674F.m.17.1.P.Seq	F	M00039171B:D11	CH09LNL
547	376987	RTA00002678F.g.21.2.P.Seq	F	M00039472C:B08	CH09LNL
548	61921	RTA00002661F.g.08.1.P.Seq	F	M00003995B:E03	CH01COH
549	373486	RTA00002672F.b.03.2.P.Seq	F	M00038635B:C08	CH09LNL
550	380355	RTA00002670F.o.06.2.P.Seq	F	M00033570C:C10	CH09LNL
551	430295	RTA00002667F.h.14.1.P.Seq	F	M00032808B:G10	CH08LNH
552	379221	RTA00002682F.n.01.1.P.Seq	F	M00040017D:G03	CH09LNL
553	373532	RTA00002672F.d.10.2.P.Seq	F	M00038991A:D01	CH09LNL
554	375633	RTA00002677F.m.05.2.P.Seq	F	M00039417B:F01	CH09LNL
555	378356	RTA00002681F.f.07.1.P.Seq	F	M00039866B:A08	CH09LNL
556	376196	RTA00002674F.m.12.1.P.Seq	F	M00039170C:F05	CH09LNL
557	375115	RTA00002673F.d.24.2.P.Seq	F	M00039066D:G08	CH09LNL
558	375115	RTA00002673F.e.01.2.P.Seq	F	M00039066D:G08	CH09LNL
559	378600	RTA00002679F.i.03.1.P.Seq	F	M00039686C:E06	CH09LNL
560	375351	RTA00002680F.e.15.1.P.Seq	F	M00039792A:B04	CH09LNL
561	25237	RTA00002710F.n.23.1.P.Seq	F	M00022671B:A08	CH03MAH
562	193503	RTA00002663F.n.15.1.P.Seq	F	M00023039D:B05	CH03MAH
563	428268	RTA00002667F.b.01.1.P.Seq	F	M00032724A:C05	CH08LNH
564	379440	RTA00002683F.j.21.2.P.Seq	F	M00040080C:C06	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
565	374502	RTA00002673F.i.08.2.P.Seq	F	M00039080C:H06	CH09LNL
566	240615	RTA00002672F.e.19.2.P.Seq	F	M00038995D:E05	CH09LNL
567	379207	RTA00002670F.b.07.2.P.Seq	F	M00033306D:G08	CH09LNL
568	427893	RTA00002665F.k.19.1.P.Seq	F	M00031419D:C04	CH08LNH
569	377530	RTA00002684F.g.19.2.P.Seq	F	M00040305A:D11	CH09LNL
570	429707	RTA00002668F.c.11.1.P.Seq	F	M00032918C:B10	CH08LNH
571	427610	RTA00002665F.i.04.1.P.Seq	F	M00028770A:D04	CH08LNH
572	100699	RTA00002662F.b.22.2.P.Seq	F	M00006680B:D02	CH02COH
573	378974	RTA00002682F.m.21.1.P.Seq	F	M00040017A:C06	CH09LNL
574	373607	RTA00002674F.d.15.1.P.Seq	F	M00039127D:E10	CH09LNL
575	262951	RTA00002665F.d.04.3.P.Seq	F	M00028215D:F03	CH08LNH
576	30748	RTA00002713F.e.11.1.P.Seq	F	M00027301B:B08	CH04MAL
577	161116	RTA00002714F.c.11.1.P.Seq	F	M00027837C:D09	CH04MAL
578	379211	RTA00002682F.p.20.1.P.Seq	F	M00040029A:G04	CH09LNL
579	430689	RTA00002669F.i.24.1.P.Seq	F	M00033243B:A05	CH08LNH
580	374122	RTA00002673F.l.22.2.P.Seq	F	M00039104D:C09	CH09LNL
581	376521	RTA00002677F.h.06.2.P.Seq	F	M00039398A:B10	CH09LNL
582	372834	RTA00002670F.b.12.2.P.Seq	F	M00033308B:G05	CH09LNL
583	379014	RTA00002682F.o.02.1.P.Seq	F	M00040022C:D06	CH09LNL
584	376344	RTA00002677F.b.18.2.P.Seq	F	M00039340B:G08	CH09LNL
585	376485	RTA00002676F.f.01.2.P.Seq	F	M00039288C:B11	CH09LNL
586	21661	RTA00002709F.e.18.1.P.Seq	F	M00005820C:E04	CH02COH
587	376539	RTA00002673F.b.18.1.P.Seq	F	M00039211A:C12	CH09LNL
588	431645	RTA00002669F.h.15.3.P.Seq	F	M00033223B:H07	CH08LNH
589	163293	RTA00002714F.c.20.1.P.Seq	F	M00028120D:F12	CH04MAL
590	178614	RTA00002713F.c.20.1.P.Seq	F	M00027263A:F10	CH04MAL
591	373274	RTA00002670F.i.22.2.P.Seq	F	M00033432B:H10	CH09LNL
592	379820	RTA00002679F.f.15.1.P.Seq	F	M00039677A:B08	CH09LNL
593	160536	RTA00002663F.f.10.1.P.Seq	F	M00022233C:A12	CH03MAH
594	373313	RTA00002671F.m.02.1.P.Seq	F	M00038328D:A03	CH09LNL
595	26429	RTA00002712F.k.23.1.P.Seq	F	M00027022D:G11	CH04MAL
596	17983	RTA00002711F.f.10.1.P.Seq	F	M00022979A:D05	CH03MAH
597	375388	RTA00002681F.j.22.2.P.Seq	F	M00039888B:D03	CH09LNL
598	63005	RTA00002712F.m.21.1.P.Seq	F	M00027094A:B03	CH04MAL
599	23030	RTA00002709F.b.10.2.P.Seq	F	M00005384A:C11	CH02COH
600	372946	RTA00002670F.l.07.2.P.Seq	F	M00033457D:A05	CH09LNL
601	375351	RTA00002680F.e.15.2.P.Seq	F	M00039792A:B04	CH09LNL
602	374502	RTA00002673F.i.08.1.P.Seq	F	M00039080C:H06	CH09LNL
603	376911	RTA00002682F.e.09.1.P.Seq	F	M00039938C:A08	CH09LNL
604	376024	RTA00002675F.n.15.1.P.Seq	F	M00039257D:C03	CH09LNL
605	377194	RTA00002679F.h.20.1.P.Seq	F	M00039685A:A08	CH09LNL
606	379643	RTA00002682F.g.08.1.P.Seq	F	M00039978A:G03	CH09LNL
607	379610	RTA00002680F.k.11.1.P.Seq	F	M00039815C:F09	CH09LNL
608	25613	RTA00002711F.g.06.1.P.Seq	F	M00023024D:F12	CH03MAH
609	207466	RTA00002664F.j.08.1.P.Seq	F	M00027733A:A02	CH04MAL
610	400052	RTA00002687F.h.13.1.P.Seq	F	M00040291D:C05	CH14EDT
611	21290	RTA00002712F.g.01.1.P.Seq	F	M00026859D:D01	CH04MAL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
612	375975	RTA00002675F.n.18.1.P.Seq	F	M00039258D:B08	CH09LNL
613	46804	RTA00002712F.n.19.1.P.Seq	F	M00027121D:C05	CH04MAL
614	69863	RTA00002712F.i.18.1.P.Seq	F	M00026935C:B04	CH04MAL
615	375285	RTA00002676F.g.18.2.P.Seq	F	M00039298B:B06	CH09LNL
616	373000	RTA00002670F.j.13.2.P.Seq	F	M00033437C:C03	CH09LNL
617	378679	RTA00002681F.f.16.1.P.Seq	F	M00039869B:F06	CH09LNL
618	45407	RTA00002712F.k.11.1.P.Seq	F	M00027016A:B06	CH04MAL
619	16838	RTA00002712F.e.23.1.P.Seq	F	M00026803A:F08	CH04MAL
620	186425	RTA00002713F.c.04.1.P.Seq	F	M00027236A:E04	CH04MAL
621	376485	RTA00002676F.e.24.2.P.Seq	F	M00039288C:B11	CH09LNL
622	41108	RTA00002712F.n.12.1.P.Seq	F	M00027108C:B03	CH04MAL
623	430876	RTA00002669F.c.02.1.P.Seq	F	M00033186C:D11	CH08LNH
624	185716	RTA00002713F.l.07.1.P.Seq	F	M00027537C:B01	CH04MAL
625	85338	RTA00002712F.b.18.1.P.Seq	F	M00023333D:C12	CH04MAL
626	185597	RTA00002713F.m.23.1.P.Seq	F	M00027596A:A10	CH04MAL
627	139348	RTA00002713F.k.23.1.P.Seq	F	M00027526D:F03	CH04MAL
628	454665	RTA00002693F.d.15.2.P.Seq	F	M00043164C:E12	CH19COP
629	186387	RTA00002713F.l.01.1.P.Seq	F	M00027528C:B10	CH04MAL
630	186387	RTA00002713F.k.24.1.P.Seq	F	M00027528C:B10	CH04MAL
631	21093	RTA00002708F.h.20.1.P.Seq	F	M00004308C:C06	CH01COH
632	20827	RTA00002710F.c.23.1.P.Seq	F	M00021671D:F12	CH03MAH
633	21290	RTA00002712F.f.24.1.P.Seq	F	M00026859D:D01	CH04MAL
634	17646	RTA00002710F.d.22.1.P.Seq	F	M00021908D:G12	CH03MAH
635	402817	RTA00002686F.a.10.1.P.Seq	F	M00039736D:G08	CH13EDT
636	42854	RTA00002713F.n.09.1.P.Seq	F	M00027615A:F10	CH04MAL
637	430876	RTA00002669F.c.02.3.P.Seq	F	M00033186C:D11	CH08LNH
638	378641	RTA00002679F.a.21.2.P.Seq	F	M00039655C:E08	CH09LNL
639	375848	RTA00002674F.m.03.2.P.Seq	F	M00039168C:A04	CH09LNL
640	36165	RTA00002708F.i.06.1.P.Seq	F	M00004340C:C07	CH01COH
641	456506	RTA00002694F.d.05.1.P.Seq	F	M00043492A:E01	CH20COHLV
642	374450	RTA00002672F.i.05.2.P.Seq	F	M00039014A:H10	CH09LNL
643	378949	RTA00002683F.o.21.2.P.Seq	F	M00040100D:B06	CH09LNL
644	373313	RTA00002671F.m.02.2.P.Seq	F	M00038328D:A03	CH09LNL
645	377861	RTA00002681F.m.20.1.P.Seq	F	M00039898A:A08	CH09LNL
646	431196	RTA00002669F.f.07.2.P.Seq	F	M00033204B:A07	CH08LNH
647	372795	RTA00002683F.a.06.1.P.Seq	F	M00040032A:B03	CH09LNL
648	42340	RTA00002661F.b.03.1.P.Seq	F	M00001439C:H06	CH01COH
649	374410	RTA00002674F.k.11.1.P.Seq	F	M00039158B:G12	CH09LNL
650	374623	RTA00002674F.a.01.2.P.Seq	F	M00039113D:A06	CH09LNL
651	431612	RTA00002669F.e.23.2.P.Seq	F	M00033202D:G06	CH08LNH
652	240615	RTA00002672F.e.19.1.P.Seq	F	M00038995D:E05	CH09LNL
653	428508	RTA00002666F.d.01.1.P.Seq	F	M00032545B:H09	CH08LNH
654	235780	RTA00002666F.d.03.1.P.Seq	F	M00032545D:G05	CH08LNH
655	17890	RTA00002710F.e.11.1.P.Seq	F	M00021955A:H02	CH03MAH
656	20100	RTA00002710F.g.11.1.P.Seq	F	M00022175D:D12	CH03MAH
657	4458	RTA00002710F.g.18.1.P.Seq	F	M00022184C:C11	CH03MAH
658	378347	RTA00002681F.h.07.2.P.Seq	F	M00039875D:A10	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
659	373477	RTA00002672F.b.23.1.P.Seq	F	M00038639B:C03	CH09LNL
660	15596	RTA00002710F.g.02.1.P.Seq	F	M00022135C:B05	CH03MAH
661	21028	RTA00002709F.l.09.1.P.Seq	F	M00007108B:A02	CH02COH
662	374063	RTA00002672F.h.15.2.P.Seq	F	M00039011D:C10	CH09LNL
663	380686	RTA00002684F.a.03.2.P.Seq	F	M00040107B:H07	CH09LNL
664	402950	RTA00002686F.g.11.1.P.Seq	F	M00040181B:H09	CH13EDT
665	428064	RTA00002665F.l.04.1.P.Seq	F	M00031485D:G02	CH08LNL
666	23310	RTA00002708F.e.10.1.P.Seq	F	M00004046C:A08	CH01COH
667	376233	RTA00002677F.b.15.2.P.Seq	F	M00039339C:F03	CH09LNL
668	375848	RTA00002674F.m.03.1.P.Seq	F	M00039168C:A04	CH09LNL
669	242251	RTA00002665F.i.08.1.P.Seq	F	M00028772C:B09	CH08LNL
670	374064	RTA00002672F.f.15.2.P.Seq	F	M00038999D:C11	CH09LNL
671	146260	RTA00002663F.d.17.1.P.Seq	F	M00022099B:D06	CH03MAH
672	375575	RTA00002677F.e.22.2.P.Seq	F	M00039385B:E09	CH09LNL
673	355518	RTA00002665F.c.15.3.P.Seq	F	M00028201B:H12	CH08LNL
674	184223	RTA00002662F.b.08.2.P.Seq	F	M00005539D:G01	CH02COH
675	213306	RTA00002664F.e.07.2.P.Seq	F	M00027078A:B02	CH04MAL
676	429566	RTA00002668F.b.04.1.P.Seq	F	M00032907A:G04	CH08LNL
677	378656	RTA00002682F.c.09.1.P.Seq	F	M00039927A:F04	CH09LNL
678	427760	RTA00002668F.e.23.1.P.Seq	F	M00032940A:C02	CH08LNL
679	372795	RTA00002683F.a.06.2.P.Seq	F	M00040032A:B03	CH09LNL
680	429340	RTA00002666F.f.12.1.P.Seq	F	M00032577A:C04	CH08LNL
681	429822	RTA00002668F.e.17.1.P.Seq	F	M00032939B:E07	CH08LNL
682	375224	RTA00002680F.d.22.2.P.Seq	F	M00039788B:A06	CH09LNL
683	378347	RTA00002681F.h.07.1.P.Seq	F	M00039875D:A10	CH09LNL
684	380109	RTA00002682F.i.17.1.P.Seq	F	M00039987C:G08	CH09LNL
685	379001	RTA00002683F.o.02.1.P.Seq	F	M00040097A:C12	CH09LNL
686	375348	RTA00002676F.i.12.3.P.Seq	F	M00039304D:B09	CH09LNL
687	377889	RTA00002672F.c.08.2.P.Seq	F	M00038661A:A07	CH09LNL
688	429883	RTA00002667F.g.05.1.P.Seq	F	M00032793A:F06	CH08LNL
689	377067	RTA00002682F.l.24.1.P.Seq	F	M00040014B:D01	CH09LNL
690	378001	RTA00002681F.m.22.2.P.Seq	F	M00039898D:C06	CH09LNL
691	45298	RTA00002710F.j.21.1.P.Seq	F	M00022433A:E02	CH03MAH
692	375431	RTA00002680F.f.03.1.P.Seq	F	M00039793D:C05	CH09LNL
693	377861	RTA00002681F.m.20.2.P.Seq	F	M00039898A:A08	CH09LNL
694	428610	RTA00002667F.e.09.1.P.Seq	F	M00032766C:A04	CH08LNL
695	20765	RTA00002710F.i.10.1.P.Seq	F	M00022363C:G12	CH03MAH
696	27601	RTA00002713F.e.23.1.P.Seq	F	M00027314C:D09	CH04MAL
697	430540	RTA00002668F.o.20.2.P.Seq	F	M00033140D:F06	CH08LNL
698	381024	RTA00002670F.h.23.2.P.Seq	F	M00033424B:A04	CH09LNL
699	16454	RTA00002709F.f.07.1.P.Seq	F	M00006599D:B02	CH02COH
700	372898	RTA00002670F.i.03.2.P.Seq	F	M00033424D:H12	CH09LNL
701	373681	RTA00002671F.d.20.1.P.Seq	F	M00038272D:F11	CH09LNL
702	82260	RTA00002684F.h.06.2.P.Seq	F	M00040307B:F01	CH09LNL
703	377343	RTA00002684F.g.04.2.P.Seq	F	M00040302C:A04	CH09LNL
704	374747	RTA00002676F.e.07.2.P.Seq	F	M00039286A:C06	CH09LNL
705	185848	RTA00002712F.m.11.1.P.Seq	F	M00027080A:B01	CH04MAL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
706	374311	RTA00002676F.e.18.2.P.Seq	F	M00039287C:A06	CH09LNL
707	278923	RTA00002667F.b.10.1.P.Seq	F	M00032726C:C01	CH08LNH
708	378667	RTA00002681F.b.11.2.P.Seq	F	M00039847A:F06	CH09LNL
709	380454	RTA00002673F.j.16.1.P.Seq	F	M00039084D:D07	CH09LNL
710	381576	RTA00002670F.i.04.2.P.Seq	F	M00033425A:C10	CH09LNL
711	375067	RTA00002675F.o.03.1.P.Seq	F	M00039260C:G03	CH09LNL
712	89706	RTA00002714F.a.11.1.P.Seq	F	M00027741B:F09	CH04MAL
713	10583	RTA00002711F.h.11.1.P.Seq	F	M00023100A:E12	CH03MAH
714	379982	RTA00002682F.i.16.1.P.Seq	F	M00039987C:E12	CH09LNL
715	378532	RTA00002680F.n.04.3.P.Seq	F	M00039828B:C05	CH09LNL
716	379776	RTA00002680F.a.22.2.P.Seq	F	M00039774C:A03	CH09LNL
717	374136	RTA00002673F.f.16.1.P.Seq	F	M00039072C:C03	CH09LNL
718	98471	RTA00002663F.j.21.1.P.Seq	F	M00022670D:H11	CH03MAH
719	125365	RTA00002668F.j.07.1.P.Seq	F	M00033019B:E10	CH08LNH
720	375431	RTA00002680F.f.03.2.P.Seq	F	M00039793D:C05	CH09LNL
721	62826	RTA00002661F.g.20.1.P.Seq	F	M00004105D:D05	CH01COH
722	379972	RTA00002679F.e.10.1.P.Seq	F	M00039672D:D10	CH09LNL
723	377554	RTA00002679F.f.10.1.P.Seq	F	M00039675D:B03	CH09LNL
724	230479	RTA00002664F.c.16.2.P.Seq	F	M00026915B:C06	CH04MAL
725	98872	RTA00002663F.j.19.1.P.Seq	F	M00022668B:B12	CH03MAH
726	42635	RTA00002679F.h.18.1.P.Seq	F	M00039684D:B08	CH09LNL
727	379044	RTA00002679F.a.10.2.P.Seq	F	M00039652B:D05	CH09LNL
728	96093	RTA00002663F.j.07.1.P.Seq	F	M00022640C:C12	CH03MAH
729	403642	RTA00002687F.d.01.2.P.Seq	F	M00039945C:F09	CH14EDT
730	400921	RTA00002685F.b.18.2.P.Seq	F	M00039371B:H06	CH12EDT
731	93587	RTA00002663F.k.10.1.P.Seq	F	M00022731A:D02	CH03MAH
732	79951	RTA00002713F.c.18.1.P.Seq	F	M00027258A:A07	CH04MAL
733	176509	RTA00002686F.b.09.1.P.Seq	F	M00039756B:H06	CH13EDT
734	451753	RTA00002694F.e.06.1.P.Seq	F	M00043634A:C10	CH20COHLV
735	186266	RTA00002713F.c.16.1.P.Seq	F	M00027256B:H09	CH04MAL
736	235052	RTA00002692F.a.15.2.P.Seq	F	M00042626B:D08	CH18CON
737	377233	RTA00002682F.e.23.1.P.Seq	F	M00039940D:G08	CH09LNL
738	378532	RTA00002680F.n.04.2.P.Seq	F	M00039828B:C05	CH09LNL
739	177932	RTA00002713F.b.22.1.P.Seq	F	M00027233B:C01	CH04MAL
740	9332	RTA00002712F.p.18.1.P.Seq	F	M00027179D:E06	CH04MAL
741	240318	RTA00002687F.d.04.2.P.Seq	F	M00039947A:D06	CH14EDT
742	404260	RTA00002687F.c.11.2.P.Seq	F	M00039942D:C01	CH14EDT
743	93767	RTA00002712F.g.09.1.P.Seq	F	M00026868C:E11	CH04MAL
744	185642	RTA00002712F.f.20.1.P.Seq	F	M00026856D:F02	CH04MAL
745	447544	RTA00002689F.e.18.3.P.Seq	F	M00042905D:D02	CH15CON
746	403274	RTA00002687F.b.10.2.P.Seq	F	M00039766A:G07	CH14EDT
747	404257	RTA00002687F.g.06.1.P.Seq	F	M00040208A:C03	CH14EDT
748	403868	RTA00002687F.k.05.2.P.Seq	F	M00040318C:H11	CH14EDT
749	450074	RTA00002691F.e.12.2.P.Seq	F	M00043392D:C11	CH17COHLV
750	404520	RTA00002687F.f.05.2.P.Seq	F	M00040202A:F05	CH14EDT
751	451789	RTA00002692F.b.04.2.P.Seq	F	M00042956C:B06	CH18CON
752	455178	RTA00002694F.b.19.1.P.Seq	F	M00043447A:C07	CH20COHLV

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
753	455136	RTA00002694F.a.08.1.P.Seq	F	M00042595A:B01	CH20COHLV
754	379001	RTA00002683F.o.02.2.P.Seq	F	M00040097A:C12	CH09LNL
755	374763	RTA00002673F.p.21.1.P.Seq	F	M00039118B:C05	CH09LNL
756	402508	RTA00002686F.o.15.1.P.Seq	F	M00040281D:B01	CH13EDT
757	431370	RTA00002669F.m.04.3.P.Seq	F	M00033288B:D12	CH08LNL
758	380500	RTA00002670F.p.19.1.P.Seq	F	M00033583B:E06	CH09LNL
759	376743	RTA00002678F.e.22.2.P.Seq	F	M00039461A:F04	CH09LNL
760	191690	RTA00002673F.m.19.1.P.Seq	F	M00039107C:E04	CH09LNL
761	374264	RTA00002671F.p.21.2.P.Seq	F	M00038620B:E09	CH09LNL
762	373020	RTA00002671F.b.20.2.P.Seq	F	M00033595A:C11	CH09LNL
763	375231	RTA00002671F.m.20.2.P.Seq	F	M00038387B:A07	CH09LNL
764	16180	RTA00002709F.j.17.1.P.Seq	F	M00006977D:A03	CH02COH
765	379403	RTA00002683F.c.17.2.P.Seq	F	M00040041C:C09	CH09LNL
766	375382	RTA00002677F.d.24.2.P.Seq	F	M00039381D:C02	CH09LNL
767	379653	RTA00002683F.c.03.2.P.Seq	F	M00040038D:G04	CH09LNL
768	377858	RTA00002681F.e.14.2.P.Seq	F	M00039864A:A07	CH09LNL
769	430861	RTA00002668F.h.18.1.P.Seq	F	M00032995C:C05	CH08LNL
770	376128	RTA00002677F.a.11.2.P.Seq	F	M00039334B:E03	CH09LNL
771	375009	RTA00002676F.n.20.2.P.Seq	F	M00039322A:F04	CH09LNL
772	429816	RTA00002667F.n.22.1.P.Seq	F	M00032871D:E11	CH08LNL
773	375657	RTA00002681F.h.13.2.P.Seq	F	M00039877C:C03	CH09LNL
774	427889	RTA00002666F.b.14.1.P.Seq	F	M00032530D:C02	CH08LNL
775	376761	RTA00002677F.g.03.2.P.Seq	F	M00039391D:F08	CH09LNL
776	44025	RTA00002684F.b.24.2.P.Seq	F	M00040115B:A04	CH09LNL
777	44025	RTA00002684F.c.01.2.P.Seq	F	M00040115B:A04	CH09LNL
778	392524	RTA00002681F.p.04.2.P.Seq	F	M00039909D:C02	CH09LNL
779	427252	RTA00002665F.b.13.1.P.Seq	F	M00028185B:A06	CH08LNL
780	374927	RTA00002673F.e.12.1.P.Seq	F	M00039068C:E06	CH09LNL
781	378226	RTA00002680F.g.09.1.P.Seq	F	M00039797C:G05	CH09LNL
782	217964	RTA00002664F.g.08.2.P.Seq	F	M00027299B:B12	CH04MAL
783	376368	RTA00002677F.b.14.2.P.Seq	F	M00039339A:H07	CH09LNL
784	377719	RTA00002677F.j.11.2.P.Seq	F	M00039407B:G02	CH09LNL
785	378081	RTA00002677F.e.16.2.P.Seq	F	M00039384C:E02	CH09LNL
786	89267	RTA00002662F.b.01.2.P.Seq	F	M00005445D:B01	CH02COH
787	374927	RTA00002673F.e.12.2.P.Seq	F	M00039068C:E06	CH09LNL
788	279054	RTA00002667F.b.23.1.P.Seq	F	M00032731B:C10	CH08LNL
789	377283	RTA00002682F.m.19.1.P.Seq	F	M00040016C:H12	CH09LNL
790	45318	RTA00002710F.l.05.1.P.Seq	F	M00022533A:A08	CH03MAH
791	188292	RTA00002664F.e.23.2.P.Seq	F	M00027162B:F05	CH04MAL
792	378872	RTA00002683F.c.20.2.P.Seq	F	M00040042B:A10	CH09LNL
793	427252	RTA00002665F.b.13.3.P.Seq	F	M00028185B:A06	CH08LNL
794	380618	RTA00002673F.j.12.2.P.Seq	F	M00039084C:G07	CH09LNL
795	35646	RTA00002667F.g.16.1.P.Seq	F	M00032797B:G02	CH08LNL
796	46407	RTA00002665F.c.10.3.P.Seq	F	M00028196D:A03	CH08LNL
797	373720	RTA00002674F.c.04.1.P.Seq	F	M00039124C:F03	CH09LNL
798	429693	RTA00002668F.f.05.1.P.Seq	F	M00032944B:B02	CH08LNL
799	377108	RTA00002678F.p.04.2.P.Seq	F	M00039636C:D11	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
800	375657	RTA00002681F.h.13.1.P.Seq	F	M00039877C:C03	CH09LNL
801	374868	RTA00002673F.d.08.2.P.Seq	F	M00039063B:D08	CH09LNL
802	428716	RTA00002667F.e.08.1.P.Seq	F	M00032766B:D12	CH08LNH
803	44025	RTA00002684F.c.01.1.P.Seq	F	M00040115B:A04	CH09LNL
804	430327	RTA00002668F.k.11.1.P.Seq	F	M00033033C:H01	CH08LNH
805	374328	RTA00002673F.c.24.1.P.Seq	F	M00039061B:F08	CH09LNL
806	376946	RTA00002682F.n.10.1.P.Seq	F	M00040019A:E01	CH09LNL
807	375522	RTA00002677F.n.08.2.P.Seq	F	M00039420D:D03	CH09LNL
808	395617	RTA00002687F.b.15.2.P.Seq	F	M00039767B:A04	CH14EDT
809	21686	RTA00002712F.g.05.1.P.Seq	F	M00026865B:A06	CH04MAL
810	452038	RTA00002692F.a.09.2.P.Seq	F	M00042623D:D07	CH18CON
811	25632	RTA00002711F.g.16.1.P.Seq	F	M00023042D:D02	CH03MAH
812	152487	RTA00002663F.e.12.1.P.Seq	F	M00022181C:D01	CH03MAH
813	378226	RTA00002680F.g.09.2.P.Seq	F	M00039797C:G05	CH09LNL
814	402446	RTA00002686F.c.04.1.P.Seq	F	M00040133B:B03	CH13EDT
815	403642	RTA00002687F.c.24.2.P.Seq	F	M00039945C:F09	CH14EDT
816	186359	RTA00002713F.g.24.1.P.Seq	F	M00027379C:B07	CH04MAL
817	404290	RTA00002688F.e.04.2.P.Seq	F	M00040395B:D11	CH14EDT
818	375443	RTA00002676F.g.19.2.P.Seq	F	M00039298B:D03	CH09LNL
819	380279	RTA00002673F.i.24.1.P.Seq	F	M00039082B:A05	CH09LNL
820	386110	RTA00002687F.e.06.1.P.Seq	F	M00039955C:C04	CH14EDT
821	380279	RTA00002673F.j.01.1.P.Seq	F	M00039082B:A05	CH09LNL
822	386986	RTA00002675F.p.06.1.P.Seq	F	M00039266A:B02	CH09LNL
823	186359	RTA00002713F.h.01.1.P.Seq	F	M00027379C:B07	CH04MAL
824	375611	RTA00002677F.o.20.2.P.Seq	F	M00039425D:E12	CH09LNL
825	378285	RTA00002679F.h.01.1.P.Seq	F	M00039681B:H09	CH09LNL
826	44025	RTA00002684F.b.24.1.P.Seq	F	M00040115B:A04	CH09LNL
827	25240	RTA00002711F.c.12.1.P.Seq	F	M00022854A:B03	CH03MAH
828	403700	RTA00002687F.g.03.2.P.Seq	F	M00040207B:D08	CH14EDT
829	404679	RTA00002687F.f.07.1.P.Seq	F	M00040203A:H06	CH14EDT
830	454806	RTA00002693F.b.12.2.P.Seq	F	M00043093C:G11	CH19COP
831	376829	RTA00002674F.f.21.2.P.Seq	F	M00039135D:G02	CH09LNL
832	456309	RTA00002694F.d.16.1.P.Seq	F	M00043518B:D06	CH20COHLV
833	374510	RTA00002672F.i.17.2.P.Seq	F	M00039015D:H04	CH09LNL
834	377232	RTA00002683F.m.08.2.P.Seq	F	M00040090B:G09	CH09LNL
835	375779	RTA00002672F.j.20.2.P.Seq	F	M00039025A:H09	CH09LNL
836	90746	RTA00002671F.a.07.2.P.Seq	F	M00033585D:A02	CH09LNL
837	453002	RTA00002692F.b.21.2.P.Seq	F	M00042970C:H10	CH18CON
838	402863	RTA00002686F.n.12.1.P.Seq	F	M00040273B:H12	CH13EDT
839	402526	RTA00002686F.p.07.1.P.Seq	F	M00040286C:C02	CH13EDT
840	412778	RTA00002685F.i.07.1.P.Seq	F	M00039533D:F04	CH12EDT
841	402273	RTA00002686F.j.18.1.P.Seq	F	M00040233C:G05	CH13EDT
842	374744	RTA00002670F.i.16.1.P.Seq	F	M00033427D:F01	CH09LNL
843	375764	RTA00002677F.o.18.2.P.Seq	F	M00039425C:G01	CH09LNL
844	428218	RTA00002667F.c.01.1.P.Seq	F	M00032731C:C07	CH08LNH
845	374809	RTA00002675F.h.01.1.P.Seq	F	M00039230D:D09	CH09LNL
846	20162	RTA00002710F.n.20.1.P.Seq	F	M00022662D:G11	CH03MAH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
847	375782	RTA00002677F.d.23.2.P.Seq	F	M00039381C:H08	CH09LNL
848	372958	RTA00002672F.c.02.1.P.Seq	F	M00038639D:F07	CH09LNL
849	403940	RTA00002688F.d.07.2.P.Seq	F	M00040387D:H05	CH14EDT
850	8490	RTA00002711F.g.03.1.P.Seq	F	M00023020C:G08	CH03MAH
851	374809	RTA00002675F.g.24.1.P.Seq	F	M00039230D:D09	CH09LNL
852	377788	RTA00002684F.g.24.2.P.Seq	F	M00040305C:H06	CH09LNL
853	13847	RTA00002711F.f.09.1.P.Seq	F	M00022976C:F04	CH03MAH
854	374172	RTA00002673F.k.16.1.P.Seq	F	M00039097D:D06	CH09LNL
855	380314	RTA00002682F.l.07.1.P.Seq	F	M00040009D:B07	CH09LNL
856	47231	RTA00002714F.b.15.1.P.Seq	F	M00027813C:F01	CH04MAL
857	400287	RTA00002685F.k.10.1.P.Seq	F	M00039584C:C01	CH12EDT
858	400533	RTA00002685F.a.02.2.P.Seq	F	M00039181D:E05	CH12EDT
859	447594	RTA00002689F.c.07.1.P.Seq	F	M00042696B:E05	CH15CON
860	147357	RTA00002711F.e.15.1.P.Seq	F	M00022928B:C01	CH03MAH
861	401141	RTA00002685F.o.22.2.P.Seq	F	M00039642D:B12	CH12EDT
862	404620	RTA00002687F.c.03.1.P.Seq	F	M00039770A:G11	CH14EDT
863	24360	RTA00002709F.l.20.1.P.Seq	F	M00007149A:G02	CH02COH
864	380618	RTA00002673F.j.12.1.P.Seq	F	M00039084C:G07	CH09LNL
865	448446	RTA00002690F.d.09.3.P.Seq	F	M00042797D:D10	CH16COP
866	402313	RTA00002686F.f.18.1.P.Seq	F	M00040174D:G03	CH13EDT
867	273151	RTA00002685F.c.05.2.P.Seq	F	M00039374C:H02	CH12EDT
868	404172	RTA00002687F.d.17.2.P.Seq	F	M00039951B:B12	CH14EDT
869	263630	RTA00002694F.e.10.1.P.Seq	F	M00043637C:H01	CH20COHLV
870	404277	RTA00002687F.d.18.1.P.Seq	F	M00039951B:C03	CH14EDT
871	403557	RTA00002687F.d.10.1.P.Seq	F	M00039948A:E03	CH14EDT
872	375161	RTA00002676F.m.24.2.P.Seq	F	M00039319B:H12	CH09LNL
873	376829	RTA00002674F.f.21.1.P.Seq	F	M00039135D:G02	CH09LNL
874	372958	RTA00002672F.c.02.2.P.Seq	F	M00038639D:F07	CH09LNL
875	21578	RTA00002709F.a.24.1.P.Seq	F	M00005351C:G05	CH02COH
876	402506	RTA00002686F.b.17.1.P.Seq	F	M00039760B:B08	CH13EDT
877	141731	RTA00002713F.b.04.1.P.Seq	F	M00027212D:E03	CH04MAL
878	37411	RTA00002661F.e.11.1.P.Seq	F	M00003770A:E05	CH01COH
879	372537	RTA00002670F.c.05.2.P.Seq	F	M00033345D:A09	CH09LNL
880	380834	RTA00002670F.c.08.2.P.Seq	F	M00033346C:A05	CH09LNL
881	401492	RTA00002685F.n.17.2.P.Seq	F	M00039609D:F07	CH12EDT
882	99998	RTA00002662F.b.23.2.P.Seq	F	M00006712C:H09	CH02COH
883	404311	RTA00002688F.d.21.2.P.Seq	F	M00040394A:D04	CH14EDT
884	231084	RTA00002664F.c.18.2.P.Seq	F	M00026918B:D01	CH04MAL
885	447679	RTA00002689F.b.11.3.P.Seq	F	M00042560A:F12	CH15CON
886	377012	RTA00002682F.d.17.1.P.Seq	F	M00039936C:C05	CH09LNL
887	226207	RTA00002664F.d.21.2.P.Seq	F	M00027035D:C06	CH04MAL
888	446183	RTA00002689F.a.12.1.P.Seq	F	M00042534A:A05	CH15CON
889	428508	RTA00002666F.c.24.1.P.Seq	F	M00032545B:H09	CH08LNH
890	157648	RTA00002714F.b.20.1.P.Seq	F	M00027818C:C07	CH04MAL
891	404609	RTA00002688F.b.15.2.P.Seq	F	M00040377C:G07	CH14EDT
892	400464	RTA00002685F.l.10.1.P.Seq	F	M00039590D:D02	CH12EDT
893	379108	RTA00002685F.l.12.1.P.Seq	F	M00039591C:D06	CH12EDT

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
894	374639	RTA00002676F.d.21.2.P.Seq	F	M00039284D:B12	CH09LNL
895	380674	RTA00002673F.j.14.2.P.Seq	F	M00039084C:H04	CH09LNL
896	380674	RTA00002673F.j.14.1.P.Seq	F	M00039084C:H04	CH09LNL
897	188972	RTA00002664F.d.20.2.P.Seq	F	M00027030C:H06	CH04MAL
898	402835	RTA00002686F.c.01.1.P.Seq	F	M00040131D:G08	CH13EDT
899	403774	RTA00002687F.d.08.2.P.Seq	F	M00039947C:G03	CH14EDT
900	374606	RTA00002673F.j.23.2.P.Seq	F	M00039096A:A05	CH09LNL
901	192535	RTA00002663F.m.14.1.P.Seq	F	M00022925C:A08	CH03MAH
902	377926	RTA00002680F.l.16.2.P.Seq	F	M00039820B:B06	CH09LNL
903	186055	RTA00002712F.i.11.1.P.Seq	F	M00026926A:E10	CH04MAL
904	380498	RTA00002684F.f.11.2.P.Seq	F	M00040129D:E10	CH09LNL
905	400236	RTA00002685F.i.18.2.P.Seq	F	M00039561A:B07	CH12EDT
906	401070	RTA00002688F.d.12.2.P.Seq	F	M00040390A:H02	CH14EDT
907	452622	RTA00002692F.b.14.2.P.Seq	F	M00042962D:C05	CH18CON
908	235052	RTA00002692F.a.15.1.P.Seq	F	M00042626B:D08	CH18CON
909	452221	RTA00002692F.c.13.2.P.Seq	F	M00042986C:G12	CH18CON
910	404581	RTA00002687F.g.11.2.P.Seq	F	M00040208D:G09	CH14EDT
911	376925	RTA00002687F.e.14.2.P.Seq	F	M00039957C:C09	CH14EDT
912	400287	RTA00002685F.k.10.2.P.Seq	F	M00039584C:C01	CH12EDT
913	403242	RTA00002687F.l.05.2.P.Seq	F	M00040323B:C12	CH14EDT
914	453313	RTA00002693F.a.07.2.P.Seq	F	M00042614B:B05	CH19COP
915	452633	RTA00002692F.f.11.2.P.Seq	F	M00043067D:D10	CH18CON
916	447679	RTA00002689F.b.11.1.P.Seq	F	M00042560A:F12	CH15CON
917	452398	RTA00002692F.f.17.1.P.Seq	F	M00043125C:A11	CH18CON
918	449797	RTA00002691F.b.22.3.P.Seq	F	M00043334B:A10	CH17COHLV
919	403916	RTA00002687F.j.11.2.P.Seq	F	M00040314D:H05	CH14EDT
920	236906	RTA00002693F.d.05.2.P.Seq	F	M00043154A:B07	CH19COP
921	404161	RTA00002687F.e.20.2.P.Seq	F	M00039958C:B09	CH14EDT
922	386110	RTA00002687F.e.06.2.P.Seq	F	M00039955C:C04	CH14EDT
923	451512	RTA00002691F.b.02.3.P.Seq	F	M00043305B:G02	CH17COHLV
924	400517	RTA00002687F.k.15.2.P.Seq	F	M00040320D:F02	CH14EDT
925	403578	RTA00002687F.i.01.2.P.Seq	F	M00040296D:E09	CH14EDT
926	403578	RTA00002687F.h.24.2.P.Seq	F	M00040296D:E09	CH14EDT
927	403371	RTA00002687F.h.19.2.P.Seq	F	M00040294D:D12	CH14EDT
928	452531	RTA00002692F.f.16.1.P.Seq	F	M00043125A:B11	CH18CON
929	454453	RTA00002693F.f.15.2.P.Seq	F	M00043215A:D02	CH19COP
930	238270	RTA00002692F.e.07.2.P.Seq	F	M00043028A:G05	CH18CON
931	14583	RTA00002687F.f.08.2.P.Seq	F	M00040203B:A05	CH14EDT
932	400464	RTA00002685F.l.10.2.P.Seq	F	M00039590D:D02	CH12EDT
933	404642	RTA00002687F.f.02.2.P.Seq	F	M00040201C:G11	CH14EDT
934	380413	RTA00002680F.k.19.1.P.Seq	F	M00039816C:D05	CH09LNL
935	287963	RTA00002693F.c.20.2.P.Seq	F	M00043148C:A09	CH19COP
936	20847	RTA00002710F.d.09.1.P.Seq	F	M00021852D:A05	CH03MAH
937	456531	RTA00002694F.b.18.1.P.Seq	F	M00043446C:E12	CH20COHLV
938	450463	RTA00002694F.a.12.1.P.Seq	F	M00042596C:D07	CH20COHLV
939	456713	RTA00002694F.d.13.1.P.Seq	F	M00043513D:G08	CH20COHLV
940	455508	RTA00002694F.a.15.1.P.Seq	F	M00042597B:E12	CH20COHLV

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
941	376138	RTA00002674F.m.05.2.P.Seq	F	M00039169A:E12	CH09LNL
942	402831	RTA00002686F.m.03.1.P.Seq	F	M00040264D:G05	CH13EDT
943	373820	RTA00002674F.d.06.2.P.Seq	F	M00039127A:G11	CH09LNL
944	85388	RTA00002674F.c.06.2.P.Seq	F	M00039124C:H08	CH09LNL
945	400732	RTA00002685F.k.24.2.P.Seq	F	M00039587C:F12	CH12EDT
946	431629	RTA00002669F.l.14.1.P.Seq	F	M00033276B:G08	CH08LNH
947	449349	RTA00002690F.d.12.3.P.Seq	F	M00042802C:C04	CH16COP
948	401124	RTA00002685F.o.11.2.P.Seq	F	M00039629D:B04	CH12EDT
949	453233	RTA00002693F.a.01.2.P.Seq	F	M00042611A:A06	CH19COP
950	124813	RTA00002685F.j.10.2.P.Seq	F	M00039564B:C01	CH12EDT
951	454627	RTA00002693F.f.09.2.P.Seq	F	M00043210C:E05	CH19COP
952	169464	RTA00002663F.i.19.1.P.Seq	F	M00022602A:E09	CH03MAH
953	451654	RTA00002692F.f.02.2.P.Seq	F	M00043044D:A09	CH18CON
954	406092	RTA00002685F.k.11.2.P.Seq	F	M00039584C:C11	CH12EDT
955	453501	RTA00002693F.d.14.2.P.Seq	F	M00043162D:C12	CH19COP
956	450845	RTA00002691F.f.10.1.P.Seq	F	M00043410C:A09	CH17COHLV
957	448177	RTA00002690F.e.12.1.P.Seq	F	M00042839B:B11	CH16COP
958	402617	RTA00002686F.b.21.1.P.Seq	F	M00040131B:D11	CH13EDT
959	378014	RTA00002680F.g.17.1.P.Seq	F	M00039799A:D10	CH09LNL
960	124813	RTA00002685F.j.10.1.P.Seq	F	M00039564B:C01	CH12EDT
961	29450	RTA00002663F.d.07.1.P.Seq	F	M00022054A:H03	CH03MAH
962	400486	RTA00002685F.e.02.1.P.Seq	F	M00039496B:D08	CH12EDT
963	44753	RTA00002713F.f.05.1.P.Seq	F	M00027324D:C05	CH04MAL
964	448177	RTA00002690F.e.12.2.P.Seq	F	M00042839B:B11	CH16COP
965	447697	RTA00002689F.e.15.3.P.Seq	F	M00042905A:F11	CH15CON
966	240318	RTA00002687F.d.04.1.P.Seq	F	M00039947A:D06	CH14EDT
967	451620	RTA00002691F.d.20.3.P.Seq	F	M00043379D:H02	CH17COHLV
968	400157	RTA00002685F.i.20.2.P.Seq	F	M00039561B:A09	CH12EDT
969	400276	RTA00002685F.h.16.2.P.Seq	F	M00039528B:B12	CH12EDT
970	449779	RTA00002691F.d.04.3.P.Seq	F	M00043367B:A08	CH17COHLV
971	400157	RTA00002685F.i.20.1.P.Seq	F	M00039561B:A09	CH12EDT
972	238133	RTA00002685F.e.03.2.P.Seq	F	M00039496B:H09	CH12EDT
973	452015	RTA00002692F.c.07.2.P.Seq	F	M00042981B:D11	CH18CON
974	400732	RTA00002685F.l.01.2.P.Seq	F	M00039587C:F12	CH12EDT
975	24984	RTA00002711F.d.21.1.P.Seq	F	M00022910A:A06	CH03MAH
976	449040	RTA00002690F.e.14.2.P.Seq	F	M00042841D:H07	CH16COP
977	377481	RTA00002671F.i.15.3.P.Seq	F	M00038303A:C03	CH09LNL
978	400910	RTA00002685F.b.07.1.P.Seq	F	M00039367B:H02	CH12EDT
979	376945	RTA00002682F.k.23.1.P.Seq	F	M00040007D:A06	CH09LNL
980	15906	RTA00002709F.e.14.1.P.Seq	F	M00005805D:D12	CH02COH
981	452781	RTA00002692F.b.16.2.P.Seq	F	M00042966B:F07	CH18CON
982	415294	RTA00002686F.f.14.1.P.Seq	F	M00040173D:B05	CH13EDT
983	401644	RTA00002685F.n.16.1.P.Seq	F	M00039608D:H01	CH12EDT
984	404402	RTA00002687F.a.19.2.P.Seq	F	M00039761D:E10	CH14EDT
985	401709	RTA00002685F.n.24.2.P.Seq	F	M00039624A:H09	CH12EDT
986	401644	RTA00002685F.n.16.2.P.Seq	F	M00039608D:H01	CH12EDT
987	452531	RTA00002692F.f.16.2.P.Seq	F	M00043125A:B11	CH18CON

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
988	400910	RTA00002685F.b.07.2.P.Seq	F	M00039367B:H02	CH12EDT
989	449235	RTA00002690F.a.22.3.P.Seq	F	M00042439B:B03	CH16COP
990	449794	RTA00002691F.c.22.2.P.Seq	F	M00043361B:A01	CH17COHLV
991	400921	RTA00002685F.b.18.1.P.Seq	F	M00039371B:H06	CH12EDT
992	373874	RTA00002672F.c.22.2.P.Seq	F	M00038663D:H10	CH09LNL
993	401050	RTA00002685F.e.09.2.P.Seq	F	M00039499C:A04	CH12EDT
994	453237	RTA00002693F.c.02.2.P.Seq	F	M00043108A:F06	CH19COP
995	449294	RTA00002690F.c.13.3.P.Seq	F	M00042770C:C04	CH16COP
996	404260	RTA00002687F.c.11.1.P.Seq	F	M00039942D:C01	CH14EDT
997	378014	RTA00002680F.g.17.2.P.Seq	F	M00039799A:D10	CH09LNL
998	404726	RTA00002688F.a.18.2.P.Seq	F	M00040371C:H05	CH14EDT
999	451347	RTA00002691F.b.11.3.P.Seq	F	M00043311C:E03	CH17COHLV
1000	401154	RTA00002685F.e.06.2.P.Seq	F	M00039497C:C06	CH12EDT
1001	401870	RTA00002686F.b.22.1.P.Seq	F	M00040131C:F03	CH13EDT
1002	400170	RTA00002685F.b.03.2.P.Seq	F	M00039366C:B07	CH12EDT
1003	25387	RTA00002711F.f.19.1.P.Seq	F	M00023001C:C08	CH03MAH
1004	377085	RTA00002678F.n.14.1.P.Seq	F	M00039619B:D02	CH09LNL
1005	403530	RTA00002688F.a.09.2.P.Seq	F	M00040368A:F01	CH14EDT
1006	372930	RTA00002670F.j.12.2.P.Seq	F	M00033437C:A07	CH09LNL
1007	401120	RTA00002685F.c.23.2.P.Seq	F	M00039379A:B03	CH12EDT
1008	403397	RTA00002687F.h.02.2.P.Seq	F	M00040219B:D02	CH14EDT
1009	449337	RTA00002690F.c.18.3.P.Seq	F	M00042774C:C05	CH16COP
1010	403561	RTA00002688F.d.06.2.P.Seq	F	M00040387C:E07	CH14EDT
1011	134182	RTA00002692F.d.13.2.P.Seq	F	M00043011A:H12	CH18CON
1012	377085	RTA00002678F.n.14.2.P.Seq	F	M00039619B:D02	CH09LNL
1013	376138	RTA00002674F.m.05.1.P.Seq	F	M00039169A:E12	CH09LNL
1014	401154	RTA00002685F.e.06.1.P.Seq	F	M00039497C:C06	CH12EDT
1015	449825	RTA00002691F.b.14.3.P.Seq	F	M00043320B:A07	CH17COHLV
1016	403896	RTA00002687F.a.04.2.P.Seq	F	M00039746C:H05	CH14EDT
1017	377632	RTA00002683F.l.18.2.P.Seq	F	M00040087D:F08	CH09LNL
1018	450845	RTA00002691F.f.10.2.P.Seq	F	M00043410C:A09	CH17COHLV
1019	450045	RTA00002691F.e.10.2.P.Seq	F	M00043391A:C10	CH17COHLV
1020	402962	RTA00002686F.d.22.1.P.Seq	F	M00040147D:H11	CH13EDT
1021	427674	RTA00002665F.i.10.1.P.Seq	F	M00028775D:F03	CH08LNL
1022	403252	RTA00002688F.c.15.2.P.Seq	F	M00040383D:C04	CH14EDT
1023	452038	RTA00002692F.a.09.1.P.Seq	F	M00042623D:D07	CH18CON
1024	401553	RTA00002685F.d.08.2.P.Seq	F	M00039482B:G02	CH12EDT
1025	451092	RTA00002691F.d.17.3.P.Seq	F	M00043377A:C03	CH17COHLV
1026	403978	RTA00002687F.g.09.2.P.Seq	F	M00040208B:A07	CH14EDT
1027	377186	RTA00002682F.m.07.1.P.Seq	F	M00040014D:F03	CH09LNL
1028	404679	RTA00002687F.f.07.2.P.Seq	F	M00040203A:H06	CH14EDT
1029	373875	RTA00002674F.c.05.1.P.Seq	F	M00039124C:H02	CH09LNL
1030	128841	RTA00002685F.o.15.2.P.Seq	F	M00039630C:H04	CH12EDT
1031	33971	RTA00002713F.h.13.1.P.Seq	F	M00027392B:H02	CH04MAL
1032	332878	RTA00002666F.h.13.1.P.Seq	F	M00032597C:B01	CH08LNL
1033	400781	RTA00002685F.j.03.2.P.Seq	F	M00039562B:G02	CH12EDT
1034	456456	RTA00002694F.b.22.1.P.Seq	F	M00043449A:E12	CH20COHLV

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1035	402337	RTA00002686F.l.07.1.P.Seq	F	M00040257D:H10	CH13EDT
1036	401974	RTA00002686F.i.15.1.P.Seq	F	M00040223A:C05	CH13EDT
1037	455141	RTA00002694F.b.14.1.P.Seq	F	M00043440C:B07	CH20COHLV
1038	402057	RTA00002686F.l.14.1.P.Seq	F	M00040260C:D04	CH13EDT
1039	402555	RTA00002686F.m.14.1.P.Seq	F	M00040267C:C04	CH13EDT
1040	406092	RTA00002685F.k.11.1.P.Seq	F	M00039584C:C11	CH12EDT
1041	374351	RTA00002674F.i.20.1.P.Seq	F	M00039147A:F10	CH09LNL
1042	402365	RTA00002686F.j.08.1.P.Seq	F	M00040230A:H02	CH13EDT
1043	401828	RTA00002686F.j.14.1.P.Seq	F	M00040232D:B07	CH13EDT
1044	447669	RTA00002689F.a.15.2.P.Seq	F	M00042513B:E06	CH15CON
1045	402588	RTA00002686F.k.18.1.P.Seq	F	M00040254B:C10	CH13EDT
1046	244858	RTA00002686F.l.02.1.P.Seq	F	M00040256A:A06	CH13EDT
1047	402339	RTA00002686F.i.20.1.P.Seq	F	M00040226A:H10	CH13EDT
1048	401766	RTA00002686F.o.16.1.P.Seq	F	M00040282A:A03	CH13EDT
1049	402952	RTA00002686F.g.14.1.P.Seq	F	M00040181D:H10	CH13EDT
1050	449669	RTA00002690F.c.10.3.P.Seq	F	M00042767B:G10	CH16COP
1051	400520	RTA00002685F.g.04.2.P.Seq	F	M00039512C:D06	CH12EDT
1052	403868	RTA00002687F.k.05.1.P.Seq	F	M00040318C:H11	CH14EDT
1053	403242	RTA00002687F.l.05.1.P.Seq	F	M00040323B:C12	CH14EDT
1054	402182	RTA00002686F.f.16.1.P.Seq	F	M00040174C:E10	CH13EDT
1055	449269	RTA00002690F.c.12.3.P.Seq	F	M00042770B:B12	CH16COP
1056	401290	RTA00002685F.n.10.1.P.Seq	F	M00039606B:D08	CH12EDT
1057	448420	RTA00002690F.d.07.3.P.Seq	F	M00042790C:C07	CH16COP
1058	374351	RTA00002674F.i.20.2.P.Seq	F	M00039147A:F10	CH09LNL
1059	448464	RTA00002690F.c.08.3.P.Seq	F	M00042765C:D04	CH16COP
1060	401079	RTA00002685F.p.05.2.P.Seq	F	M00039643C:B04	CH12EDT
1061	403916	RTA00002687F.j.11.1.P.Seq	F	M00040314D:H05	CH14EDT
1062	401374	RTA00002685F.p.07.2.P.Seq	F	M00039645C:E01	CH12EDT
1063	400503	RTA00002685F.k.02.1.P.Seq	F	M00039570B:D10	CH12EDT
1064	219825	RTA00002664F.h.06.2.P.Seq	F	M00027396D:G08	CH04MAL
1065	377732	RTA00002681F.p.09.2.P.Seq	F	M00039910C:G10	CH09LNL
1066	380348	RTA00002684F.d.12.1.P.Seq	F	M00040121B:C05	CH09LNL
1067	449549	RTA00002690F.a.09.3.P.Seq	F	M00042431C:F01	CH16COP
1068	402223	RTA00002686F.f.05.1.P.Seq	F	M00040169B:F08	CH13EDT
1069	401727	RTA00002685F.o.23.2.P.Seq	F	M00039642D:H09	CH12EDT
1070	379878	RTA00002682F.h.12.1.P.Seq	F	M00039984A:C02	CH09LNL
1071	378602	RTA00002681F.a.08.2.P.Seq	F	M00039839C:E05	CH09LNL
1072	448065	RTA00002690F.c.22.3.P.Seq	F	M00042781A:A07	CH16COP
1073	403493	RTA00002687F.j.03.1.P.Seq	F	M00040313D:E04	CH14EDT
1074	400517	RTA00002687F.k.15.1.P.Seq	F	M00040320D:F02	CH14EDT
1075	456636	RTA00002694F.e.05.1.P.Seq	F	M00043632D:F09	CH20COHLV
1076	400101	RTA00002685F.o.04.1.P.Seq	F	M00039625B:G08	CH12EDT
1077	403578	RTA00002687F.i.01.1.P.Seq	F	M00040296D:E09	CH14EDT
1078	402419	RTA00002686F.g.20.1.P.Seq	F	M00040184C:A11	CH13EDT
1079	375161	RTA00002676F.n.01.2.P.Seq	F	M00039319B:H12	CH09LNL
1080	401851	RTA00002686F.d.07.1.P.Seq	F	M00040143A:H05	CH13EDT
1081	400567	RTA00002685F.a.14.2.P.Seq	F	M00039361B:E01	CH12EDT

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1082	376641	RTA00002677F.d.01.2.P.Seq	F	M00039345A:D09	CH09LNL
1083	376641	RTA00002677F.c.24.2.P.Seq	F	M00039345A:D09	CH09LNL
1084	400450	RTA00002685F.j.22.1.P.Seq	F	M00039570A:D10	CH12EDT
1085	375373	RTA00002676F.h.12.1.P.Seq	F	M00039300C:C09	CH09LNL
1086	375373	RTA00002676F.h.12.2.P.Seq	F	M00039300C:C09	CH09LNL
1087	413643	RTA00002685F.n.05.2.P.Seq	F	M00039604D:G03	CH12EDT
1088	448874	RTA00002690F.c.02.3.P.Seq	F	M00042759B:G11	CH16COP
1089	376511	RTA00002674F.h.04.1.P.Seq	F	M00039140A:B08	CH09LNL
1090	374040	RTA00002674F.h.21.1.P.Seq	F	M00039142D:B11	CH09LNL
1091	454132	RTA00002693F.e.18.1.P.Seq	F	M00043191A:A07	CH19COP
1092	404581	RTA00002687F.g.11.1.P.Seq	F	M00040208D:G09	CH14EDT
1093	260521	RTA00002689F.c.13.1.P.Seq	F	M00042702B:G02	CH15CON
1094	379564	RTA00002687F.o.12.1.P.Seq	F	M00040346A:C11	CH14EDT
1095	452491	RTA00002692F.f.05.2.P.Seq	F	M00043046D:B11	CH18CON
1096	403541	RTA00002687F.p.20.2.P.Seq	F	M00040364A:E05	CH14EDT
1097	404636	RTA00002688F.b.11.2.P.Seq	F	M00040376C:G02	CH14EDT
1098	379564	RTA00002687F.o.12.2.P.Seq	F	M00040346A:C11	CH14EDT
1099	451548	RTA00002691F.b.09.3.P.Seq	F	M00043310C:G06	CH17COHLV
1100	454308	RTA00002693F.f.14.1.P.Seq	F	M00043213B:B12	CH19COP
1101	401184	RTA00002685F.d.04.2.P.Seq	F	M00039380C:C09	CH12EDT
1102	401290	RTA00002685F.n.10.2.P.Seq	F	M00039606B:D08	CH12EDT
1103	400101	RTA00002685F.o.04.2.P.Seq	F	M00039625B:G08	CH12EDT
1104	454308	RTA00002693F.f.14.2.P.Seq	F	M00043213B:B12	CH19COP
1105	452622	RTA00002692F.b.14.1.P.Seq	F	M00042962D:C05	CH18CON
1106	450012	RTA00002691F.d.09.3.P.Seq	F	M00043370B:C08	CH17COHLV
1107	400503	RTA00002685F.k.02.2.P.Seq	F	M00039570B:D10	CH12EDT
1108	400450	RTA00002685F.j.22.2.P.Seq	F	M00039570A:D10	CH12EDT
1109	446166	RTA00002689F.c.17.1.P.Seq	F	M00042711B:A11	CH15CON
1110	456233	RTA00002694F.e.08.1.P.Seq	F	M00043636B:C06	CH20COHLV
1111	25443	RTA00002710F.d.15.1.P.Seq	F	M00021866D:A03	CH03MAH
1112	404119	RTA00002688F.d.17.2.P.Seq	F	M00040392C:B12	CH14EDT
1113	403642	RTA00002687F.d.01.1.P.Seq	F	M00039945C:F09	CH14EDT
1114	403493	RTA00002687F.j.03.2.P.Seq	F	M00040313D:E04	CH14EDT
1115	454132	RTA00002693F.e.18.2.P.Seq	F	M00043191A:A07	CH19COP
1116	450607	RTA00002691F.d.12.3.P.Seq	F	M00043372C:G05	CH17COHLV
1117	451718	RTA00002692F.e.24.2.P.Seq	F	M00043044B:A12	CH18CON
1118	453907	RTA00002693F.b.08.2.P.Seq	F	M00043087B:G07	CH19COP
1119	447669	RTA00002689F.a.15.3.P.Seq	F	M00042538B:E06	CH15CON
1120	404044	RTA00002687F.p.11.1.P.Seq	F	M00040351D:A11	CH14EDT
1121	449617	RTA00002690F.e.16.2.P.Seq	F	M00042849D:F11	CH16COP
1122	452723	RTA00002692F.e.18.2.P.Seq	F	M00043036C:E05	CH18CON
1123	270014	RTA00002685F.i.15.2.P.Seq	F	M00039536C:H11	CH12EDT
1124	401198	RTA00002685F.i.14.2.P.Seq	F	M00039536C:C10	CH12EDT
1125	452414	RTA00002692F.e.12.1.P.Seq	F	M00043032C:A10	CH18CON
1126	453019	RTA00002692F.d.18.2.P.Seq	F	M00043013A:H10	CH18CON
1127	403642	RTA00002687F.c.24.1.P.Seq	F	M00039945C:F09	CH14EDT
1128	401437	RTA00002685F.c.18.2.P.Seq	F	M00039377D:E12	CH12EDT

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1129	452414	RTA00002692F.e.12.2.P.Seq	F	M00043032C:A10	CH18CON
1130	404122	RTA00002687F.n.10.1.P.Seq	F	M00040334D:B02	CH14EDT
1131	400567	RTA00002685F.a.14.1.P.Seq	F	M00039361B:E01	CH12EDT
1132	401437	RTA00002685F.c.18.1.P.Seq	F	M00039377D:E12	CH12EDT
1133	404642	RTA00002687F.f.02.1.P.Seq	F	M00040201C:G11	CH14EDT
1134	376007	RTA00002676F.f.22.2.P.Seq	F	M00039293B:C11	CH09LNL
1135	402835	RTA00002686F.b.24.1.P.Seq	F	M00040131D:G08	CH13EDT
1136	403774	RTA00002687F.d.08.1.P.Seq	F	M00039947C:G03	CH14EDT
1137	45505	RTA00002712F.d.04.1.P.Seq	F	M00023377B:F01	CH04MAL
1138	452071	RTA00002692F.c.05.2.P.Seq	F	M00042979B:E02	CH18CON
1139	449832	RTA00002691F.e.13.1.P.Seq	F	M00043393A:B08	CH17COHLV
1140	379004	RTA00002683F.n.09.2.P.Seq	F	M00040093B:C02	CH09LNL
1141	455211	RTA00002694F.b.07.1.P.Seq	F	M00043430B:C02	CH20COHLV
1142	379021	RTA00002683F.n.13.2.P.Seq	F	M00040093D:D03	CH09LNL
1143	376279	RTA00002680F.d.10.2.P.Seq	F	M00039785D:G05	CH09LNL
1144	374373	RTA00002681F.n.21.1.P.Seq	F	M00039903A:H07	CH09LNL
1145	97668	RTA00002686F.d.19.1.P.Seq	F	M00040145D:D03	CH13EDT
1146	400407	RTA00002685F.a.05.2.P.Seq	F	M00039184A:D03	CH12EDT
1147	402904	RTA00002686F.n.15.1.P.Seq	F	M00040274A:H11	CH13EDT
1148	403912	RTA00002687F.j.19.1.P.Seq	F	M00040317A:H03	CH14EDT
1149	400511	RTA00002685F.b.23.2.P.Seq	F	M00039372C:D12	CH12EDT
1150	402746	RTA00002686F.a.14.1.P.Seq	F	M00039740B:F10	CH13EDT
1151	403849	RTA00002687F.n.09.2.P.Seq	F	M00040333D:G05	CH14EDT
1152	401471	RTA00002685F.o.10.1.P.Seq	F	M00039629B:F01	CH12EDT
1153	404362	RTA00002687F.o.06.2.P.Seq	F	M00040342B:D12	CH14EDT
1154	373641	RTA00002677F.i.09.2.P.Seq	F	M00039403A:G12	CH09LNL
1155	401952	RTA00002686F.j.10.1.P.Seq	F	M00040231B:C08	CH13EDT
1156	400685	RTA00002685F.m.09.2.P.Seq	F	M00039597D:F04	CH12EDT
1157	402689	RTA00002686F.n.05.1.P.Seq	F	M00040271B:E12	CH13EDT
1158	380462	RTA00002670F.o.01.2.P.Seq	F	M00033570B:E06	CH09LNL
1159	400078	RTA00002685F.m.15.2.P.Seq	F	M00039600A:A11	CH12EDT
1160	373748	RTA00002671F.l.06.3.P.Seq	F	M00038325D:F12	CH09LNL
1161	401392	RTA00002685F.f.08.2.P.Seq	F	M00039505C:E03	CH12EDT
1162	20548	RTA00002710F.h.15.1.P.Seq	F	M00022247A:E02	CH03MAH
1163	376279	RTA00002680F.d.10.1.P.Seq	F	M00039785D:G05	CH09LNL
1164	374428	RTA00002672F.a.20.1.P.Seq	F	M00038633B:G02	CH09LNL
1165	374428	RTA00002672F.a.20.2.P.Seq	F	M00038633B:G02	CH09LNL
1166	372914	RTA00002679F.j.21.1.P.Seq	F	M00039696A:E05	CH09LNL
1167	378320	RTA00002681F.l.14.2.P.Seq	F	M00039894C:H07	CH09LNL
1168	235422	RTA00002665F.h.19.1.P.Seq	F	M00028768C:D05	CH08LNH
1169	402473	RTA00002686F.p.11.1.P.Seq	F	M00040287C:B09	CH13EDT
1170	374828	RTA00002674F.m.10.1.P.Seq	F	M00039170A:B10	CH09LNL
1171	403912	RTA00002687F.j.19.2.P.Seq	F	M00040317A:H03	CH14EDT
1172	401471	RTA00002685F.o.10.2.P.Seq	F	M00039629B:F01	CH12EDT
1173	404362	RTA00002687F.o.06.1.P.Seq	F	M00040342B:D12	CH14EDT
1174	403849	RTA00002687F.n.09.1.P.Seq	F	M00040333D:G05	CH14EDT
1175	395617	RTA00002687F.b.15.1.P.Seq	F	M00039767B:A04	CH14EDT

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1176	401709	RTA00002685F.o.01.2.P.Seq	F	M00039624A:H09	CH12EDT
1177	404464	RTA00002687F.o.22.1.P.Seq	F	M00040347D:F09	CH14EDT
1178	447795	RTA00002689F.e.06.3.P.Seq	F	M00042895C:G01	CH15CON
1179	18139	RTA00002708F.f.10.1.P.Seq	F	M00004139B:B10	CH01COH
1180	403898	RTA00002687F.a.05.1.P.Seq	F	M00039746C:H06	CH14EDT
1181	453312	RTA00002693F.a.21.2.P.Seq	F	M00043078D:D04	CH19COP
1182	404172	RTA00002687F.d.17.1.P.Seq	F	M00039951B:B12	CH14EDT
1183	400973	RTA00002685F.c.06.2.P.Seq	F	M00039374C:H12	CH12EDT
1184	450198	RTA00002691F.e.23.2.P.Seq	F	M00043405A:D11	CH17COHLV
1185	451502	RTA00002691F.f.03.2.P.Seq	F	M00043406B:G12	CH17COHLV
1186	454414	RTA00002693F.f.18.2.P.Seq	F	M00043220B:C04	CH19COP
1187	453752	RTA00002693F.b.02.2.P.Seq	F	M00043081D:F05	CH19COP
1188	403700	RTA00002687F.g.03.1.P.Seq	F	M00040207B:D08	CH14EDT
1189	403371	RTA00002687F.h.19.1.P.Seq	F	M00040294D:D12	CH14EDT
1190	14583	RTA00002687F.f.08.1.P.Seq	F	M00040203B:A05	CH14EDT
1191	404161	RTA00002687F.e.20.1.P.Seq	F	M00039958C:B09	CH14EDT
1192	403274	RTA00002687F.b.10.1.P.Seq	F	M00039766A:G07	CH14EDT
1193	373465	RTA00002671F.o.09.1.P.Seq	F	M00038615A:H12	CH09LNL
1194	402582	RTA00002686F.m.08.1.P.Seq	F	M00040265D:C08	CH13EDT
1195	402241	RTA00002686F.l.16.1.P.Seq	F	M00040261C:F01	CH13EDT
1196	380451	RTA00002670F.p.12.1.P.Seq	F	M00033581D:D08	CH09LNL
1197	455938	RTA00002694F.d.24.1.P.Seq	F	M00043528C:A02	CH20COHLV
1198	374297	RTA00002672F.i.02.2.P.Seq	F	M00039013D:F02	CH09LNL
1199	402624	RTA00002686F.p.13.1.P.Seq	F	M00040287D:D07	CH13EDT
1200	402322	RTA00002686F.j.16.1.P.Seq	F	M00040233A:H02	CH13EDT
1201	449504	RTA00002690F.c.11.2.P.Seq	F	M00042769C:E09	CH16COP
1202	226704	RTA00002664F.a.11.1.P.Seq	F	M00023352D:H03	CH04MAL
1203	271092	RTA00002690F.b.23.2.P.Seq	F	M00042756D:A10	CH16COP
1204	400864	RTA00002685F.g.17.2.P.Seq	F	M00039517B:G12	CH12EDT
1205	235855	RTA00002667F.o.06.1.P.Seq	F	M00032876C:D06	CH08LNL
1206	402789	RTA00002686F.g.16.1.P.Seq	F	M00040183A:F07	CH13EDT
1207	19826	RTA00002710F.k.05.1.P.Seq	F	M00022467C:B12	CH03MAH
1208	380157	RTA00002682F.h.19.1.P.Seq	F	M00039984D:G12	CH09LNL
1209	401187	RTA00002685F.e.15.2.P.Seq	F	M00039500C:C04	CH12EDT
1210	427346	RTA00002665F.b.01.3.P.Seq	F	M00028066C:D07	CH08LNL
1211	402866	RTA00002686F.c.15.1.P.Seq	F	M00040138B:H03	CH13EDT
1212	376712	RTA00002677F.c.13.2.P.Seq	F	M00039343B:F12	CH09LNL
1213	401655	RTA00002685F.c.22.1.P.Seq	F	M00039378D:H07	CH12EDT
1214	400147	RTA00002685F.g.10.1.P.Seq	F	M00039515A:A06	CH12EDT
1215	400864	RTA00002685F.g.17.1.P.Seq	F	M00039517B:G12	CH12EDT
1216	451600	RTA00002691F.b.19.3.P.Seq	F	M00043328D:H02	CH17COHLV
1217	400147	RTA00002685F.g.10.2.P.Seq	F	M00039515A:A06	CH12EDT
1218	401655	RTA00002685F.c.22.2.P.Seq	F	M00039378D:H07	CH12EDT
1219	449307	RTA00002690F.a.10.3.P.Seq	F	M00042431D:C10	CH16COP
1220	403121	RTA00002688F.a.01.2.P.Seq	F	M00040366A:B01	CH14EDT
1221	451718	RTA00002692F.e.24.1.P.Seq	F	M00043044B:A12	CH18CON
1222	294345	RTA00002685F.g.14.1.P.Seq	F	M00039515D:C11	CH12EDT

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1223	186541	RTA00002712F.p.23.2.P.Seq	F	M00027181D:A05	CH04MAL
1224	403898	RTA00002687F.a.05.2.P.Seq	F	M00039746C:H06	CH14EDT
1225	403541	RTA00002687F.p.20.1.P.Seq	F	M00040364A:E05	CH14EDT
1226	450773	RTA00002691F.d.24.3.P.Seq	F	M00043383D:A02	CH17COHLV
1227	376236	RTA00002685F.l.24.2.P.Seq	F	M00039595C:E05	CH12EDT
1228	422357	RTA00002688F.c.21.1.P.Seq	F	M00040385C:D02	CH14EDT
1229	404532	RTA00002687F.p.10.2.P.Seq	F	M00040351B:F02	CH14EDT
1230	403693	RTA00002687F.j.23.1.P.Seq	F	M00040317D:F02	CH14EDT
1231	403693	RTA00002687F.j.23.2.P.Seq	F	M00040317D:F02	CH14EDT
1232	401515	RTA00002685F.o.02.2.P.Seq	F	M00039624B:F12	CH12EDT
1233	404532	RTA00002687F.p.10.1.P.Seq	F	M00040351B:F02	CH14EDT
1234	452077	RTA00002692F.d.01.2.P.Seq	F	M00043002A:E05	CH18CON
1235	18003	RTA00002711F.b.04.1.P.Seq	F	M00022821C:C09	CH03MAH
1236	377014	RTA00002682F.f.13.1.P.Seq	F	M00039973D:C08	CH09LNL
1237	404232	RTA00002687F.n.12.2.P.Seq	F	M00040334D:C07	CH14EDT
1238	404232	RTA00002687F.n.12.1.P.Seq	F	M00040334D:C07	CH14EDT
1239	406263	RTA00002685F.d.14.1.P.Seq	F	M00039493A:C04	CH12EDT
1240	452077	RTA00002692F.c.24.2.P.Seq	F	M00043002A:E05	CH18CON
1241	454349	RTA00002693F.c.09.2.P.Seq	F	M00043133B:C11	CH19COP
1242	447671	RTA00002689F.e.12.1.P.Seq	F	M00042904B:E07	CH15CON
1243	447603	RTA00002693F.b.14.2.P.Seq	F	M00043095A:F09	CH19COP
1244	456764	RTA00002694F.c.14.1.P.Seq	F	M00043465B:H02	CH20COHLV
1245	401827	RTA00002686F.l.19.1.P.Seq	F	M00040262B:B06	CH13EDT
1246	404520	RTA00002687F.f.05.1.P.Seq	F	M00040202A:F05	CH14EDT
1247	449798	RTA00002691F.d.02.3.P.Seq	F	M00043366A:A02	CH17COHLV
1248	450993	RTA00002691F.c.12.3.P.Seq	F	M00043350D:B11	CH17COHLV
1249	377471	RTA00002691F.c.02.3.P.Seq	F	M00043339A:F11	CH17COHLV
1250	400404	RTA00002686F.a.17.1.P.Seq	F	M00039752B:G08	CH13EDT
1251	19106	RTA00002691F.e.08.2.P.Seq	F	M00043389C:E03	CH17COHLV
1252	404024	RTA00002687F.e.18.1.P.Seq	F	M00039958A:A08	CH14EDT
1253	446404	RTA00002689F.b.14.1.P.Seq	F	M00042566C:C05	CH15CON
1254	392921	RTA00002677F.k.12.2.P.Seq	F	M00039411C:E07	CH09LNL
1255	376850	RTA00002678F.e.10.2.P.Seq	F	M00039458B:H11	CH09LNL
1256	453011	RTA00002692F.f.10.2.P.Seq	F	M00043066B:H11	CH18CON
1257	234811	RTA00002691F.a.03.3.P.Seq	F	M00042352D:C01	CH17COHLV
1258	402708	RTA00002686F.m.11.1.P.Seq	F	M00040267A:E06	CH13EDT
1259	451013	RTA00002691F.f.08.2.P.Seq	F	M00043409B:B03	CH17COHLV
1260	453011	RTA00002692F.f.10.1.P.Seq	F	M00043066B:H11	CH18CON
1261	380462	RTA00002670F.n.24.2.P.Seq	F	M00033570B:E06	CH09LNL
1262	379602	RTA00002681F.c.21.2.P.Seq	F	M00039855C:F01	CH09LNL
1263	403896	RTA00002687F.a.04.1.P.Seq	F	M00039746C:H05	CH14EDT
1264	403397	RTA00002687F.h.02.1.P.Seq	F	M00040219B:D02	CH14EDT
1265	271723	RTA00002686F.b.05.1.P.Seq	F	M00039755A:B08	CH13EDT
1266	451379	RTA00002691F.b.12.2.P.Seq	F	M00043312C:E08	CH17COHLV
1267	456624	RTA00002694F.e.02.1.P.Seq	F	M00043616B:F02	CH20COHLV
1268	375483	RTA00002686F.n.14.1.P.Seq	F	M00040274A:D07	CH13EDT
1269	402229	RTA00002686F.i.09.1.P.Seq	F	M00040221A:G11	CH13EDT

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1270	377039	RTA00002686F.o.12.1.P.Seq	F	M00040280C:H05	CH13EDT
1271	18041	RTA00002710F.h.21.1.P.Seq	F	M00022262D:G03	CH03MAH
1272	401381	RTA00002685F.o.08.1.P.Seq	F	M00039626D:F04	CH12EDT
1273	428491	RTA00002666F.c.05.1.P.Seq	F	M00032535D:H01	CH08LNL
1274	54656	RTA00002661F.i.22.2.P.Seq	F	M00004372B:F07	CH01COH
1275	379183	RTA00002679F.i.17.1.P.Seq	F	M00039688C:G06	CH09LNL
1276	25594	RTA00002711F.f.07.1.P.Seq	F	M00022968B:E02	CH03MAH
1277	403355	RTA00002687F.d.11.1.P.Seq	F	M00039948D:D11	CH14EDT
1278	16789	RTA00002709F.b.09.2.P.Seq	F	M00005382B:F08	CH02COH
1279	23292	RTA00002708F.c.02.1.P.Seq	F	M00003750D:E06	CH01COH
1280	373982	RTA00002673F.b.24.2.P.Seq	F	M00039058A:A04	CH09LNL
1281	373982	RTA00002673F.c.01.2.P.Seq	F	M00039058A:A04	CH09LNL
1282	449911	RTA00002691F.e.02.2.P.Seq	F	M00043384B:B02	CH17COHLV
1283	450633	RTA00002691F.f.02.2.P.Seq	F	M00043405C:G12	CH17COHLV
1284	23939	RTA00002713F.j.14.1.P.Seq	F	M00027486A:F06	CH04MAL
1285	450633	RTA00002691F.f.02.1.P.Seq	F	M00043405C:G12	CH17COHLV
1286	379122	RTA00002672F.n.14.1.P.Seq	F	M00039039B:F09	CH09LNL
1287	449429	RTA00002690F.a.16.3.P.Seq	F	M00042437A:D04	CH16COP
1288	430578	RTA00002668F.g.18.1.P.Seq	F	M00032984C:G05	CH08LNL
1289	425824	RTA00002687F.b.17.1.P.Seq	F	M00039767C:E12	CH14EDT
1290	425824	RTA00002687F.b.17.2.P.Seq	F	M00039767C:E12	CH14EDT
1291	401266	RTA00002685F.i.11.2.P.Seq	F	M00039535D:D10	CH12EDT
1292	377949	RTA00002674F.p.04.1.P.Seq	F	M00039200A:C10	CH09LNL
1293	12926	RTA00002710F.e.21.1.P.Seq	F	M00022005C:C06	CH03MAH
1294	378242	RTA00002679F.c.20.2.P.Seq	F	M00039664D:G07	CH09LNL
1295	401781	RTA00002686F.e.08.1.P.Seq	F	M00040160B:A10	CH13EDT
1296	453101	RTA00002693F.c.16.2.P.Seq	F	M00043143B:A10	CH19COP
1297	377592	RTA00002677F.l.12.2.P.Seq	F	M00039415D:E01	CH09LNL
1298	404340	RTA00002687F.b.05.1.P.Seq	F	M00039764C:D07	CH14EDT
1299	400968	RTA00002685F.h.01.2.P.Seq	F	M00039521D:H03	CH12EDT
1300	400968	RTA00002685F.g.24.2.P.Seq	F	M00039521D:H03	CH12EDT
1301	374417	RTA00002671F.j.15.3.P.Seq	F	M00038315C:G11	CH09LNL
1302	374621	RTA00002675F.p.02.1.P.Seq	F	M00039263D:A12	CH09LNL
1303	19063	RTA00002708F.i.14.1.P.Seq	F	M00004361A:H02	CH01COH
1304	135941	RTA00002713F.g.06.1.P.Seq	F	M00027359B:G05	CH04MAL
1305	403355	RTA00002687F.d.11.2.P.Seq	F	M00039948D:D11	CH14EDT
1306	375226	RTA00002677F.m.08.2.P.Seq	F	M00039417C:A01	CH09LNL
1307	222658	RTA00002664F.e.14.2.P.Seq	F	M00027103B:A09	CH04MAL
1308	447978	RTA00002690F.d.11.3.P.Seq	F	M00042800A:A03	CH16COP
1309	431346	RTA00002669F.g.24.1.P.Seq	F	M00033218A:C04	CH08LNL
1310	455579	RTA00002694F.a.10.1.P.Seq	F	M00042596B:F06	CH20COHLV
1311	13406	RTA00002709F.l.14.1.P.Seq	F	M00007124D:H10	CH02COH
1312	378364	RTA00002674F.o.17.1.P.Seq	F	M00039196D:A07	CH09LNL
1313	373788	RTA00002671F.c.16.2.P.Seq	F	M00038259A:G08	CH09LNL
1314	403548	RTA00002688F.a.10.2.P.Seq	F	M00040368D:E09	CH14EDT
1315	22425	RTA00002709F.c.08.2.P.Seq	F	M00005498A:H06	CH02COH
1316	452238	RTA00002692F.c.21.2.P.Seq	F	M00042998A:G04	CH18CON

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1317	446680	RTA00002689F.c.04.1.P.Seq	F	M00042693D:E04	CH15CON
1318	142922	RTA00002712F.g.02.1.P.Seq	F	M00026860B:C05	CH04MAL
1319	450196	RTA00002691F.c.19.3.P.Seq	F	M00043359B:D10	CH17COHLV
1320	26017	RTA00002709F.d.04.1.P.Seq	F	M00005601D:D08	CH02COH
1321	380355	RTA00002670F.o.06.1.P.Seq	F	M00033570C:C10	CH09LNL
1322	25232	RTA00002710F.n.22.1.P.Seq	F	M00022667D:B02	CH03MAH
1323	378952	RTA00002683F.h.11.1.P.Seq	F	M00040070B:B07	CH09LNL
1324	404487	RTA00002687F.c.13.2.P.Seq	F	M00039943B:F10	CH14EDT
1325	48482	RTA00002712F.p.06.1.P.Seq	F	M00027159D:F03	CH04MAL
1326	373705	RTA00002673F.a.13.1.P.Seq	F	M00039052C:F07	CH09LNL
1327	373705	RTA00002673F.a.13.2.P.Seq	F	M00039052C:F07	CH09LNL
1328	21162	RTA00002709F.c.03.1.P.Seq	F	M00005449B:D01	CH02COH
1329	15203	RTA00002710F.a.21.1.P.Seq	F	M00007972B:H12	CH03MAH
1330	21162	RTA00002709F.c.03.2.P.Seq	F	M00005449B:D01	CH02COH
1331	401013	RTA00002685F.o.16.2.P.Seq	F	M00039641A:A05	CH12EDT
1332	404449	RTA00002687F.c.04.2.P.Seq	F	M00039770C:E04	CH14EDT
1333	429672	RTA00002668F.b.10.1.P.Seq	F	M00032909A:B06	CH08LNH
1334	48541	RTA00002712F.i.07.1.P.Seq	F	M00026922C:B02	CH04MAL
1335	378424	RTA00002681F.a.03.2.P.Seq	F	M00039839B:B01	CH09LNL
1336	49540	RTA00002712F.d.24.1.P.Seq	F	M00023399C:E10	CH04MAL
1337	379170	RTA00002672F.i.21.1.P.Seq	F	M00039016D:G06	CH09LNL
1338	179540	RTA00002683F.o.20.2.P.Seq	F	M00040100C:E05	CH09LNL
1339	451269	RTA00002691F.f.11.1.P.Seq	F	M00043411B:D08	CH17COHLV
1340	449832	RTA00002691F.e.13.2.P.Seq	F	M00043393A:B08	CH17COHLV
1341	380119	RTA00002670F.m.20.2.P.Seq	F	M00033560D:G07	CH09LNL
1342	153094	RTA00002714F.a.12.1.P.Seq	F	M00027743A:C03	CH04MAL
1343	448749	RTA00002690F.d.14.2.P.Seq	F	M00042806C:F07	CH16COP
1344	448749	RTA00002690F.d.14.3.P.Seq	F	M00042806C:F07	CH16COP
1345	454816	RTA00002693F.b.16.1.P.Seq	F	M00043096A:G04	CH19COP
1346	374744	RTA00002670F.i.16.2.P.Seq	F	M00033427D:F01	CH09LNL
1347	404449	RTA00002687F.c.04.1.P.Seq	F	M00039770C:E04	CH14EDT
1348	58005	RTA00002661F.h.14.1.P.Seq	F	M00004222C:E03	CH01COH
1349	451379	RTA00002691F.b.12.3.P.Seq	F	M00043312C:E08	CH17COHLV
1350	456323	RTA00002694F.d.21.1.P.Seq	F	M00043526B:D10	CH20COHLV
1351	455957	RTA00002694F.c.15.1.P.Seq	F	M00043465C:A03	CH20COHLV
1352	428063	RTA00002666F.l.05.1.P.Seq	F	M00032638C:G08	CH08LNH
1353	374722	RTA00002676F.j.19.3.P.Seq	F	M00039310A:C07	CH09LNL
1354	428407	RTA00002665F.p.12.1.P.Seq	F	M00032510D:F12	CH08LNH
1355	378000	RTA00002681F.j.16.1.P.Seq	F	M00039887D:C04	CH09LNL
1356	452717	RTA00002692F.b.17.2.P.Seq	F	M00042966C:E06	CH18CON
1357	378000	RTA00002681F.j.16.2.P.Seq	F	M00039887D:C04	CH09LNL
1358	448356	RTA00002690F.c.03.3.P.Seq	F	M00042760A:C12	CH16COP
1359	456629	RTA00002694F.d.04.1.P.Seq	F	M00043491C:F04	CH20COHLV
1360	431346	RTA00002669F.g.24.2.P.Seq	F	M00033218A:C04	CH08LNH
1361	377206	RTA00002682F.m.14.1.P.Seq	F	M00040015C:F08	CH09LNL
1362	453036	RTA00002692F.b.11.2.P.Seq	F	M00042960D:H08	CH18CON
1363	402632	RTA00002686F.g.15.1.P.Seq	F	M00040182D:D06	CH13EDT

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1364	230532	RTA00002664F.c.11.2.P.Seq	F	M00026901A:G07	CH04MAL
1365	30755	RTA00002663F.e.03.1.P.Seq	F	M00022138A:E05	CH03MAH
1366	451438	RTA00002691F.d.23.3.P.Seq	F	M00043383C:F12	CH17COHLV
1367	379011	RTA00002681F.n.23.1.P.Seq	F	M00039903C:D01	CH09LNL
1368	404048	RTA00002687F.g.01.1.P.Seq	F	M00040206A:A07	CH14EDT
1369	404048	RTA00002687F.g.01.2.P.Seq	F	M00040206A:A07	CH14EDT
1370	452398	RTA00002692F.f.17.2.P.Seq	F	M00043125C:A11	CH18CON
1371	403686	RTA00002687F.d.03.1.P.Seq	F	M00039946B:F08	CH14EDT
1372	403686	RTA00002687F.d.03.2.P.Seq	F	M00039946B:F08	CH14EDT
1373	404048	RTA00002687F.f.24.2.P.Seq	F	M00040206A:A07	CH14EDT
1374	404048	RTA00002687F.f.24.1.P.Seq	F	M00040206A:A07	CH14EDT
1375	450627	RTA00002691F.f.01.2.P.Seq	F	M00043405C:G02	CH17COHLV
1376	375589	RTA00002680F.f.06.2.P.Seq	F	M00039794A:E04	CH09LNL
1377	379011	RTA00002681F.n.23.2.P.Seq	F	M00039903C:D01	CH09LNL
1378	16789	RTA00002709F.b.09.1.P.Seq	F	M00005382B:F08	CH02COH
1379	427346	RTA00002665F.a.24.3.P.Seq	F	M00028066C:D07	CH08LNH
1380	49540	RTA00002712F.e.01.1.P.Seq	F	M00023399C:E10	CH04MAL
1381	14440	RTA00002674F.e.14.2.P.Seq	F	M00039129C:D04	CH09LNL
1382	391401	RTA00002682F.k.11.1.P.Seq	F	M00040004D:B03	CH09LNL
1383	43782	RTA00002662F.d.21.2.P.Seq	F	M00007165B:G11	CH02COH
1384	212635	RTA00002666F.p.01.1.P.Seq	F	M00032688D:D11	CH08LNH
1385	15618	RTA00002710F.o.05.1.P.Seq	F	M00022684A:C02	CH03MAH
1386	18501	RTA00002669F.g.23.3.P.Seq	F	M00033217B:H07	CH08LNH
1387	400310	RTA00002688F.b.05.2.P.Seq	F	M00040375C:B06	CH14EDT
1388	403796	RTA00002687F.h.17.1.P.Seq	F	M00040293D:G04	CH14EDT
1389	452314	RTA00002694F.a.21.1.P.Seq	F	M00043416C:A02	CH20COHLV
1390	119179	RTA00002712F.k.20.1.P.Seq	F	M00027021A:G02	CH04MAL
1391	167451	RTA00002663F.j.11.1.P.Seq	F	M00022646A:H10	CH03MAH
1392	450523	RTA00002691F.e.19.2.P.Seq	F	M00043401D:G08	CH17COHLV
1393	289535	RTA00002693F.f.06.1.P.Seq	F	M00043202B:F01	CH19COP
1394	374736	RTA00002673F.o.08.2.P.Seq	F	M00039112B:C05	CH09LNL
1395	378912	RTA00002672F.n.01.2.P.Seq	F	M00039036C:B05	CH09LNL
1396	134877	RTA00002662F.d.05.2.P.Seq	F	M00007026B:H09	CH02COH
1397	372811	RTA00002670F.c.12.2.P.Seq	F	M00033347C:F02	CH09LNL
1398	373296	RTA00002672F.e.08.2.P.Seq	F	M00038994A:A10	CH09LNL
1399	373296	RTA00002672F.e.08.1.P.Seq	F	M00038994A:A10	CH09LNL
1400	452903	RTA00002692F.f.08.2.P.Seq	F	M00043060D:G12	CH18CON
1401	450067	RTA00002691F.c.17.3.P.Seq	F	M00043352D:C03	CH17COHLV
1402	451013	RTA00002691F.f.08.1.P.Seq	F	M00043409B:B03	CH17COHLV
1403	212635	RTA00002666F.o.24.1.P.Seq	F	M00032688D:D11	CH08LNH
1404	452367	RTA00002692F.c.02.2.P.Seq	F	M00042976A:H04	CH18CON
1405	450627	RTA00002691F.e.24.1.P.Seq	F	M00043405C:G02	CH17COHLV
1406	186438	RTA00002713F.i.15.1.P.Seq	F	M00027462A:D07	CH04MAL
1407	431066	RTA00002669F.c.17.3.P.Seq	F	M00033189D:F08	CH08LNH
1408	378912	RTA00002672F.m.24.2.P.Seq	F	M00039036C:B05	CH09LNL
1409	15731	RTA00002709F.l.13.1.P.Seq	F	M00007116C:G02	CH02COH
1410	377187	RTA00002683F.d.21.2.P.Seq	F	M00040047C:F05	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1411	376107	RTA00002677F.a.08.2.P.Seq	F	M00039333D:D09	CH09LNL
1412	450580	RTA00002691F.c.20.3.P.Seq	F	M00043359C:G01	CH17COHLV
1413	379942	RTA00002679F.l.21.1.P.Seq	F	M00039707A:D02	CH09LNL
1414	375589	RTA00002680F.f.06.1.P.Seq	F	M00039794A:E04	CH09LNL
1415	375789	RTA00002674F.a.16.1.P.Seq	F	M00039120C:H03	CH09LNL
1416	456227	RTA00002694F.c.16.1.P.Seq	F	M00043465C:C09	CH20COHLV
1417	455852	RTA00002694F.a.02.1.P.Seq	F	M00042592A:H10	CH20COHLV
1418	25169	RTA00002710F.m.05.1.P.Seq	F	M00022579C:C11	CH03MAH
1419	376524	RTA00002678F.h.23.2.P.Seq	F	M00039477A:B03	CH09LNL
1420	449562	RTA00002690F.b.13.2.P.Seq	F	M00042515C:F08	CH16COP
1421	449562	RTA00002690F.b.13.3.P.Seq	F	M00042515C:F08	CH16COP
1422	286001	RTA00002690F.b.08.2.P.Seq	F	M00042511A:H04	CH16COP
1423	286001	RTA00002690F.b.08.3.P.Seq	F	M00042511A:H04	CH16COP
1424	380322	RTA00002683F.p.21.1.P.Seq	F	M00040106B:B09	CH09LNL
1425	401603	RTA00002685F.f.23.2.P.Seq	F	M00039510C:G02	CH12EDT
1426	376541	RTA00002678F.d.13.2.P.Seq	F	M00039456A:C08	CH09LNL
1427	449123	RTA00002690F.a.13.3.P.Seq	F	M00042435A:A11	CH16COP
1428	418358	RTA00002686F.m.07.1.P.Seq	F	M00040265D:B07	CH13EDT
1429	380263	RTA00002689F.a.22.1.P.Seq	F	M00042543C:G04	CH15CON
1430	455748	RTA00002694F.b.06.1.P.Seq	F	M00043428D:G08	CH20COHLV
1431	451679	RTA00002693F.a.04.2.P.Seq	F	M00042612D:F06	CH19COP
1432	396332	RTA00002686F.k.14.1.P.Seq	F	M00040252C:C06	CH13EDT
1433	377578	RTA00002683F.b.11.2.P.Seq	F	M00040037A:E11	CH09LNL
1434	20061	RTA00002710F.m.14.1.P.Seq	F	M00022597D:A06	CH03MAH
1435	402494	RTA00002686F.h.16.1.P.Seq	F	M00040191A:B09	CH13EDT
1436	372798	RTA00002670F.c.18.2.P.Seq	F	M00033349D:F05	CH09LNL
1437	236295	RTA00002679F.a.19.2.P.Seq	F	M00039655B:H09	CH09LNL
1438	451570	RTA00002691F.c.03.3.P.Seq	F	M00043340B:H08	CH17COHLV
1439	35847	RTA00002708F.h.03.1.P.Seq	F	M00004239B:F11	CH01COH
1440	455706	RTA00002694F.b.10.1.P.Seq	F	M00043433B:G09	CH20COHLV
1441	346310	RTA00002684F.d.18.1.P.Seq	F	M00040122D:A02	CH09LNL
1442	189561	RTA00002676F.j.09.3.P.Seq	F	M00039308B:G08	CH09LNL
1443	403200	RTA00002687F.j.24.1.P.Seq	F	M00040318A:B02	CH14EDT
1444	401413	RTA00002685F.i.03.2.P.Seq	F	M00039530B:E02	CH12EDT
1445	448680	RTA00002690F.b.02.3.P.Seq	F	M00042440B:E09	CH16COP
1446	117060	RTA00002679F.h.24.1.P.Seq	F	M00039686C:C05	CH09LNL
1447	403200	RTA00002687F.j.24.2.P.Seq	F	M00040318A:B02	CH14EDT
1448	448589	RTA00002690F.a.07.3.P.Seq	F	M00042349D:D07	CH16COP
1449	373806	RTA00002674F.o.02.1.P.Seq	F	M00039179A:G09	CH09LNL
1450	377055	RTA00002682F.k.13.1.P.Seq	F	M00040005B:C11	CH09LNL
1451	373111	RTA00002670F.n.14.2.P.Seq	F	M00033566C:E08	CH09LNL
1452	12350	RTA00002713F.a.05.1.P.Seq	F	M00027195C:E04	CH04MAL
1453	450366	RTA00002691F.c.06.3.P.Seq	F	M00043344D:E04	CH17COHLV
1454	397851	RTA00002680F.b.04.2.P.Seq	F	M00039775A:A09	CH09LNL
1455	403200	RTA00002687F.k.01.2.P.Seq	F	M00040318A:B02	CH14EDT
1456	403200	RTA00002687F.k.01.1.P.Seq	F	M00040318A:B02	CH14EDT
1457	401142	RTA00002687F.i.24.2.P.Seq	F	M00040313C:D05	CH14EDT

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1458	375221	RTA00002679F.k.19.1.P.Seq	F	M00039702A:B02	CH09LNL
1459	403471	RTA00002687F.a.14.1.P.Seq	F	M00039749D:D05	CH14EDT
1460	12270	RTA00002711F.f.23.1.P.Seq	F	M00023007C:E10	CH03MAH
1461	401013	RTA00002685F.o.16.1.P.Seq	F	M00039641A:A05	CH12EDT
1462	74344	RTA00002661F.f.10.1.P.Seq	F	M00003902A:C03	CH01COH
1463	423432	RTA00002687F.l.10.2.P.Seq	F	M00040323C:G11	CH14EDT
1464	423432	RTA00002687F.l.10.1.P.Seq	F	M00040323C:G11	CH14EDT
1465	379560	RTA00002682F.g.18.1.P.Seq	F	M00039981A:E08	CH09LNL
1466	122669	RTA00002712F.f.22.1.P.Seq	F	M00026857D:G12	CH04MAL
1467	373319	RTA00002671F.c.17.2.P.Seq	F	M00038259B:A02	CH09LNL
1468	448034	RTA00002690F.b.16.2.P.Seq	F	M00042751C:C12	CH16COP
1469	376366	RTA00002677F.h.05.2.P.Seq	F	M00039397B:H09	CH09LNL
1470	452253	RTA00002692F.f.04.2.P.Seq	F	M00043045D:G12	CH18CON
1471	401601	RTA00002685F.f.18.2.P.Seq	F	M00039508C:G01	CH12EDT
1472	373647	RTA00002672F.d.04.1.P.Seq	F	M00038664C:E04	CH09LNL
1473	379721	RTA00002676F.b.20.2.P.Seq	F	M00039276B:H09	CH09LNL
1474	446404	RTA00002689F.a.02.3.P.Seq	F	M00042887C:D07	CH15CON
1475	403738	RTA00002687F.a.10.2.P.Seq	F	M00039748A:F11	CH14EDT
1476	376887	RTA00002674F.f.23.2.P.Seq	F	M00039135D:H02	CH09LNL
1477	373787	RTA00002677F.l.04.2.P.Seq	F	M00039414D:G03	CH09LNL
1478	401375	RTA00002685F.n.04.1.P.Seq	F	M00039604B:E05	CH12EDT
1479	401375	RTA00002685F.n.04.2.P.Seq	F	M00039604B:E05	CH12EDT
1480	403232	RTA00002687F.g.20.2.P.Seq	F	M00040218C:C02	CH14EDT
1481	403232	RTA00002687F.g.20.1.P.Seq	F	M00040218C:C02	CH14EDT
1482	449080	RTA00002690F.a.04.2.P.Seq	F	M00042347D:H11	CH16COP
1483	430973	RTA00002669F.a.03.4.P.Seq	F	M00033176B:E12	CH08LNH
1484	374742	RTA00002676F.c.12.2.P.Seq	F	M00039279B:C11	CH09LNL
1485	449741	RTA00002690F.a.23.2.P.Seq	F	M00042856B:H02	CH16COP
1486	45341	RTA00002710F.k.19.1.P.Seq	F	M00022499A:B02	CH03MAH
1487	451220	RTA00002691F.f.07.2.P.Seq	F	M00043408B:D11	CH17COHLV
1488	22067	RTA00002708F.f.12.1.P.Seq	F	M00004140D:C03	CH01COH
1489	378952	RTA00002683F.h.11.2.P.Seq	F	M00040070B:B07	CH09LNL
1490	401435	RTA00002685F.n.14.2.P.Seq	F	M00039607D:E08	CH12EDT
1491	375284	RTA00002676F.g.21.2.P.Seq	F	M00039298D:B04	CH09LNL
1492	449080	RTA00002690F.a.04.3.P.Seq	F	M00042347D:H11	CH16COP
1493	37897	RTA00002661F.b.15.1.P.Seq	F	M00001476B:G10	CH01COH
1494	7572	RTA00002709F.h.03.1.P.Seq	F	M00006809B:B09	CH02COH
1495	377076	RTA00002682F.f.14.1.P.Seq	F	M00039973D:D12	CH09LNL
1496	374828	RTA00002674F.m.10.2.P.Seq	F	M00039170A:B10	CH09LNL
1497	400295	RTA00002685F.a.17.2.P.Seq	F	M00039363A:C09	CH12EDT
1498	401435	RTA00002685F.n.14.1.P.Seq	F	M00039607D:E08	CH12EDT
1499	374680	RTA00002676F.c.14.1.P.Seq	F	M00039279C:B08	CH09LNL
1500	399018	RTA00002684F.d.20.2.P.Seq	F	M00040123A:A09	CH09LNL
1501	376351	RTA00002678F.c.19.2.P.Seq	F	M00039452C:G09	CH09LNL
1502	19699	RTA00002710F.f.18.1.P.Seq	F	M00022105C:C12	CH03MAH
1503	394113	RTA00002665F.d.15.3.P.Seq	F	M00028314D:F05	CH08LNH
1504	452652	RTA00002692F.a.16.1.P.Seq	F	M00042627C:D01	CH18CON

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1505	450791	RTA00002691F.b.23.3.P.Seq	F	M00043338B:A03	CH17COHLV
1506	20112	RTA00002711F.b.16.1.P.Seq	F	M00022830D:D01	CH03MAH
1507	455142	RTA00002694F.b.08.1.P.Seq	F	M00043431D:B08	CH20COHLV
1508	117060	RTA00002679F.i.01.1.P.Seq	F	M00039686C:C05	CH09LNL
1509	447859	RTA00002689F.d.13.1.P.Seq	F	M00042737C:H04	CH15CON
1510	452572	RTA00002692F.e.16.1.P.Seq	F	M00043034D:C01	CH18CON
1511	448639	RTA00002690F.a.06.3.P.Seq	F	M00042348B:E05	CH16COP
1512	378947	RTA00002683F.o.12.2.P.Seq	F	M00040098C:B01	CH09LNL
1513	403599	RTA00002687F.i.12.2.P.Seq	F	M00040299B:F10	CH14EDT
1514	404084	RTA00002688F.d.16.2.P.Seq	F	M00040392B:H01	CH14EDT
1515	375243	RTA00002680F.d.24.1.P.Seq	F	M00039788C:A01	CH09LNL
1516	229665	RTA00002664F.c.08.2.P.Seq	F	M00026885A:H09	CH04MAL
1517	450270	RTA00002691F.a.18.3.P.Seq	F	M00042518D:D04	CH17COHLV
1518	448841	RTA00002690F.d.10.3.P.Seq	F	M00042799D:F08	CH16COP
1519	447613	RTA00002689F.c.11.1.P.Seq	F	M00042698D:E01	CH15CON
1520	453909	RTA00002693F.d.24.2.P.Seq	F	M00043173D:G03	CH19COP
1521	400213	RTA00002685F.a.06.2.P.Seq	F	M00039184B:B09	CH12EDT
1522	403738	RTA00002687F.a.10.1.P.Seq	F	M00039748A:F11	CH14EDT
1523	456725	RTA00002694F.e.14.1.P.Seq	F	M00043648A:G07	CH20COHLV
1524	230842	RTA00002665F.n.15.1.P.Seq	F	M00032492A:C01	CH08LNH
1525	450149	RTA00002692F.a.20.2.P.Seq	F	M00042630A:C05	CH18CON
1526	34343	RTA00002709F.a.13.1.P.Seq	F	M00005297D:H08	CH02COH
1527	403956	RTA00002688F.c.12.2.P.Seq	F	M00040383A:H02	CH14EDT
1528	375243	RTA00002680F.e.01.2.P.Seq	F	M00039788C:A01	CH09LNL
1529	375243	RTA00002680F.d.24.2.P.Seq	F	M00039788C:A01	CH09LNL
1530	373647	RTA00002672F.d.04.2.P.Seq	F	M00038664C:E04	CH09LNL
1531	376897	RTA00002674F.i.20.1.P.Seq	F	M00039167B:H09	CH09LNL
1532	23468	RTA00002708F.e.02.1.P.Seq	F	M00003991C:F06	CH01COH
1533	455184	RTA00002694F.a.05.1.P.Seq	F	M00042593A:C02	CH20COHLV
1534	455327	RTA00002694F.a.22.1.P.Seq	F	M00043417C:D05	CH20COHLV
1535	455189	RTA00002694F.c.09.1.P.Seq	F	M00043461D:C02	CH20COHLV
1536	455688	RTA00002694F.c.18.1.P.Seq	F	M00043476A:F07	CH20COHLV
1537	456286	RTA00002694F.b.23.1.P.Seq	F	M00043450C:C06	CH20COHLV
1538	455883	RTA00002694F.a.23.1.P.Seq	F	M00043418A:H10	CH20COHLV
1539	456308	RTA00002694F.d.22.1.P.Seq	F	M00043527C:E09	CH20COHLV
1540	452720	RTA00002694F.d.14.1.P.Seq	F	M00043516B:H09	CH20COHLV
1541	455319	RTA00002694F.b.13.1.P.Seq	F	M00043437D:D04	CH20COHLV
1542	455813	RTA00002694F.c.24.1.P.Seq	F	M00043483B:G10	CH20COHLV
1543	451814	RTA00002692F.e.20.2.P.Seq	F	M00043040B:B07	CH18CON
1544	448639	RTA00002690F.b.07.3.P.Seq	F	M00042470C:E05	CH16COP
1545	450578	RTA00002691F.b.20.3.P.Seq	F	M00043332C:G04	CH17COHLV
1546	451193	RTA00002691F.b.01.3.P.Seq	F	M00043304C:D02	CH17COHLV
1547	451981	RTA00002692F.c.23.2.P.Seq	F	M00043001D:D03	CH18CON
1548	447859	RTA00002689F.d.13.2.P.Seq	F	M00042737C:H04	CH15CON
1549	449415	RTA00002690F.a.23.3.P.Seq	F	M00042439B:D03	CH16COP
1550	451193	RTA00002691F.a.24.2.P.Seq	F	M00043304C:D02	CH17COHLV
1551	452032	RTA00002692F.e.04.2.P.Seq	F	M00043026C:D07	CH18CON

1552	452028	RTA00002692F.b.03.2.P.Seq	F	M00042955C:D05	CH18CON
1553	453981	RTA00002693F.c.07.2.P.Seq	F	M00043131B:A09	CH19COP
1554	422703	RTA00002687F.h.04.1.P.Seq	F	M00040219D:E08	CH14EDT
1555	450966	RTA00002691F.e.05.2.P.Seq	F	M00043386A:B08	CH17COHLV
1556	451058	RTA00002691F.b.24.3.P.Seq	F	M00043338B:C11	CH17COHLV
1557	451058	RTA00002691F.c.01.3.P.Seq	F	M00043338B:C11	CH17COHLV
1558	414331	RTA00002685F.c.14.2.P.Seq	F	M00039376D:H07	CH12EDT
1559	453398	RTA00002693F.a.14.2.P.Seq	F	M00043073A:C12	CH19COP
1560	454962	RTA00002693F.e.10.2.P.Seq	F	M00043184A:H08	CH19COP
1561	451193	RTA00002691F.a.24.3.P.Seq	F	M00043304C:D02	CH17COHLV
1562	447859	RTA00002689F.d.13.3.P.Seq	F	M00042737C:H04	CH15CON
1563	454335	RTA00002693F.e.14.2.P.Seq	F	M00043187A:C04	CH19COP
1564	456522	RTA00002694F.e.16.1.P.Seq	F	M00043649B:E07	CH20COHLV
1565	379167	RTA00002692F.c.09.2.P.Seq	F	M00042983C:A11	CH18CON
1566	402763	RTA00002686F.c.11.1.P.Seq	F	M00040136C:F08	CH13EDT
1567	450956	RTA00002691F.b.04.3.P.Seq	F	M00043306C:B03	CH17COHLV
1568	448999	RTA00002690F.d.08.3.P.Seq	F	M00042792A:H01	CH16COP
1569	448479	RTA00002691F.a.20.3.P.Seq	F	M00043296B:G09	CH17COHLV
1570	414331	RTA00002685F.c.14.1.P.Seq	F	M00039376D:H07	CH12EDT
1571	390124	RTA00002693F.d.13.2.P.Seq	F	M00043162A:B08	CH19COP
1572	174250	RTA00002689F.c.09.1.P.Seq	F	M00042697D:C07	CH15CON
1573	448991	RTA00002690F.d.02.3.P.Seq	F	M00042784A:H06	CH16COP
1574	453909	RTA00002693F.e.01.2.P.Seq	F	M00043173D:G03	CH19COP
1575	448933	RTA00002693F.c.05.1.P.Seq	F	M00043109C:G01	CH19COP
1576	449032	RTA00002690F.a.15.3.P.Seq	F	M00042436B:H09	CH16COP
1577	448853	RTA00002690F.b.03.3.P.Seq	F	M00042463A:F09	CH16COP
1578	449496	RTA00002690F.e.06.2.P.Seq	F	M00042830B:E02	CH16COP
1579	451546	RTA00002691F.a.04.3.P.Seq	F	M00042352D:G09	CH17COHLV
1580	451297	RTA00002691F.f.05.1.P.Seq	F	M00043407C:E05	CH17COHLV
1581	289519	RTA00002691F.d.18.2.P.Seq	F	M00043378A:H10	CH17COHLV
1582	448933	RTA00002693F.c.05.2.P.Seq	F	M00043109C:G01	CH19COP
1583	450806	RTA00002691F.c.14.3.P.Seq	F	M00043351D:A11	CH17COHLV
1584	450452	RTA00002691F.d.07.3.P.Seq	F	M00043368C:F09	CH17COHLV
1585	450754	RTA00002691F.d.03.2.P.Seq	F	M00043366C:H05	CH17COHLV
1586	452455	RTA00002692F.e.10.1.P.Seq	F	M00043029C:A06	CH18CON
1587	452032	RTA00002692F.e.04.1.P.Seq	F	M00043026C:D07	CH18CON
1588	454776	RTA00002693F.f.11.2.P.Seq	F	M00043211A:F01	CH19COP
1589	452579	RTA00002692F.e.19.1.P.Seq	F	M00043036D:C09	CH18CON
1590	451297	RTA00002691F.f.05.2.P.Seq	F	M00043407C:E05	CH17COHLV
1591	446923	RTA00002690F.d.05.3.P.Seq	F	M00042788C:F11	CH16COP
1592	449911	RTA00002691F.e.02.1.P.Seq	F	M00043384B:B02	CH17COHLV
1593	452241	RTA00002692F.c.10.2.P.Seq	F	M00042983C:G06	CH18CON
1594	452455	RTA00002692F.e.10.2.P.Seq	F	M00043029C:A06	CH18CON
1595	451052	RTA00002691F.a.10.3.P.Seq	F	M00042448A:C09	CH17COHLV
1596	450754	RTA00002691F.d.03.3.P.Seq	F	M00043366C:H05	CH17COHLV
1597	449524	RTA00002690F.a.11.3.P.Seq	F	M00042432D:E02	CH16COP
1598	453468	RTA00002693F.f.02.1.P.Seq	F	M00043200B:C08	CH19COP
1599	447583	RTA00002690F.b.20.3.P.Seq	F	M00042756B:F11	CH16COP
1600	450956	RTA00002691F.b.04.2.P.Seq	F	M00043306C:B03	CH17COHLV

1601	450609	RTA00002691F.a.13.3.P.Seq	F	M00042453B:G09	CH17COHLV
1602	447528	RTA00002689F.c.10.1.P.Seq	F	M00042698D:D10	CH15CON
1603	450617	RTA00002691F.e.11.2.P.Seq	F	M00043391A:G08	CH17COHLV
1604	450617	RTA00002691F.e.11.1.P.Seq	F	M00043391A:G08	CH17COHLV
1605	422703	RTA00002687F.h.04.2.P.Seq	F	M00040219D:E08	CH14EDT
1606	449538	RTA00002690F.b.17.3.P.Seq	F	M00042752A:E11	CH16COP
1607	411128	RTA00002720F.a.02.4.P.Seq	F	M00043022A:E12	CH18CON
1608	453398	RTA00002693F.a.14.1.P.Seq	F	M00043073A:C12	CH19COP
1609	447984	RTA00002693F.e.20.2.P.Seq	F	M00043192C:B12	CH19COP
1610	452010	RTA00002692F.c.19.2.P.Seq	F	M00042997B:D06	CH18CON
1611	456185	RTA00002694F.e.07.1.P.Seq	F	M00043635C:C11	CH20COHLV
1612	38403	RTA00002693F.c.11.2.P.Seq	F	M00043138D:B11	CH19COP
1613	449595	RTA00002690F.c.14.3.P.Seq	F	M00042771C:F06	CH16COP
1614	235312	RTA00002691F.a.02.3.P.Seq	F	M00042352C:H03	CH17COHLV
1615	449285	RTA00002690F.d.24.3.P.Seq	F	M00042823C:C02	CH16COP
1616	450562	RTA00002691F.c.08.3.P.Seq	F	M00043346A:G01	CH17COHLV
1617	451196	RTA00002691F.a.23.3.P.Seq	F	M00043304B:D05	CH17COHLV
1618	446445	RTA00002689F.c.23.1.P.Seq	F	M00042717A:C07	CH15CON
1619	449538	RTA00002690F.b.17.2.P.Seq	F	M00042752A:E11	CH16COP
1620	449627	RTA00002690F.a.08.3.P.Seq	F	M00042431B:G08	CH16COP
1621	448552	RTA00002690F.d.16.3.P.Seq	F	M00042807D:D05	CH16COP
1622	451559	RTA00002691F.a.11.3.P.Seq	F	M00042448C:H12	CH17COHLV
1623	377284	RTA00002683F.g.06.1.P.Seq	F	M00040060C:H10	CH09LNL
1624	449496	RTA00002690F.e.06.1.P.Seq	F	M00042830B:E02	CH16COP
1625	147196	RTA00002691F.e.20.1.P.Seq	F	M00043402C:D08	CH17COHLV
1626	373494	RTA00002690F.e.20.1.P.Seq	F	M00042852C:A01	CH16COP
1627	456478	RTA00002694F.e.13.1.P.Seq	F	M00043640C:E03	CH20COHLV
1628	452430	RTA00002692F.b.15.2.P.Seq	F	M00042964D:A03	CH18CON
1629	449146	RTA00002690F.e.19.2.P.Seq	F	M00042852B:A03	CH16COP
1630	451619	RTA00002691F.b.17.3.P.Seq	F	M00043324D:H11	CH17COHLV
1631	376897	RTA00002674F.l.20.2.P.Seq	F	M00039167B:H09	CH09LNL
1632	378557	RTA00002680F.i.06.2.P.Seq	F	M00039807A:D01	CH09LNL
1633	452076	RTA00002692F.c.20.2.P.Seq	F	M00042998A:E03	CH18CON
1634	456351	RTA00002694F.e.11.1.P.Seq	F	M00043638A:D06	CH20COHLV
1635	401588	RTA00002685F.i.06.2.P.Seq	F	M00039533B:G08	CH12EDT
1636	452330	RTA00002692F.c.22.2.P.Seq	F	M00043001B:H10	CH18CON
1637	346310	RTA00002684F.d.18.2.P.Seq	F	M00040122D:A02	CH09LNL
1638	449285	RTA00002690F.e.01.2.P.Seq	F	M00042823C:C02	CH16COP
1639	377284	RTA00002683F.g.06.2.P.Seq	F	M00040060C:H10	CH09LNL
1640	377603	RTA00002683F.m.02.2.P.Seq	F	M00040089B:E04	CH09LNL
1641	378557	RTA00002680F.i.06.1.P.Seq	F	M00039807A:D01	CH09LNL
1642	403669	RTA00002687F.l.20.2.P.Seq	F	M00040326A:F04	CH14EDT
1643	447388	RTA00002689F.e.17.3.P.Seq	F	M00042905B:C03	CH15CON
1644	452409	RTA00002692F.b.20.2.P.Seq	F	M00042970C:A04	CH18CON
1645	13625	RTA00002710F.b.08.1.P.Seq	F	M00007994A:G02	CH03MAH
1646	447069	RTA00002689F.b.15.1.P.Seq	F	M00042567B:H10	CH15CON
1647	289519	RTA00002691F.d.18.3.P.Seq	F	M00043378A:H10	CH17COHLV
1648	32699	RTA00002713F.i.24.1.P.Seq	F	M00027475B:E10	CH04MAL
1649	373697	RTA00002678F.c.24.2.P.Seq	F	M00039454B:A11	CH09LNL

1650	32699	RTA00002713F.j.01.1.P.Seq	F	M00027475B:E10	CH04MAL
1651	452572	RTA00002692F.e.16.2.P.Seq	F	M00043034D:C01	CH18CON
1652	9607	RTA00002710F.j.16.1.P.Seq	F	M00022416A:A07	CH03MAH
1653	374753	RTA00002676F.k.23.3.P.Seq	F	M00039313D:G04	CH09LNL
1654	403599	RTA00002687F.i.12.1.P.Seq	F	M00040299B:F10	CH14EDT
1655	430304	RTA00002667F.k.03.1.P.Seq	F	M00032830D:G03	CH08LNL
1656	428458	RTA00002665F.p.13.1.P.Seq	F	M00032510D:G06	CH08LNL
1657	427699	RTA00002665F.e.18.1.P.Seq	F	M00028362A:G11	CH08LNL
1658	380597	RTA00002673F.i.15.2.P.Seq	F	M00039081B:G06	CH09LNL
1659	404377	RTA00002687F.a.21.2.P.Seq	F	M00039762B:F07	CH14EDT
1660	374036	RTA00002671F.o.20.2.P.Seq	F	M00038616D:B12	CH09LNL
1661	404377	RTA00002687F.a.21.1.P.Seq	F	M00039762B:F07	CH14EDT
1662	400665	RTA00002688F.d.14.2.P.Seq	F	M00040391A:D10	CH14EDT
1663	427374	RTA00002665F.c.22.3.P.Seq	F	M00028207D:E09	CH08LNL
1664	227947	RTA00002684F.h.08.2.P.Seq	F	M00040307C:F10	CH09LNL
1665	429182	RTA00002666F.g.23.1.P.Seq	F	M00032592A:H11	CH08LNL
1666	374036	RTA00002671F.o.20.1.P.Seq	F	M00038616D:B12	CH09LNL
1667	373614	RTA00002671F.m.06.2.P.Seq	F	M00038329A:E08	CH09LNL
1668	453281	RTA00002693F.a.03.1.P.Seq	F	M00042611D:B12	CH19COP
1669	290131	RTA00002689F.b.08.1.P.Seq	F	M00042558A:F03	CH15CON
1670	373838	RTA00002672F.c.19.2.P.Seq	F	M00038663B:H06	CH09LNL
1671	424689	RTA00002687F.d.16.2.P.Seq	F	M00039951A:B07	CH14EDT
1672	424689	RTA00002687F.d.16.1.P.Seq	F	M00039951A:B07	CH14EDT
1673	380239	RTA00002680F.j.02.1.P.Seq	F	M00039810A:H10	CH09LNL
1674	430566	RTA00002666F.d.12.1.P.Seq	F	M00032551B:G05	CH08LNL
1675	401792	RTA00002686F.e.12.1.P.Seq	F	M00040162A:E01	CH13EDT
1676	380596	RTA00002671F.a.03.1.P.Seq	F	M00033584D:G11	CH09LNL
1677	447737	RTA00002689F.c.15.1.P.Seq	F	M00042704A:F09	CH15CON
1678	450261	RTA00002691F.e.09.1.P.Seq	F	M00043389D:D07	CH17COHLV
1679	453281	RTA00002693F.a.03.2.P.Seq	F	M00042611D:B12	CH19COP
1680	378994	RTA00002670F.f.03.1.P.Seq	F	M00033376A:C12	CH09LNL
1681	25910	RTA00002710F.i.19.1.P.Seq	F	M00022373C:B07	CH03MAH
1682	379097	RTA00002683F.o.14.2.P.Seq	F	M00040098D:E04	CH09LNL
1683	426895	RTA00002691F.c.16.3.P.Seq	F	M00043352D:B05	CH17COHLV
1684	159000	RTA00002712F.i.22.1.P.Seq	F	M00026944B:E03	CH04MAL
1685	377088	RTA00002682F.m.06.1.P.Seq	F	M00040014D:D10	CH09LNL
1686	20990	RTA00002670F.f.13.2.P.Seq	F	M00033377D:A05	CH09LNL
1687	379131	RTA00002682F.p.04.1.P.Seq	F	M00040026B:F06	CH09LNL
1688	179262	RTA00002712F.g.21.1.P.Seq	F	M00026878A:F05	CH04MAL
1689	378947	RTA00002683F.o.12.1.P.Seq	F	M00040098C:B01	CH09LNL
1690	20733	RTA00002710F.j.19.1.P.Seq	F	M00022421B:C11	CH03MAH
1691	403471	RTA00002687F.a.14.2.P.Seq	F	M00039749D:D05	CH14EDT
1692	43568	RTA00002709F.a.10.1.P.Seq	F	M00005018A:B05	CH02COH
1693	380354	RTA00002670F.n.23.2.P.Seq	F	M00033570B:C08	CH09LNL
1694	379896	RTA00002680F.a.24.1.P.Seq	F	M00039774C:C09	CH09LNL
1695	379896	RTA00002680F.b.01.1.P.Seq	F	M00039774C:C09	CH09LNL
1696	379896	RTA00002680F.b.01.2.P.Seq	F	M00039774C:C09	CH09LNL
1697	379896	RTA00002680F.a.24.2.P.Seq	F	M00039774C:C09	CH09LNL
1698	377679	RTA00002678F.a.09.2.P.Seq	F	M00039431B:F04	CH09LNL

1699	254091	RTA00002677F.a.13.2.P.Seq	F	M00039335A:E08	CH09LNL
1700	378144	RTA00002677F.e.17.2.P.Seq	F	M00039384C:F08	CH09LNL
1701	402690	RTA00002688F.c.23.2.P.Seq	F	M00040386A:A02	CH14EDT
1702	427553	RTA00002665F.d.08.3.P.Seq	F	M00028220A:B04	CH08LNLH
1703	427716	RTA00002665F.i.13.1.P.Seq	F	M00028777B:G12	CH08LNLH
1704	453877	RTA00002693F.d.16.2.P.Seq	F	M00043165B:G01	CH19COP
1705	379808	RTA00002680F.j.16.1.P.Seq	F	M00039813B:B01	CH09LNL
1706	431082	RTA00002669F.i.16.2.P.Seq	F	M00033231D:G10	CH08LNLH
1707	373571	RTA00002671F.l.09.3.P.Seq	F	M00038326B:D04	CH09LNL
1708	24045	RTA00002709F.l.17.1.P.Seq	F	M00007136A:A03	CH02COH
1709	403669	RTA00002687F.l.20.1.P.Seq	F	M00040326A:F04	CH14EDT
1710	224172	RTA00002687F.e.15.2.P.Seq	F	M00039957D:A12	CH14EDT
1711	159680	RTA00002663F.f.14.1.P.Seq	F	M00022257A:B09	CH03MAH
1712	24408	RTA00002709F.a.16.1.P.Seq	F	M00005308A:D06	CH02COH
1713	456127	RTA00002694F.c.04.1.P.Seq	F	M00043453B:B09	CH20COHLV
1714	374680	RTA00002676F.c.14.2.P.Seq	F	M00039279C:B08	CH09LNL
1715	429089	RTA00002666F.n.14.1.P.Seq	F	M00032668D:G12	CH08LNLH
1716	378934	RTA00002682F.p.19.1.P.Seq	F	M00040029A:B03	CH09LNL
1717	224172	RTA00002687F.e.15.1.P.Seq	F	M00039957D:A12	CH14EDT
1718	264667	RTA00002682F.e.17.1.P.Seq	F	M00039940A:D07	CH09LNL
1719	378714	RTA00002672F.g.10.2.P.Seq	F	M00039002D:G11	CH09LNL
1720	46948	RTA00002663F.h.06.1.P.Seq	F	M00022489C:G04	CH03MAH
1721	16774	RTA00002709F.b.02.1.P.Seq	F	M00005352C:A02	CH02COH
1722	99513	RTA00002712F.a.17.1.P.Seq	F	M00023300D:C11	CH04MAL
1723	26599	RTA00002713F.n.04.1.P.Seq	F	M00027602B:C01	CH04MAL
1724	455850	RTA00002694F.a.01.1.P.Seq	F	M00042591D:H03	CH20COHLV
1725	374235	RTA00002674F.h.13.1.P.Seq	F	M00039141C:E01	CH09LNL
1726	376661	RTA00002689F.e.11.3.P.Seq	F	M00042902D:B08	CH15CON
1727	403014	RTA00002688F.a.07.2.P.Seq	F	M00040368A:A12	CH14EDT
1728	450261	RTA00002691F.e.09.2.P.Seq	F	M00043389D:D07	CH17COHLV
1729	377092	RTA00002678F.o.15.2.P.Seq	F	M00039633D:D05	CH09LNL
1730	378073	RTA00002681F.j.10.1.P.Seq	F	M00039885C:D01	CH09LNL
1731	403014	RTA00002688F.a.07.1.P.Seq	F	M00040368A:A12	CH14EDT
1732	403974	RTA00002687F.o.10.2.P.Seq	F	M00040345D:A09	CH14EDT
1733	403974	RTA00002687F.o.10.1.P.Seq	F	M00040345D:A09	CH14EDT
1734	378073	RTA00002681F.j.10.2.P.Seq	F	M00039885C:D01	CH09LNL
1735	379614	RTA00002681F.d.09.1.P.Seq	F	M00039859A:F06	CH09LNL
1736	378994	RTA00002670F.f.03.2.P.Seq	F	M00033376A:C12	CH09LNL
1737	18306	RTA00002708F.a.02.1.P.Seq	F	M00001351A:B02	CH01COH
1738	373347	RTA00002674F.o.07.1.P.Seq	F	M00039180A:A07	CH09LNL
1739	377557	RTA00002671F.i.19.3.P.Seq	F	M00038303D:E07	CH09LNL
1740	402056	RTA00002686F.l.12.1.P.Seq	F	M00040260B:D02	CH13EDT
1741	402424	RTA00002686F.k.15.1.P.Seq	F	M00040253C:A05	CH13EDT
1742	379575	RTA00002679F.p.23.1.P.Seq	F	M00039771C:E11	CH09LNL
1743	22651	RTA00002708F.f.13.1.P.Seq	F	M00004144A:H05	CH01COH
1744	376151	RTA00002675F.n.04.1.P.Seq	F	M00039255C:E12	CH09LNL
1745	377183	RTA00002683F.e.15.1.P.Seq	F	M00040052D:F12	CH09LNL
1746	379094	RTA00002672F.o.07.2.P.Seq	F	M00039043B:E01	CH09LNL
1747	38891	RTA00002677F.h.24.2.P.Seq	F	M00039401B:D02	CH09LNL

1748	378308	RTA00002630F.i.15.2.P.Seq	F	M00039820A:H11	CH09LNL
1749	376933	RTA00002683F.f.08.2.P.Seq	F	M00040055D:A06	CH09LNL
1750	44295	RTA00002663F.f.17.1.P.Seq	F	M00022264B:G10	CH03MAH
1751	384025	RTA00002670F.k.20.1.P.Seq	F	M00033454A:D09	CH09LNL
1752	374408	RTA00002669F.f.10.3.P.Seq	F	M00033205A:F03	CH08LNLH
1753	446139	RTA00002689F.b.13.1.P.Seq	F	M00042565C:A08	CH15CON
1754	380247	RTA00002683F.c.11.2.P.Seq	F	M00040040A:A06	CH09LNL
1755	31966	RTA00002713F.i.16.1.P.Seq	F	M00027462B:H07	CH04MAL
1756	9564	RTA00002708F.h.04.1.P.Seq	F	M00004241B:H07	CH01COH
1757	94106	RTA00002712F.j.01.1.P.Seq	F	M00026946A:F12	CH04MAL
1758	376896	RTA00002677F.i.03.2.P.Seq	F	M00039402B:E03	CH09LNL
1759	376469	RTA00002674F.h.06.1.P.Seq	F	M00039140D:A04	CH09LNL
1760	455147	RTA00002694F.c.06.1.P.Seq	F	M00043458A:B12	CH20COHLV
1761	375381	RTA00002683F.a.02.2.P.Seq	F	M00040031A:E06	CH09LNL
1762	160196	RTA00002663F.f.11.1.P.Seq	F	M00022234C:D06	CH03MAH
1763	185945	RTA00002713F.b.21.1.P.Seq	F	M00027232D:B08	CH04MAL
1764	446139	RTA00002689F.b.13.3.P.Seq	F	M00042565C:A08	CH15CON
1765	379182	RTA00002682F.c.15.1.P.Seq	F	M00039928B:G05	CH09LNL
1766	376200	RTA00002693F.f.08.2.P.Seq	F	M00043203A:B09	CH19COP
1767	379506	RTA00002681F.c.10.2.P.Seq	F	M00039851C:D12	CH09LNL
1768	35715	RTA00002708F.a.04.1.P.Seq	F	M00001356A:H11	CH01COH
1769	428500	RTA00002665F.p.06.1.P.Seq	F	M00032508B:H03	CH08LNLH
1770	428812	RTA00002667F.a.10.1.P.Seq	F	M00032712B:G02	CH08LNLH
1771	378911	RTA00002672F.n.24.2.P.Seq	F	M00039042B:B02	CH09LNL
1772	373697	RTA00002678F.d.01.2.P.Seq	F	M00039454B:A11	CH09LNL
1773	372886	RTA00002670F.b.22.2.P.Seq	F	M00033343C:H08	CH09LNL
1774	378911	RTA00002672F.o.01.2.P.Seq	F	M00039042B:B02	CH09LNL
1775	122451	RTA00002663F.a.12.1.P.Seq	F	M00008026B:C11	CH03MAH
1776	19867	RTA00002711F.c.13.1.P.Seq	F	M00022856C:A07	CH03MAH
1777	37372	RTA00002708F.f.20.1.P.Seq	F	M00004155D:A10	CH01COH
1778	431419	RTA00002669F.j.23.3.P.Seq	F	M00033261C:D12	CH08LNLH
1779	186360	RTA00002713F.a.21.1.P.Seq	F	M00027207B:F07	CH04MAL
1780	430751	RTA00002669F.j.11.2.P.Seq	F	M00033248A:B02	CH08LNLH
1781	372572	RTA00002670F.g.20.1.P.Seq	F	M00033410B:C09	CH09LNL
1782	376913	RTA00002683F.m.04.2.P.Seq	F	M00040089C:E06	CH09LNL
1783	376990	RTA00002683F.f.09.2.P.Seq	F	M00040055D:B01	CH09LNL
1784	58508	RTA00002661F.e.17.1.P.Seq	F	M00003786A:A11	CH01COH
1785	189139	RTA00002664F.b.14.2.P.Seq	F	M00026851B:F01	CH04MAL
1786	384025	RTA00002670F.k.20.2.P.Seq	F	M00033454A:D09	CH09LNL
1787	379126	RTA00002683F.n.05.2.P.Seq	F	M00040092B:F05	CH09LNL
1788	377633	RTA00002684F.g.15.2.P.Seq	F	M00040304B:F06	CH09LNL
1789	430284	RTA00002667F.k.06.1.P.Seq	F	M00032831C:G07	CH08LNLH
1790	374773	RTA00002676F.l.22.3.P.Seq	F	M00039316A:C01	CH09LNL
1791	403761	RTA00002687F.m.03.1.P.Seq	F	M00040327B:G06	CH14EDT
1792	375547	RTA00002677F.m.04.2.P.Seq	F	M00039417A:E12	CH09LNL
1793	80436	RTA00002661F.c.09.1.P.Seq	F	M00001582A:E02	CH01COH
1794	189139	RTA00002664F.b.14.1.P.Seq	F	M00026851B:F01	CH04MAL
1795	376614	RTA00002677F.c.05.2.P.Seq	F	M00039341D:D07	CH09LNL
1796	404513	RTA00002688F.d.13.1.P.Seq	F	M00040390B:F02	CH14EDT

1797	375714	RTA00002677F.m.13.2.P.Seq	F	M00039417C:G01	CH09LNL
1798	51564	RTA00002712F.d.23.1.P.Seq	F	M00023398B:D12	CH04MAL
1799	399551	RTA00002687F.f.13.2.P.Seq	F	M00040203D:H11	CH14EDT
1800	133512	RTA00002693F.e.24.2.P.Seq	F	M00043200A:H09	CH19COP
1801	375176	RTA00002675F.p.13.1.P.Seq	F	M00039266D:H04	CH09LNL
1802	375704	RTA00002676F.h.13.2.P.Seq	F	M00039300C:G04	CH09LNL
1803	399551	RTA00002687F.f.13.1.P.Seq	F	M00040203D:H11	CH14EDT
1804	403357	RTA00002687F.i.05.2.P.Seq	F	M00040298B:G02	CH14EDT
1805	34513	RTA00002709F.c.22.1.P.Seq	F	M00005555A:A10	CH02COH
1806	121871	RTA00002713F.a.09.1.P.Seq	F	M00027198B:B08	CH04MAL
1807	32095	RTA00002662F.d.15.2.P.Seq	F	M00007112C:B10	CH02COH
1808	403183	RTA00002687F.n.02.1.P.Seq	F	M00040332D:B05	CH14EDT
1809	168691	RTA00002663F.j.02.1.P.Seq	F	M00022615D:G05	CH03MAH
1810	430854	RTA00002668F.p.21.2.P.Seq	F	M00033173D:C01	CH08LNL
1811	377987	RTA00002679F.h.08.1.P.Seq	F	M00039682A:C08	CH09LNL
1812	428408	RTA00002665F.p.23.1.P.Seq	F	M00032513D:F01	CH08LNL
1813	375930	RTA00002677F.h.03.2.P.Seq	F	M00039396D:B04	CH09LNL
1814	28453	RTA00002711F.h.07.1.P.Seq	F	M00023094A:B11	CH03MAH
1815	119478	RTA00002686F.n.07.1.P.Seq	F	M00040271C:D08	CH13EDT
1816	403189	RTA00002687F.g.16.2.P.Seq	F	M00040217D:B07	CH14EDT
1817	129692	RTA00002679F.e.13.1.P.Seq	F	M00039673A:F09	CH09LNL
1818	86668	RTA00002664F.a.10.2.P.Seq	F	M00023352B:F03	CH04MAL
1819	403357	RTA00002687F.i.05.1.P.Seq	F	M00040298B:G02	CH14EDT
1820	373198	RTA00002670F.p.01.2.P.Seq	F	M00033578D:G02	CH09LNL
1821	373198	RTA00002670F.o.24.2.P.Seq	F	M00033578D:G02	CH09LNL
1822	25233	RTA00002711F.b.06.1.P.Seq	F	M00022823C:C01	CH03MAH
1823	403429	RTA00002687F.a.07.2.P.Seq	F	M00039746D:D11	CH14EDT
1824	417119	RTA00002686F.i.14.1.P.Seq	F	M00040222D:G02	CH13EDT
1825	376066	RTA00002680F.c.12.2.P.Seq	F	M00039781D:D10	CH09LNL
1826	403189	RTA00002687F.g.16.1.P.Seq	F	M00040217D:B07	CH14EDT
1827	403429	RTA00002687F.a.07.1.P.Seq	F	M00039746D:D11	CH14EDT
1828	430975	RTA00002669F.j.06.3.P.Seq	F	M00033246C:E08	CH08LNL
1829	427544	RTA00002665F.e.03.1.P.Seq	F	M00028354A:B12	CH08LNL
1830	401155	RTA00002685F.o.12.1.P.Seq	F	M00039630A:C08	CH12EDT
1831	377005	RTA00002682F.k.15.1.P.Seq	F	M00040005D:B07	CH09LNL
1832	379032	RTA00002683F.a.07.1.P.Seq	F	M00040032A:D09	CH09LNL
1833	400097	RTA00002685F.g.19.2.P.Seq	F	M00039521A:A02	CH12EDT
1834	383401	RTA00002670F.k.13.2.P.Seq	F	M00033450C:A02	CH09LNL
1835	379032	RTA00002683F.a.07.2.P.Seq	F	M00040032A:D09	CH09LNL
1836	429663	RTA00002667F.m.21.1.P.Seq	F	M00032864B:B09	CH08LNL
1837	374018	RTA00002672F.a.14.2.P.Seq	F	M00038632C:B09	CH09LNL
1838	375409	RTA00002678F.n.02.2.P.Seq	F	M00039616B:C01	CH09LNL
1839	401155	RTA00002685F.o.12.2.P.Seq	F	M00039630A:C08	CH12EDT
1840	13958	RTA00002711F.b.02.1.P.Seq	F	M00022817A:H02	CH03MAH
1841	38767	RTA00002687F.a.11.1.P.Seq	F	M00039748C:F11	CH14EDT
1842	29398	RTA00002663F.c.23.1.P.Seq	F	M00022015B:B07	CH03MAH
1843	12453	RTA00002709F.c.23.2.P.Seq	F	M00005556B:D02	CH02COH
1844	38767	RTA00002687F.a.11.2.P.Seq	F	M00039748C:F11	CH14EDT
1845	279885	RTA00002671F.f.05.2.P.Seq	F	M00038279C:A11	CH09LNL

1846	188592	RTA00002664F.e.18.2.P.Seq	F	M00027141C:H03	CH04MAL
1847	376469	RTA00002674F.h.06.2.P.Seq	F	M00039140D:A04	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1	10600	RTA00002891F.j.07.1.P.Seq	F	M00003753B:D07	CH01COH
2	18827	RTA00002900F.p.12.1.P.Seq	F	M00005413D:A05	CH02COH
3	1759	RTA00002923F.f.23.1.P.Seq	F	M00039248C:A08	CH09LNL
4	10924	RTA00002907F.k.12.1.P.Seq	F	M00022224A:C07	CH03MAH
5	45331	RTA00002903F.l.10.1.P.Seq	F	M00007037D:D10	CH02COH
6	42233	RTA00002912F.g.24.1.P.Seq	F	M00027359B:A06	CH04MAL
7	7211	RTA00002909F.h.06.1.P.Seq	F	M00022634A:C07	CH03MAH
8	21395	RTA00002890F.k.16.1.P.Seq	F	M00001637D:C12	CH01COH
9	3093	RTA00002923F.e.03.1.P.Seq	F	M00039225A:D11	CH09LNL
10	15806	RTA00002894F.f.07.1.P.Seq	F	M00003991A:C11	CH01COH
11	19739	RTA00002896F.d.12.1.P.Seq	F	M00004147C:E01	CH01COH
12	140879	RTA00002905F.c.17.1.P.Seq	F	M00007985C:D08	CH03MAH
13	29706	RTA00002908F.l.22.1.P.Seq	F	M00022487B:A08	CH03MAH
14	109581	RTA00002918F.i.08.1.P.Seq	F	M00032908A:D08	CH08LNL
15	25009	RTA00002906F.k.11.1.P.Seq	F	M00022016B:F01	CH03MAH
16	8328	RTA00002888F.e.07.1.P.Seq	F	M00001451C:E10	CH01COH
17	15045	RTA00002887F.e.06.1.P.Seq	F	M00001393C:E08	CH01COH
18	21216	RTA00002898F.p.22.1.P.Seq	F	M00004416B:G10	CH01COH
19	185754	RTA00002912F.l.09.1.P.Seq	F	M00027506B:G01	CH04MAL
20	11881	RTA00002909F.h.10.1.P.Seq	F	M00022638A:D03	CH03MAH
21	185989	RTA00002910F.h.12.1.P.Seq	F	M00022924C:F04	CH03MAH
22	9667	RTA00002923F.a.03.1.P.Seq	F	M00039162D:C04	CH09LNL
23	15817	RTA00002903F.o.03.1.P.Seq	F	M00007103D:C02	CH02COH
24	10198	RTA00002923F.j.09.1.P.Seq	F	M00039294C:B09	CH09LNL
25	6355	RTA00002894F.p.12.1.P.Seq	F	M00004055D:D05	CH01COH
26	12227	RTA00002909F.e.18.1.P.Seq	F	M00022601B:G06	CH03MAH
27	11047	RTA00002893F.o.06.1.P.Seq	F	M00003960D:C12	CH01COH
28	1870	RTA00002910F.m.08.1.P.Seq	F	M00023020C:H03	CH03MAH
29	20065	RTA00002908F.m.09.1.P.Seq	F	M00022491A:A08	CH03MAH
30	19454	RTA00002900F.m.23.1.P.Seq	F	M00005379A:D10	CH02COH
31	48048	RTA00002922F.m.13.1.P.Seq	F	M00039124D:H01	CH09LNL
32	19799	RTA00002908F.h.19.1.P.Seq	F	M00022449D:F08	CH03MAH
33	185562	RTA00002911F.m.07.1.P.Seq	F	M00027093A:H02	CH04MAL
34	24214	RTA00002891F.k.19.1.P.Seq	F	M00003764D:F07	CH01COH
35	5172	RTA00002908F.p.22.1.P.Seq	F	M00022525B:D09	CH03MAH
36	50495	RTA00002898F.c.16.1.P.Seq	F	M00004321C:C11	CH01COH
37	43287	RTA00002908F.k.16.1.P.Seq	F	M00022470D:B02	CH03MAH
38	15324	RTA00002905F.p.20.1.P.Seq	F	M00021e97C:B07	CH03MAH
39	22157	RTA00002888F.g.07.1.P.Seq	F	M00001461D:B10	CH01COH
40	15249	RTA00002915F.l.08.1.P.Seq	F	M00032489B:G12	CH08LNL
41	2764	RTA00002925F.c.11.1.P.Seq	F	M00039829B:E01	CH09LNL
42	23838	RTA00002889F.b.14.1.P.Seq	F	M00001513B:D10	CH01COH
43	11074	RTA00002899F.g.22.1.P.Seq	F	M00004e03C:C10	CH01COH
44	18367	RTA00002922F.b.09.1.P.Seq	F	M00038e19D:C12	CH09LNL
45	21703	RTA00002903F.m.08.1.P.Seq	F	M00007059B:D07	CH02COH
46	21470	RTA00002895F.c.14.1.P.Seq	F	M000040e7B:D03	CH01COH
47	15492	RTA00002907F.p.06.1.P.Seq	F	M00022282B:C09	CH03MAH
48	4022	RTA00002897F.i.22.1.P.Seq	F	M000042e9B:B04	CH01COH
49	21579	RTA00002891F.e.03.1.P.Seq	F	M00001e86B:H01	CH01COH
50	186283	RTA00002913F.c.06.1.P.Seq	F	M00027801B:D07	CH04MAL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
51	5410	RTA00002921F.i.08.1.P.Seq	F	M00033445D:G03	CH09LNL
52	22420	RTA00002901F.e.19.1.P.Seq	F	M00005474C:H09	CH02COH
53	140553	RTA00002916F.n.02.1.P.Seq	F	M00032638B:F02	CH08LNL
54	23849	RTA00002887F.a.22.1.P.Seq	F	M00001386B:F11	CH01COH
55	21945	RTA00002895F.l.22.1.P.Seq	F	M00004103C:E10	CH01COH
56	7867	RTA00002901F.p.08.1.P.Seq	F	M00005710B:H03	CH02COH
57	14533	RTA00002896F.l.01.1.P.Seq	F	M00004179C:B06	CH01COH
58	5790	RTA00002919F.g.17.1.P.Seq	F	M00033080C:A07	CH08LNL
59	186153	RTA00002911F.i.24.1.P.Seq	F	M00027017A:B09	CH04MAL
60	10561	RTA00002899F.h.08.1.P.Seq	F	M00004606D:H09	CH01COH
61	24572	RTA00002893F.l.08.1.P.Seq	F	M00003926A:F11	CH01COH
62	13138	RTA00002888F.m.03.1.P.Seq	F	M00001488C:A03	CH01COH
63	6701	RTA00002922F.g.18.1.P.Seq	F	M00039055C:A01	CH09LNL
64	12751	RTA00002904F.c.10.1.P.Seq	F	M00007202B:F01	CH02COH
65	3583	RTA00002916F.n.21.1.P.Seq	F	M00032644C:B05	CH08LNL
66	12673	RTA00002901F.d.24.1.P.Seq	F	M00005463A:G02	CH02COH
67	15243	RTA00002901F.l.21.1.P.Seq	F	M00005623B:G01	CH02COH
68	21022	RTA00002922F.k.24.1.P.Seq	F	M00039111A:C12	CH09LNL
69	36596	RTA00002919F.g.24.1.P.Seq	F	M00033081D:D11	CH08LNL
70	4932	RTA00002890F.c.14.1.P.Seq	F	M00001596A:D02	CH01COH
71	42413	RTA00002900F.o.14.1.P.Seq	F	M00005401D:F09	CH02COH
72	1090	RTA00002918F.g.20.1.P.Seq	F	M00032892C:C12	CH08LNL
73	44737	RTA00002901F.a.20.1.P.Seq	F	M00005434A:C03	CH02COH
74	4183	RTA00002918F.n.23.1.P.Seq	F	M00032988B:G01	CH08LNL
75	41882	RTA00002902F.d.12.1.P.Seq	F	M00006586D:D04	CH02COH
76	500	RTA00002925F.o.18.1.P.Seq	F	M00040034A:E06	CH09LNL
77	5435	RTA00002921F.f.20.1.P.Seq	F	M00033420B:E08	CH09LNL
78	15829	RTA00002900F.j.01.1.P.Seq	F	M00005314A:G10	CH02COH
79	154083	RTA00002907F.a.06.1.P.Seq	F	M00022096D:A03	CH03MAH
80	24381	RTA00002910F.i.16.1.P.Seq	F	M00022953B:D06	CH03MAH
81	107940	RTA00002930F.f.07.1.P.Seq	F	M00055735A:H08	CH15CON
82	24761	RTA00002902F.l.21.1.P.Seq	F	M00006756C:A02	CH02COH
83	10734	RTA00002924F.e.02.1.P.Seq	F	M00039457D:C02	CH09LNL
84	40540	RTA00002897F.p.23.1.P.Seq	F	M00004303C:C05	CH01COH
85	23692	RTA00002930F.i.07.1.P.Seq	F	M00056057C:F06	CH15CON
86	7896	RTA00002906F.j.08.1.P.Seq	F	M00021998B:D09	CH03MAH
87	24387	RTA00002896F.e.09.1.P.Seq	F	M00004151B:A07	CH01COH
88	2420	RTA00002889F.h.02.1.P.Seq	F	M00001546B:C11	CH01COH
89	10431	RTA00002887F.p.07.1.P.Seq	F	M00001429B:G05	CH01COH
90	14665	RTA00002908F.g.07.1.P.Seq	F	M00022425A:C09	CH03MAH
91	10302	RTA00002906F.o.03.1.P.Seq	F	M00022081A:B07	CH03MAH
92	28436	RTA00002908F.f.08.1.P.Seq	F	M00022415C:D12	CH03MAH
93	17829	RTA00002889F.g.11.1.P.Seq	F	M00001544B:E06	CH01COH
94	10390	RTA00002906F.e.13.1.P.Seq	F	M00021923A:B12	CH03MAH
95	11619	RTA00002913F.c.07.1.P.Seq	F	M00027806C:H05	CH04MAL
96	6890	RTA00002918F.m.19.1.P.Seq	F	M00032979D:H07	CH08LNL
97	10110	RTA00002897F.g.13.1.P.Seq	F	M00004245C:G10	CH01COH
98	21511	RTA00002892F.h.24.2.P.Seq	F	M00003821C:E12	CH01COH
99	9287	RTA00002899F.h.14.1.P.Seq	F	M00004608A:C10	CH01COH
100	16575	RTA00002895F.n.02.1.P.Seq	F	M00004110D:F09	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
101	16857	RTA00002899F.h.17.1.P.Seq	F	M00004609A:E09	CH01COH
102	33329	RTA00002891F.p.14.1.P.Seq	F	M00003787D:A10	CH01COH
103	40652	RTA00002896F.f.21.1.P.Seq	F	M00004153B:E03	CH01COH
104	8070	RTA00002925F.c.09.1.P.Seq	F	M00039828B:H06	CH09LNL
105	15880	RTA00002887F.g.11.1.P.Seq	F	M00001397C:H08	CH01COH
106	87418	RTA00002901F.g.10.1.P.Seq	F	M00005500A:D04	CH02COH
107	9961	RTA00002903F.l.21.1.P.Seq	F	M00007046D:C09	CH02COH
108	9966	RTA00002911F.o.20.1.P.Seq	F	M00027168B:H08	CH04MAL
109	17513	RTA00002906F.d.03.1.P.Seq	F	M00021896D:A05	CH03MAH
110	24835	RTA00002924F.f.18.1.P.Seq	F	M00039554D:B09	CH09LNL
111	15200	RTA00002891F.j.08.1.P.Seq	F	M00003758B:F06	CH01COH
112	124098	RTA00002905F.e.23.1.P.Seq	F	M00008020D:D05	CH03MAH
113	3786	RTA00002901F.e.05.1.P.Seq	F	M00005466C:B01	CH02COH
114	154121	RTA00002906F.p.02.1.P.Seq	F	M00022088B:F10	CH03MAH
115	5746	RTA00002918F.l.09.1.P.Seq	F	M00032945D:B07	CH08LNH
116	33700	RTA00002901F.e.09.1.P.Seq	F	M00005468A:C04	CH02COH
117	5660	RTA00002890F.b.11.1.P.Seq	F	M00001591B:H05	CH01COH
118	22732	RTA00002924F.o.23.1.P.Seq	F	M00039785C:H12	CH09LNL
119	14720	RTA00002892F.j.05.1.P.Seq	F	M00003825A:H10	CH01COH
120	13658	RTA00002896F.c.04.1.P.Seq	F	M00004143B:B04	CH01COH
121	23150	RTA00002887F.a.01.1.P.Seq	F	M00001384A:A07	CH01COH
122	11970	RTA00002903F.k.03.1.P.Seq	F	M00007002C:A10	CH02COH
123	10686	RTA00002915F.p.02.2.P.Seq	F	M00032519D:F08	CH08LNH
124	9588	RTA00002923F.m.10.1.P.Seq	F	M00039331B:F09	CH09LNL
125	8500	RTA00002925F.e.21.1.P.Seq	F	M00039860D:B02	CH09LNL
126	8615	RTA00002907F.l.17.1.P.Seq	F	M00022238C:G04	CH03MAH
127	7524	RTA00002886F.e.16.1.P.Seq	F	M00001348B:B03	CH01COH
128	325	RTA00002912F.g.02.1.P.Seq	F	M00027332B:H09	CH04MAL
129	10214	RTA00002889F.o.01.1.P.Seq	F	M00001570A:B07	CH01COH
130	23534	RTA00002889F.c.22.1.P.Seq	F	M00001533D:A01	CH01COH
131	7473	RTA00002893F.o.20.1.P.Seq	F	M00003965D:D11	CH01COH
132	185625	RTA00002912F.f.10.1.P.Seq	F	M00027314D:E02	CH04MAL
133	3920	RTA00002917F.m.07.1.P.Seq	F	M00032773D:F08	CH08LNH
134	8458	RTA00002889F.m.02.1.P.Seq	F	M00001562D:B07	CH01COH
135	20263	RTA00002906F.n.08.1.P.Seq	F	M00022073C:C07	CH03MAH
136	186141	RTA00002912F.f.04.1.P.Seq	F	M00027311A:H09	CH04MAL
137	4852	RTA00002919F.i.15.1.P.Seq	F	M00033150B:E02	CH08LNH
138	2146	RTA00002926F.a.21.1.P.Seq	F	M00040061C:C08	CH09LNL
139	3522	RTA00002897F.h.23.1.P.Seq	F	M00004263C:D03	CH01COH
140	20027	RTA00002909F.g.21.1.P.Seq	F	M00022627B:H03	CH03MAH
141	15650	RTA00002925F.g.04.1.P.Seq	F	M00039874A:B06	CH09LNL
142	21031	RTA00002901F.h.21.1.P.Seq	F	M00005520B:H05	CH02COH
143	95610	RTA00002909F.h.18.1.P.Seq	F	M00022642A:G08	CH03MAH
144	903	RTA00002912F.o.03.1.P.Seq	F	M00027591A:E04	CH04MAL
145	17284	RTA00002916F.k.18.1.P.Seq	F	M00032620B:F06	CH08LNH
146	15556	RTA00002895F.m.01.1.P.Seq	F	M00004104A:A12	CH01COH
147	11013	RTA00002897F.b.08.1.P.Seq	F	M00004214D:A05	CH01COH
148	15358	RTA00002903F.n.18.1.P.Seq	F	M00007098A:E10	CH02COH
149	10792	RTA00002894F.a.10.1.P.Seq	F	M00003974C:E11	CH01COH
150	25507	RTA00002901F.n.07.1.P.Seq	F	M00005643D:A05	CH02COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
151	19978	RTA00002908F.k.21.1.P.Seq	F	M00022472D:B01	CH03MAH
152	31133	RTA00002905F.f.23.1.P.Seq	F	M00008045C:A05	CH03MAH
153	4503	RTA00002893F.h.14.1.P.Seq	F	M00003906A:C02	CH01COH
154	9017	RTA00002886F.i.03.1.P.Seq	F	M00001358A:E08	CH01COH
155	6635	RTA00002895F.a.07.1.P.Seq	F	M00004057D:G01	CH01COH
156	10220	RTA00002921F.d.09.1.P.Seq	F	M00033360C:A03	CH09LNL
157	9831	RTA00002896F.b.08.1.P.Seq	F	M00004139B:F01	CH01COH
158	17291	RTA00002888F.c.10.1.P.Seq	F	M00001442A:F08	CH01COH
159	9802	RTA00002916F.l.12.1.P.Seq	F	M00032628C:B06	CH08LNL
160	133828	RTA00002908F.b.21.1.P.Seq	F	M00022374C:E11	CH03MAH
161	25870	RTA00002909F.m.23.1.P.Seq	F	M00022702D:E02	CH03MAH
162	27324	RTA00002912F.i.22.1.P.Seq	F	M00027433B:D12	CH04MAL
163	98159	RTA00002910F.f.19.1.P.Seq	F	M00022897B:F06	CH03MAH
164	21264	RTA00002903F.d.15.1.P.Seq	F	M00006904D:A02	CH02COH
165	186199	RTA00002911F.b.13.2.P.Seq	F	M00023394D:D10	CH04MAL
166	28794	RTA00002887F.i.14.1.P.Seq	F	M00001403C:B03	CH01COH
167	23180	RTA00002895F.j.17.1.P.Seq	F	M00004093A:C03	CH01COH
168	21022	RTA00002922F.l.01.1.P.Seq	F	M00039111A:C12	CH09LNL
169	14370	RTA00002893F.i.17.1.P.Seq	F	M00003911C:A09	CH01COH
170	4804	RTA00002918F.a.19.1.P.Seq	F	M00032826C:D10	CH08LNL
171	7066	RTA00002919F.o.07.1.P.Seq	F	M00033246A:H12	CH08LNL
172	48227	RTA00002903F.o.18.1.P.Seq	F	M00007117A:C11	CH02COH
173	20171	RTA00002886F.i.15.1.P.Seq	F	M00001359A:H10	CH01COH
174	10555	RTA00002894F.p.10.1.P.Seq	F	M00004055C:B10	CH01COH
175	12523	RTA00002914F.m.08.1.P.Seq	F	M00028361B:H08	CH08LNL
176	23767	RTA00002896F.i.21.1.P.Seq	F	M00004171B:B03	CH01COH
177	16849	RTA00002918F.b.07.1.P.Seq	F	M00032829D:A05	CH08LNL
178	185866	RTA00002911F.c.18.2.P.Seq	F	M00026818C:E01	CH04MAL
179	29927	RTA00002899F.b.20.1.P.Seq	F	M00004445C:F07	CH01COH
180	21975	RTA00002902F.a.01.1.P.Seq	F	M00005743D:A12	CH02COH
181	24456	RTA00002903F.b.20.1.P.Seq	F	M00006877C:F11	CH02COH
182	6034	RTA00002901F.a.12.1.P.Seq	F	M00005423A:C11	CH02COH
183	11362	RTA00002887F.h.06.1.P.Seq	F	M00001399C:A01	CH01COH
184	20671	RTA00002905F.a.22.1.P.Seq	F	M00007947A:B06	CH03MAH
185	8059	RTA00002917F.b.02.1.P.Seq	F	M00032671B:D06	CH08LNL
186	12037	RTA00002897F.d.11.1.P.Seq	F	M00004229B:B06	CH01COH
187	13209	RTA00002897F.d.20.1.P.Seq	F	M00004230D:B05	CH01COH
188	23660	RTA00002915F.i.21.1.P.Seq	F	M00031416D:H05	CH08LNL
189	4747	RTA00002919F.c.23.1.P.Seq	F	M00033041A:B11	CH08LNL
190	24532	RTA00002919F.m.16.1.P.Seq	F	M00033218C:F07	CH08LNL
191	8576	RTA00002890F.h.13.1.P.Seq	F	M00001616D:F03	CH01COH
192	12056	RTA00002893F.g.12.1.P.Seq	F	M00003900C:D12	CH01COH
193	895	RTA00002921F.b.11.1.P.Seq	F	M00033303C:F09	CH09LNL
194	7212	RTA00002897F.j.04.1.P.Seq	F	M00004270A:E09	CH01COH
195	108296	RTA00002907F.h.20.1.P.Seq	F	M00022193C:C09	CH03MAH
196	115713	RTA00002906F.a.22.1.P.Seq	F	M00021852C:H02	CH03MAH
197	7334	RTA00002910F.l.08.1.P.Seq	F	M00023004C:A01	CH03MAH
198	1090	RTA00002918F.g.20.2.P.Seq	F	M00032892C:C12	CH08LNL
199	7913	RTA00002886F.j.13.1.P.Seq	F	M00001362A:F09	CH01COH
200	12139	RTA00002923F.o.02.1.P.Seq	F	M00039349D:B11	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
201	17148	RTA00002895F.i.14.1.P.Seq	F	M00004102A:E03	CH01COH
202	2314	RTA00002891F.g.10.1.P.Seq	F	M00001771B:E06	CH01COH
203	18660	RTA00002903F.m.03.1.P.Seq	F	M00007048C:A12	CH02COH
204	21799	RTA00002900F.n.09.1.P.Seq	F	M00005385D:F07	CH02COH
205	16612	RTA00002893F.j.17.1.P.Seq	F	M00003915C:D10	CH01COH
206	168067	RTA00002909F.a.17.1.P.Seq	F	M00022537B:C06	CH03MAH
207	21197	RTA00002891F.c.19.1.P.Seq	F	M00001680A:A01	CH01COH
208	45015	RTA00002905F.o.17.1.P.Seq	F	M00021678D:H04	CH03MAH
209	15381	RTA00002903F.m.19.1.P.Seq	F	M00007070C:C01	CH02COH
210	1402	RTA00002896F.i.04.1.P.Seq	F	M00004166C:B10	CH01COH
211	69026	RTA00002893F.f.05.1.P.Seq	F	M00003887C:E09	CH01COH
212	33119	RTA00002922F.i.07.1.P.Seq	F	M00039067A:C05	CH09LNL
213	1166	RTA00002891F.c.05.1.P.Seq	F	M00001677B:H08	CH01COH
214	14345	RTA00002891F.b.06.1.P.Seq	F	M00001671C:F03	CH01COH
215	10589	RTA00002908F.d.16.1.P.Seq	F	M00022392B:F01	CH03MAH
216	13281	RTA00002916F.p.01.1.P.Seq	F	M00032652C:C07	CH08LNL
217	13281	RTA00002916F.o.24.1.P.Seq	F	M00032652C:C07	CH08LNL
218	12248	RTA00002898F.h.08.1.P.Seq	F	M00004351B:G07	CH01COH
219	164955	RTA00002909F.n.09.1.P.Seq	F	M00022706D:G08	CH03MAH
220	15686	RTA00002907F.f.24.1.P.Seq	F	M00022170C:C01	CH03MAH
221	15686	RTA00002907F.g.01.1.P.Seq	F	M00022170C:C01	CH03MAH
222	34228	RTA00002891F.d.14.1.P.Seq	F	M00001683B:F11	CH01COH
223	6530	RTA00002900F.p.04.1.P.Seq	F	M00005409D:B02	CH02COH
224	1964	RTA00002903F.c.10.1.P.Seq	F	M00006885A:F07	CH02COH
225	10547	RTA00002893F.e.16.1.P.Seq	F	M00003884A:E12	CH01COH
226	13393	RTA00002901F.a.06.1.P.Seq	F	M00005422B:B08	CH02COH
227	14809	RTA00002915F.e.08.2.P.Seq	F	M00028773C:C05	CH08LNL
228	46850	RTA00002907F.e.21.1.P.Seq	F	M00022158B:B09	CH03MAH
229	5398	RTA00002911F.i.13.1.P.Seq	F	M00027004C:C11	CH04MAL
230	27569	RTA00002910F.l.14.1.P.Seq	F	M00023007D:D03	CH03MAH
231	26277	RTA00002898F.g.19.1.P.Seq	F	M00004347C:A05	CH01COH
232	185914	RTA00002912F.k.01.1.P.Seq	F	M00027467A:C07	CH04MAL
233	14274	RTA00002895F.c.09.1.P.Seq	F	M00004066D:G10	CH01COH
234	28396	RTA00002907F.g.02.1.P.Seq	F	M00022171A:F03	CH03MAH
235	22991	RTA00002916F.k.07.1.P.Seq	F	M00032614C:B10	CH08LNL
236	6321	RTA00002908F.b.17.1.P.Seq	F	M00022372D:H12	CH03MAH
237	21822	RTA00002903F.a.17.1.P.Seq	F	M00006861D:H10	CH02COH
238	8440	RTA00002923F.k.09.1.P.Seq	F	M00039302B:E10	CH09LNL
239	14677	RTA00002905F.c.05.1.P.Seq	F	M00007975D:F12	CH03MAH
240	135005	RTA00002902F.d.23.1.P.Seq	F	M00006592A:A12	CH02COH
241	5091	RTA00002895F.n.19.1.P.Seq	F	M00004115A:G12	CH01COH
242	24760	RTA00002923F.h.18.1.P.Seq	F	M00039270D:D02	CH09LNL
243	21833	RTA00002926F.f.22.2.P.Seq	F	M00040123C:A10	CH09LNL
244	12176	RTA00002886F.g.18.1.P.Seq	F	M00001353A:H07	CH01COH
245	14407	RTA00002901F.c.20.1.P.Seq	F	M00005452D:E05	CH02COH
246	186319	RTA00002912F.d.24.1.P.Seq	F	M00027290C:F06	CH04MAL
247	30135	RTA00002907F.i.21.2.P.Seq	F	M00022208C:F08	CH03MAH
248	33142	RTA00002901F.l.01.1.P.Seq	F	M00005607B:C04	CH02COH
249	33142	RTA00002901F.k.24.1.P.Seq	F	M00005607B:C04	CH02COH
250	16232	RTA00002900F.n.10.1.P.Seq	F	M00005387A:B03	CH02COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
251	23954	RTA00002894F.k.06.1.P.Seq	F	M00004036B:A11	CH01COH
252	12399	RTA00002918F.n.10.1.P.Seq	F	M00032985D:G09	CH08LNH
253	30853	RTA00002907F.j.16.2.P.Seq	F	M00022216D:D10	CH03MAH
254	8615	RTA00002907F.l.17.2.P.Seq	F	M00022238C:G04	CH03MAH
255	142359	RTA00002905F.c.10.1.P.Seq	F	M00007980B:A07	CH03MAH
256	9565	RTA00002926F.g.08.2.P.Seq	F	M00040127C:D02	CH09LNL
257	17334	RTA00002902F.d.03.1.P.Seq	F	M00006582D:A09	CH02COH
258	12540	RTA00002886F.f.03.1.P.Seq	F	M00001349C:B04	CH01COH
259	17289	RTA00002926F.f.14.2.P.Seq	F	M00040118D:C05	CH09LNL
260	46798	RTA00002907F.i.13.2.P.Seq	F	M00022202C:C04	CH03MAH
261	7797	RTA00002905F.b.06.1.P.Seq	F	M00007953D:F07	CH03MAH
262	1945	RTA00002896F.p.04.1.P.Seq	F	M00004201D:C03	CH01COH
263	6084	RTA00002896F.o.02.1.P.Seq	F	M00004195A:F07	CH01COH
264	6091	RTA00002930F.c.03.1.P.Seq	F	M00042915B:G11	CH15CON
265	186105	RTA00002930F.c.10.1.P.Seq	F	M00055430A:A01	CH15CON
266	11341	RTA00002930F.h.07.1.P.Seq	F	M00055961C:B10	CH15CON
267	2520	RTA00002930F.e.10.1.P.Seq	F	M00055639A:E06	CH15CON
268	136735	RTA00002903F.k.06.1.P.Seq	F	M00007006C:C12	CH02COH
269	8336	RTA00002900F.e.20.1.P.Seq	F	M00004873B:G04	CH02COH
270	13926	RTA00002907F.h.19.1.P.Seq	F	M00022193B:A09	CH03MAH
271	11119	RTA00002906F.k.01.1.P.Seq	F	M00022009C:A08	CH03MAH
272	11119	RTA00002906F.j.24.1.P.Seq	F	M00022009C:A08	CH03MAH
273	11726	RTA00002906F.l.07.1.P.Seq	F	M00022051B:D07	CH03MAH
274	6799	RTA00002925F.g.21.1.P.Seq	F	M00039885C:D11	CH09LNL
275	17266	RTA00002889F.g.09.1.P.Seq	F	M00001544B:B05	CH01COH
276	9479	RTA00002924F.g.04.1.P.Seq	F	M00039560B:G09	CH09LNL
277	185557	RTA00002912F.j.13.1.P.Seq	F	M00027457B:E11	CH04MAL
278	27872	RTA00002906F.e.14.1.P.Seq	F	M00021923D:H02	CH03MAH
279	15513	RTA00002924F.g.21.1.P.Seq	F	M00039617C:A10	CH09LNL
280	4446	RTA00002891F.m.15.1.P.Seq	F	M00003773A:F10	CH01COH
281	1681	RTA00002916F.g.07.1.P.Seq	F	M00032577D:F01	CH08LNH
282	24243	RTA00002887F.n.13.1.P.Seq	F	M00001424D:D02	CH01COH
283	16049	RTA00002900F.c.11.1.P.Seq	F	M00004846A:A10	CH02COH
284	186267	RTA00002910F.h.11.1.P.Seq	F	M00022924B:A05	CH03MAH
285	4543	RTA00002925F.h.22.1.P.Seq	F	M00039895D:C04	CH09LNL
286	6176	RTA00002914F.d.23.1.P.Seq	F	M00028188C:H11	CH08LNH
287	29043	RTA00002906F.h.17.1.P.Seq	F	M00021974D:F01	CH03MAH
288	696	RTA00002922F.o.15.1.P.Seq	F	M00039143A:F04	CH09LNL
289	7225	RTA00002891F.l.22.1.P.Seq	F	M00003770C:A10	CH01COH
290	25609	RTA00002899F.h.15.1.P.Seq	F	M00004608A:H04	CH01COH
291	6295	RTA00002922F.o.24.1.P.Seq	F	M00039146B:G04	CH09LNL
292	186319	RTA00002912F.e.01.1.P.Seq	F	M00027290C:F06	CH04MAL
293	4539	RTA00002889F.d.04.1.P.Seq	F	M00001534C:E07	CH01COH
294	17841	RTA00002891F.m.06.1.P.Seq	F	M00003771D:A03	CH01COH
295	13720	RTA00002924F.c.05.1.P.Seq	F	M00039430A:E04	CH09LNL
296	7300	RTA00002925F.a.14.1.P.Seq	F	M00039806B:D05	CH09LNL
297	186280	RTA00002912F.f.13.1.P.Seq	F	M00027316C:C03	CH04MAL
298	185585	RTA00002912F.n.04.1.P.Seq	F	M00027569A:E05	CH04MAL
299	3447	RTA00002900F.l.11.1.P.Seq	F	M00005364B:E10	CH02COH
300	14487	RTA00002889F.f.19.1.P.Seq	F	M00001542B:F09	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
301	5338	RTA00002901F.g.16.1.P.Seq	F	M00005505A:F01	CH02COH
302	7766	RTA00002917F.e.07.1.P.Seq	F	M00032700A:E09	CH08LNH
303	7450	RTA00002899F.g.09.1.P.Seq	F	M00004509D:C06	CH01COH
304	15369	RTA00002908F.m.18.1.P.Seq	F	M00022494D:A05	CH03MAH
305	4954	RTA00002919F.i.17.1.P.Seq	F	M00033150C:A11	CH08LNH
306	17189	RTA00002900F.j.11.1.P.Seq	F	M00005333D:D08	CH02COH
307	186561	RTA00002912F.m.23.1.P.Seq	F	M00027549C:G03	CH04MAL
308	44645	RTA00002896F.h.22.1.P.Seq	F	M00004165C:A11	CH01COH
309	11404	RTA00002924F.a.24.1.P.Seq	F	M00039413C:E06	CH09LNL
310	38212	RTA00002893F.m.22.1.P.Seq	F	M00003942A:D01	CH01COH
311	22099	RTA00002890F.m.09.1.P.Seq	F	M00001648A:D10	CH01COH
312	25041	RTA00002890F.p.12.1.P.Seq	F	M00001661D:F06	CH01COH
313	185938	RTA00002911F.p.01.1.P.Seq	F	M00027173C:E11	CH04MAL
314	9414	RTA00002908F.o.06.1.P.Seq	F	M00022509B:D11	CH03MAH
315	185707	RTA00002911F.o.19.1.P.Seq	F	M00027167C:B10	CH04MAL
316	185499	RTA00002912F.n.19.1.P.Seq	F	M00027586A:C09	CH04MAL
317	25704	RTA00002912F.n.22.1.P.Seq	F	M00027589B:G07	CH04MAL
318	21068	RTA00002896F.h.18.1.P.Seq	F	M00004164B:E12	CH01COH
319	13440	RTA00002917F.e.18.1.P.Seq	F	M00032711B:F01	CH08LNH
320	3907	RTA00002923F.i.18.1.P.Seq	F	M00039285B:G04	CH09LNL
321	21391	RTA00002896F.g.03.1.P.Seq	F	M00004158D:E08	CH01COH
322	6755	RTA00002918F.l.01.1.P.Seq	F	M00032944A:B07	CH08LNH
323	155939	RTA00002907F.j.23.1.P.Seq	F	M00022218B:B12	CH03MAH
324	8100	RTA00002896F.g.21.1.P.Seq	F	M00004160D:F06	CH01COH
325	4785	RTA00002919F.j.18.1.P.Seq	F	M00033183B:F10	CH08LNH
326	14947	RTA00002902F.k.23.1.P.Seq	F	M00006743A:D04	CH02COH
327	8295	RTA00002903F.k.23.1.P.Seq	F	M00007031A:E02	CH02COH
328	156277	RTA00002907F.l.13.1.P.Seq	F	M00022237D:D06	CH03MAH
329	22751	RTA00002897F.l.15.1.P.Seq	F	M00004282C:A12	CH01COH
330	7869	RTA00002917F.j.15.1.P.Seq	F	M00032749D:G03	CH08LNH
331	156009	RTA00002907F.k.05.1.P.Seq	F	M00022220A:A07	CH03MAH
332	9453	RTA00002907F.k.21.1.P.Seq	F	M00022228B:B11	CH03MAH
333	186052	RTA00002912F.h.08.1.P.Seq	F	M00027364B:E12	CH04MAL
334	669	RTA00002917F.f.22.1.P.Seq	F	M00032723D:H02	CH08LNH
335	11609	RTA00002899F.f.23.1.P.Seq	F	M00004507D:E03	CH01COH
336	186075	RTA00002911F.k.19.1.P.Seq	F	M00027057C:D10	CH04MAL
337	935	RTA00002911F.l.20.1.P.Seq	F	M00027081A:A08	CH04MAL
338	11430	RTA00002892F.e.07.2.P.Seq	F	M00003808B:E07	CH01COH
339	185938	RTA00002911F.o.24.1.P.Seq	F	M00027173C:E11	CH04MAL
340	12394	RTA00002915F.m.15.2.P.Seq	F	M00032497D:B10	CH08LNH
341	186588	RTA00002911F.l.03.1.P.Seq	F	M00027064B:D06	CH04MAL
342	23174	RTA00002909F.e.17.1.P.Seq	F	M00022600D:B05	CH03MAH
343	4727	RTA00002905F.g.19.1.P.Seq	F	M00008059D:B08	CH03MAH
344	17048	RTA00002887F.l.10.1.P.Seq	F	M00001416B:A05	CH01COH
345	2354	RTA00002916F.o.03.1.P.Seq	F	M00032645D:C01	CH08LNH
346	1987	RTA00002894F.a.13.1.P.Seq	F	M00003974D:E02	CH01COH
347	24483	RTA00002897F.i.21.1.P.Seq	F	M00004269A:G11	CH01COH
348	33337	RTA00002896F.f.08.1.P.Seq	F	M00004155A:H03	CH01COH
349	11641	RTA00002916F.m.19.1.P.Seq	F	M00032637A:F09	CH08LNH
350	10307	RTA00002910F.l.01.1.P.Seq	F	M00022995C:G07	CH03MAH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
351	20388	RTA00002906F.a.04.1.P.Seq	F	M00021700D:H03	CH03MAH
352	24687	RTA00002903F.m.02.1.P.Seq	F	M00007048B:E11	CH02COH
353	10414	RTA00002919F.n.19.1.P.Seq	F	M00033232B:C08	CH08LNH
354	11058	RTA00002892F.h.16.2.P.Seq	F	M00003820B:F11	CH01COH
355	6574	RTA00002917F.o.17.1.P.Seq	F	M00032797D:D08	CH08LNH
356	18782	RTA00002905F.f.07.1.P.Seq	F	M00008021C:G12	CH03MAH
357	35896	RTA00002896F.d.04.1.P.Seq	F	M00004146C:B04	CH01COH
358	3518	RTA00002930F.j.10.1.P.Seq	F	M00056217D:E10	CH15CON
359	8820	RTA00002915F.f.17.2.P.Seq	F	M00028782A:F01	CH08LNH
360	10208	RTA00002897F.h.08.1.P.Seq	F	M00004251D:D03	CH01COH
361	2089	RTA00002896F.g.14.1.P.Seq	F	M00004159D:F12	CH01COH
362	170919	RTA00002909F.p.03.1.P.Seq	F	M00022727A:G01	CH03MAH
363	8727	RTA00002917F.o.02.1.P.Seq	F	M00032791B:H11	CH08LNH
364	33184	RTA00002898F.d.08.1.P.Seq	F	M00004324A:D10	CH01COH
365	27973	RTA00002905F.g.13.1.P.Seq	F	M00008055D:G03	CH03MAH
366	15835	RTA00002897F.k.13.1.P.Seq	F	M00004278C:B10	CH01COH
367	10273	RTA00002903F.n.03.1.P.Seq	F	M00007081B:E09	CH02COH
368	2832	RTA00002899F.f.03.1.P.Seq	F	M00004502A:D12	CH01COH
369	32022	RTA00002903F.m.12.1.P.Seq	F	M00007060D:G07	CH02COH
370	68176	RTA00002893F.g.11.1.P.Seq	F	M00003898C:A01	CH01COH
371	29378	RTA00002915F.n.14.2.P.Seq	F	M00032508A:E03	CH08LNH
372	23235	RTA00002925F.k.02.1.P.Seq	F	M00039929B:E06	CH09LNL
373	12111	RTA00002895F.o.17.1.P.Seq	F	M00004122C:D01	CH01COH
374	5737	RTA00002924F.k.02.1.P.Seq	F	M00039672C:D05	CH09LNL
375	72475	RTA00002915F.l.15.1.P.Seq	F	M00032490D:E08	CH08LNH
376	7027	RTA00002907F.o.01.1.P.Seq	F	M00022264A:B02	CH03MAH
377	17165	RTA00002903F.d.19.1.P.Seq	F	M00006907A:C09	CH02COH
378	26446	RTA00002894F.m.17.1.P.Seq	F	M00004047C:B09	CH01COH
379	6755	RTA00002918F.k.24.1.P.Seq	F	M00032944A:B07	CH08LNH
380	9336	RTA00002909F.n.02.1.P.Seq	F	M00022703D:B11	CH03MAH
381	6960	RTA00002916F.o.08.1.P.Seq	F	M00032647B:F06	CH08LNH
382	472	RTA00002911F.g.01.1.P.Seq	F	M00026936D:C07	CH04MAL
383	9460	RTA00002908F.c.03.1.P.Seq	F	M00022376D:D05	CH03MAH
384	10307	RTA00002910F.k.24.1.P.Seq	F	M00022995C:G07	CH03MAH
385	4623	RTA00002923F.d.22.1.P.Seq	F	M00039222B:A04	CH09LNL
386	141167	RTA00002905F.c.09.1.P.Seq	F	M00007980A:B01	CH03MAH
387	34011	RTA00002898F.m.10.1.P.Seq	F	M00004385C:H12	CH01COH
388	5965	RTA00002915F.a.07.1.P.Seq	F	M00028620C:C07	CH08LNH
389	12336	RTA00002915F.g.04.1.P.Seq	F	M00028784A:D12	CH08LNH
390	36492	RTA00002893F.f.18.1.P.Seq	F	M00003891B:H02	CH01COH
391	29803	RTA00002908F.k.06.1.P.Seq	F	M00022467D:B03	CH03MAH
392	4420	RTA00002920F.a.15.1.P.Seq	F	M00033326B:B05	CH08LNH
393	15097	RTA00002923F.b.06.1.P.Seq	F	M00039175A:F01	CH09LNL
394	19133	RTA00002894F.g.03.1.P.Seq	F	M00003993C:D07	CH01COH
395	9810	RTA00002905F.c.03.1.P.Seq	F	M00007975C:A10	CH03MAH
396	31562	RTA00002897F.a.09.1.P.Seq	F	M00004210A:A03	CH01COH
397	1499	RTA00002912F.k.12.1.P.Seq	F	M00027475D:A01	CH04MAL
398	29531	RTA00002907F.o.05.1.P.Seq	F	M00022265A:F11	CH03MAH
399	4287	RTA00002918F.j.20.1.P.Seq	F	M00032928C:D02	CH08LNH
400	28660	RTA00002905F.p.11.1.P.Seq	F	M00021690A:C03	CH03MAH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
401	4596	RTA00002898F.f.21.1.P.Seq	F	M00004341C:E05	CH01COH
402	21774	RTA00002898F.c.20.1.P.Seq	F	M00004322B:D03	CH01COH
403	5611	RTA00002915F.e.12.1.P.Seq	F	M00028774D:E10	CH08LNH
404	7030	RTA00002894F.l.13.1.P.Seq	F	M00004042B:A11	CH01COH
405	11736	RTA00002898F.e.09.1.P.Seq	F	M00004330A:A01	CH01COH
406	94732	RTA00002910F.e.17.1.P.Seq	F	M00022856D:A07	CH03MAH
407	30283	RTA00002923F.g.19.1.P.Seq	F	M00039255D:B01	CH09LNL
408	129779	RTA00002904F.a.18.1.P.Seq	F	M00007155C:D07	CH02COH
409	4635	RTA00002900F.j.21.1.P.Seq	F	M00005349C:C02	CH02COH
410	5879	RTA00002893F.f.08.1.P.Seq	F	M00003888B:F09	CH01COH
411	119206	RTA00002905F.m.16.1.P.Seq	F	M00021650D:A11	CH03MAH
412	6946	RTA00002930F.g.19.2.P.Seq	F	M00055880B:H10	CH15CON
413	42462	RTA00002902F.f.12.1.P.Seq	F	M00006631D:D02	CH02COH
414	24285	RTA00002896F.m.17.1.P.Seq	F	M00004189A:C12	CH01COH
415	13769	RTA00002901F.a.17.1.P.Seq	F	M00005423C:D07	CH02COH
416	17039	RTA00002896F.i.14.1.P.Seq	F	M00004169A:E04	CH01COH
417	14397	RTA00002896F.j.11.1.P.Seq	F	M00004172D:B12	CH01COH
418	14351	RTA00002888F.c.21.1.P.Seq	F	M00001444C:D11	CH01COH
419	5579	RTA00002893F.j.11.1.P.Seq	F	M00003914A:A08	CH01COH
420	24186	RTA00002914F.n.02.1.P.Seq	F	M00028366B:B08	CH08LNH
421	11433	RTA00002921F.c.06.1.P.Seq	F	M00033342B:F03	CH09LNL
422	186635	RTA00002911F.f.06.1.P.Seq	F	M00026907D:E07	CH04MAL
423	5955	RTA00002915F.d.18.1.P.Seq	F	M00028771A:E02	CH08LNH
424	22053	RTA00002894F.k.09.1.P.Seq	F	M00004036D:C12	CH01COH
425	9259	RTA00002918F.b.09.1.P.Seq	F	M00032830D:D02	CH08LNH
426	25437	RTA00002905F.o.23.1.P.Seq	F	M00021681C:C09	CH03MAH
427	8488	RTA00002916F.i.02.1.P.Seq	F	M00032590B:H01	CH08LNH
428	4884	RTA00002919F.o.12.1.P.Seq	F	M00033248D:H11	CH08LNH
429	9804	RTA00002915F.c.19.1.P.Seq	F	M00028764B:D03	CH08LNH
430	179954	RTA00002910F.j.04.1.P.Seq	F	M00022964A:B03	CH03MAH
431	186532	RTA00002912F.a.01.1.P.Seq	F	M00027189C:B10	CH04MAL
432	11015	RTA00002894F.i.15.1.P.Seq	F	M00004029D:A01	CH01COH
433	8824	RTA00002903F.b.17.1.P.Seq	F	M00006877B:C09	CH02COH
434	4063	RTA00002916F.k.01.1.P.Seq	F	M00032613A:E11	CH08LNH
435	7964	RTA00002896F.i.18.1.P.Seq	F	M00004170A:F03	CH01COH
436	9238	RTA00002915F.j.20.1.P.Seq	F	M00032473B:A03	CH08LNH
437	2841	RTA00002914F.f.15.1.P.Seq	F	M00028196A:G03	CH08LNH
438	11203	RTA00002886F.p.16.1.P.Seq	F	M00001382D:H08	CH01COH
439	8800	RTA00002888F.c.20.1.P.Seq	F	M00001444B:E04	CH01COH
440	3224	RTA00002916F.d.23.1.P.Seq	F	M00032556D:A03	CH08LNH
441	95423	RTA00002909F.k.24.1.P.Seq	F	M00022674C:H08	CH03MAH
442	7911	RTA00002926F.c.11.2.P.Seq	F	M00040079D:D09	CH09LNL
443	88052	RTA00002925F.p.11.1.P.Seq	F	M00040041D:F01	CH09LNL
444	32736	RTA00002900F.l.20.1.P.Seq	F	M00005367D:A11	CH02COH
445	20811	RTA00002896F.n.14.1.P.Seq	F	M00004192C:B06	CH01COH
446	12856	RTA00002908F.b.07.1.P.Seq	F	M00022368A:B11	CH03MAH
447	12190	RTA00002899F.b.10.1.P.Seq	F	M00004430B:B10	CH01COH
448	10546	RTA00002901F.o.08.1.P.Seq	F	M00005689C:B02	CH02COH
449	21041	RTA00002898F.k.08.1.P.Seq	F	M00004372A:E12	CH01COH
450	16484	RTA00002894F.c.04.1.P.Seq	F	M00003979B:A04	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
451	7741	RTA00002894F.i.08.1.P.Seq	F	M00004028B:F10	CH01COH
452	14921	RTA00002926F.c.15.2.P.Seq	F	M00040081C:E02	CH09LNL
453	17571	RTA00002900F.m.16.1.P.Seq	F	M00005375D:A10	CH02COH
454	46881	RTA00002901F.l.20.1.P.Seq	F	M00005622A:H02	CH02COH
455	21533	RTA00002898F.j.10.1.P.Seq	F	M00004365C:C09	CH01COH
456	19010	RTA00002916F.k.08.1.P.Seq	F	M00032614D:D08	CH08LNL
457	48768	RTA00002886F.n.01.1.P.Seq	F	M00001374C:B10	CH01COH
458	7515	RTA00002892F.p.22.2.P.Seq	F	M00003855C:F02	CH01COH
459	17326	RTA00002898F.h.02.1.P.Seq	F	M00004350A:A04	CH01COH
460	3902	RTA00002901F.d.17.1.P.Seq	F	M00005460D:C11	CH02COH
461	12400	RTA00002901F.d.18.1.P.Seq	F	M00005461A:D12	CH02COH
462	186543	RTA00002912F.a.06.1.P.Seq	F	M00027193C:A07	CH04MAL
463	4063	RTA00002916F.j.24.1.P.Seq	F	M00032613A:E11	CH08LNL
464	6267	RTA00002910F.d.20.1.P.Seq	F	M00022835C:A09	CH03MAH
465	21349	RTA00002901F.c.04.1.P.Seq	F	M00005445D:F11	CH02COH
466	1123	RTA00002894F.i.24.1.P.Seq	F	M00004031C:G06	CH01COH
467	4401	RTA00002918F.m.18.1.P.Seq	F	M00032979D:C11	CH08LNL
468	15255	RTA00002925F.p.10.1.P.Seq	F	M00040041A:G08	CH09LNL
469	10991	RTA00002933F.a.15.1.P.Seq	F	M00043077C:G10	CH19COP
470	48768	RTA00002886F.m.24.1.P.Seq	F	M00001374C:B10	CH01COH
471	20406	RTA00002900F.c.20.1.P.Seq	F	M00004852D:C06	CH02COH
472	39784	RTA00002886F.g.05.1.P.Seq	F	M00001352B:B02	CH01COH
473	36567	RTA00002886F.n.06.1.P.Seq	F	M00001375B:D04	CH01COH
474	14817	RTA00002902F.a.18.1.P.Seq	F	M00005771D:C02	CH02COH
475	156277	RTA00002907F.l.13.2.P.Seq	F	M00022237D:D06	CH03MAH
476	6898	RTA00002907F.a.22.1.P.Seq	F	M00022104A:G08	CH03MAH
477	17376	RTA00002902F.c.03.1.P.Seq	F	M00005819D:F09	CH02COH
478	186535	RTA00002912F.d.12.1.P.Seq	F	M00027270A:D04	CH04MAL
479	91616	RTA00002910F.b.24.1.P.Seq	F	M00022812A:G01	CH03MAH
480	91616	RTA00002910F.c.01.1.P.Seq	F	M00022812A:G01	CH03MAH
481	6993	RTA00002896F.j.12.1.P.Seq	F	M00004172D:F04	CH01COH
482	12443	RTA00002916F.a.20.1.P.Seq	F	M00032534B:E12	CH08LNL
483	28585	RTA00002901F.j.16.1.P.Seq	F	M00005570A:D05	CH02COH
484	9453	RTA00002907F.k.21.2.P.Seq	F	M00022228B:B11	CH03MAH
485	156009	RTA00002907F.k.05.2.P.Seq	F	M00022220A:A07	CH03MAH
486	5958	RTA00002908F.n.22.2.P.Seq	F	M00022507C:C08	CH03MAH
487	155939	RTA00002907F.j.23.2.P.Seq	F	M00022218B:B12	CH03MAH
488	16695	RTA00002886F.g.22.1.P.Seq	F	M00001353D:E05	CH01COH
489	10118	RTA00002886F.h.18.1.P.Seq	F	M00001356D:E06	CH01COH
490	13288	RTA00002930F.b.21.1.P.Seq	F	M00042891C:G08	CH15CON
491	3210	RTA00002910F.h.22.1.P.Seq	F	M00022945A:H09	CH03MAH
492	15014	RTA00002934F.a.18.1.P.Seq	F	M00043528A:E11	CH20COHLV
493	22087	RTA00002890F.i.19.1.P.Seq	F	M00001624A:C01	CH01COH
494	31948	RTA00002908F.i.12.1.P.Seq	F	M00022454C:B08	CH03MAH
495	11593	RTA00002906F.p.21.1.P.Seq	F	M00022094B:G02	CH03MAH
496	3131	RTA00002908F.m.17.1.P.Seq	F	M00022494B:D06	CH03MAH
497	151263	RTA00002906F.i.21.1.P.Seq	F	M00021991D:F09	CH03MAH
498	177542	RTA00002910F.h.23.1.P.Seq	F	M00022945B:F11	CH03MAH
499	9738	RTA00002924F.f.23.1.P.Seq	F	M00039559B:C07	CH09LNL
500	15313	RTA00002925F.f.05.1.P.Seq	F	M00039865A:C09	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
501	19724	RTA00002906F.p.05.1.P.Seq	F	M00022088D:E10	CH03MAH
502	10731	RTA00002893F.m.11.1.P.Seq	F	M00003938C:A05	CH01COH
503	10257	RTA00002901F.h.09.1.P.Seq	F	M00005512B:H01	CH02COH
504	186468	RTA00002913F.b.18.1.P.Seq	F	M00027746A:D06	CH04MAL
505	14736	RTA00002908F.g.22.1.P.Seq	F	M00022436C:F11	CH03MAH
506	33267	RTA00002889F.h.14.1.P.Seq	F	M00001548B:D06	CH01COH
507	7719	RTA00002908F.e.11.1.P.Seq	F	M00022403C:E12	CH03MAH
508	185539	RTA00002913F.b.03.1.P.Seq	F	M00027717C:C06	CH04MAL
509	14825	RTA00002924F.f.19.1.P.Seq	F	M00039556C:G05	CH09LNL
510	3917	RTA00002906F.p.15.1.P.Seq	F	M00022092D:A11	CH03MAH
511	18718	RTA00002895F.h.05.1.P.Seq	F	M00004085B:H02	CH01COH
512	186762	RTA00002918F.b.11.1.P.Seq	F	M00032831A:C07	CH08LNL
513	2732	RTA00002925F.i.07.1.P.Seq	F	M00039900B:G04	CH09LNL
514	7684	RTA00002924F.j.17.1.P.Seq	F	M00039668C:F01	CH09LNL
515	6852	RTA00002922F.c.22.1.P.Seq	F	M00039001A:B10	CH09LNL
516	1422	RTA00002924F.c.09.1.P.Seq	F	M00039433C:E03	CH09LNL
517	5560	RTA00002917F.i.01.1.P.Seq	F	M00032734C:C05	CH08LNL
518	48734	RTA00002908F.l.23.1.P.Seq	F	M00022487C:C02	CH03MAH
519	10486	RTA00002899F.g.07.1.P.Seq	F	M00004509B:B10	CH01COH
520	33514	RTA00002890F.j.03.1.P.Seq	F	M00001626A:D07	CH01COH
521	5821	RTA00002917F.m.01.1.P.Seq	F	M00032772D:D03	CH08LNL
522	5821	RTA00002917F.l.24.1.P.Seq	F	M00032772D:D03	CH08LNL
523	21940	RTA00002896F.a.03.1.P.Seq	F	M00004134A:A08	CH01COH
524	185724	RTA00002912F.m.08.1.P.Seq	F	M00027523A:H05	CH04MAL
525	182887	RTA00002910F.k.21.1.P.Seq	F	M00022992A:H06	CH03MAH
526	21346	RTA00002901F.g.24.1.P.Seq	F	M00005507B:A03	CH02COH
527	5501	RTA00002887F.n.12.1.P.Seq	F	M00001424B:H06	CH01COH
528	13961	RTA00002892F.j.14.1.P.Seq	F	M00003828A:D11	CH01COH
529	16784	RTA00002886F.a.09.1.P.Seq	F	M00001338D:D01	CH01COH
530	17628	RTA00002916F.f.10.1.P.Seq	F	M00032568B:F08	CH08LNL
531	3304	RTA00002898F.d.05.1.P.Seq	F	M00004324A:B03	CH01COH
532	14895	RTA00002901F.g.14.1.P.Seq	F	M00005504C:F12	CH02COH
533	16036	RTA00002891F.k.09.1.P.Seq	F	M00003763B:B10	CH01COH
534	23877	RTA00002891F.k.15.1.P.Seq	F	M00003764B:F11	CH01COH
535	186784	RTA00002930F.i.17.1.P.Seq	F	M00056105A:D06	CH15CON
536	13591	RTA00002901F.f.15.1.P.Seq	F	M00005485C:H04	CH02COH
537	17916	RTA00002906F.p.08.1.P.Seq	F	M00022090B:A10	CH03MAH
538	40594	RTA00002897F.i.15.1.P.Seq	F	M00004266B:F07	CH01COH
539	9677	RTA00002925F.i.21.1.P.Seq	F	M00039915B:E08	CH09LNL
540	7736	RTA00002887F.e.03.1.P.Seq	F	M00001393B:C03	CH01COH
541	2474	RTA00002917F.e.15.1.P.Seq	F	M00032707D:F08	CH08LNL
542	23810	RTA00002892F.i.06.1.P.Seq	F	M00003822D:A02	CH01COH
543	24633	RTA00002907F.i.19.1.P.Seq	F	M00022208B:D03	CH03MAH
544	72081	RTA00002925F.k.03.1.P.Seq	F	M00039929D:H10	CH09LNL
545	5991	RTA00002916F.i.17.1.P.Seq	F	M00032597A:H02	CH08LNL
546	14596	RTA00002911F.n.15.1.P.Seq	F	M00027131A:B03	CH04MAL
547	6923	RTA00002896F.d.01.1.P.Seq	F	M00004146B:E08	CH01COH
548	6923	RTA00002896F.c.24.1.P.Seq	F	M00004146B:E08	CH01COH
549	21851	RTA00002887F.d.09.1.P.Seq	F	M00001391D:D03	CH01COH
550	3935	RTA00002925F.j.08.1.P.Seq	F	M00039921C:H11	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
551	13328	RTA00002909F.h.08.1.P.Seq	F	M00022634B:H09	CH03MAH
552	2492	RTA00002887F.e.11.1.P.Seq	F	M00001393D:E02	CH01COH
553	11960	RTA00002917F.b.03.1.P.Seq	F	M00032671B:D08	CH08LNL
554	186084	RTA00002912F.f.18.1.P.Seq	F	M00027319D:F07	CH04MAL
555	13644	RTA00002925F.a.09.1.P.Seq	F	M00039805B:B06	CH09LNL
556	5707	RTA00002909F.k.13.1.P.Seq	F	M00022672C:H04	CH03MAH
557	95700	RTA00002911F.p.14.1.P.Seq	F	M00027182B:G06	CH04MAL
558	342	RTA00002922F.i.23.1.P.Seq	F	M00039076D:G04	CH09LNL
559	8481	RTA00002887F.c.12.1.P.Seq	F	M00001389D:D06	CH01COH
560	12575	RTA00002916F.i.12.1.P.Seq	F	M00032594C:F05	CH08LNL
561	40712	RTA00002921F.d.08.1.P.Seq	F	M00033359C:H05	CH09LNL
562	10768	RTA00002886F.d.24.1.P.Seq	F	M00001346B:G11	CH01COH
563	38781	RTA00002889F.k.23.1.P.Seq	F	M00001559A:H09	CH01COH
564	8790	RTA00002888F.g.08.1.P.Seq	F	M00001461D:C10	CH01COH
565	10167	RTA00002916F.k.22.1.P.Seq	F	M00032621A:F11	CH08LNL
566	13706	RTA00002905F.e.21.1.P.Seq	F	M00008019B:A01	CH03MAH
567	124172	RTA00002900F.a.09.1.P.Seq	F	M00004824A:D12	CH02COH
568	92126	RTA00002910F.g.12.1.P.Seq	F	M00022904C:D04	CH03MAH
569	5830	RTA00002916F.j.09.1.P.Seq	F	M00032605B:D09	CH08LNL
570	15154	RTA00002886F.p.13.1.P.Seq	F	M00001382D:A07	CH01COH
571	25813	RTA00002910F.i.12.1.P.Seq	F	M00022952A:B02	CH03MAH
572	17268	RTA00002886F.d.07.1.P.Seq	F	M00001344D:E08	CH01COH
573	13684	RTA00002915F.j.09.1.P.Seq	F	M00031485B:G05	CH08LNL
574	13460	RTA00002898F.f.19.1.P.Seq	F	M00004341C:A09	CH01COH
575	25115	RTA00002919F.p.18.1.P.Seq	F	M00033311B:G10	CH08LNL
576	19949	RTA00002905F.e.17.1.P.Seq	F	M00008016B:E09	CH03MAH
577	24266	RTA00002917F.k.06.1.P.Seq	F	M00032759A:A03	CH08LNL
578	8243	RTA00002901F.o.17.1.P.Seq	F	M00005703B:E03	CH02COH
579	12576	RTA00002900F.k.23.1.P.Seq	F	M00005359B:B03	CH02COH
580	28531	RTA00002909F.c.04.1.P.Seq	F	M00022559D:G10	CH03MAH
581	15153	RTA00002894F.o.21.1.P.Seq	F	M00004054A:D03	CH01COH
582	9498	RTA00002894F.e.04.1.P.Seq	F	M00003985D:B02	CH01COH
583	48140	RTA00002914F.h.13.1.P.Seq	F	M00028211A:F10	CH08LNL
584	7626	RTA00002895F.b.04.1.P.Seq	F	M00004061B:E05	CH01COH
585	22668	RTA00002896F.p.17.1.P.Seq	F	M00004204C:H08	CH01COH
586	45691	RTA00002908F.a.11.1.P.Seq	F	M00022305A:B04	CH03MAH
587	30429	RTA00002904F.a.19.1.P.Seq	F	M00007155D:C09	CH02COH
588	46969	RTA00002909F.g.02.1.P.Seq	F	M00022618C:E04	CH03MAH
589	44030	RTA00002900F.o.23.1.P.Seq	F	M00005405C:D01	CH02COH
590	142548	RTA00002905F.h.10.1.P.Seq	F	M00008073A:D01	CH03MAH
591	18455	RTA00002905F.g.18.1.P.Seq	F	M00008059B:F08	CH03MAH
592	7501	RTA00002894F.g.05.1.P.Seq	F	M00003993D:B03	CH01COH
593	7280	RTA00002893F.n.22.1.P.Seq	F	M00003959D:A05	CH01COH
594	19339	RTA00002898F.l.12.1.P.Seq	F	M00004376D:A12	CH01COH
595	30194	RTA00002922F.k.05.1.P.Seq	F	M00039100A:G04	CH09LNL
596	32650	RTA00002911F.i.05.1.P.Seq	F	M00026994D:D07	CH04MAL
597	10510	RTA00002905F.d.17.1.P.Seq	F	M00008001B:F05	CH03MAH
598	13539	RTA00002898F.f.03.1.P.Seq	F	M00004336A:A01	CH01COH
599	20149	RTA00002917F.o.03.1.P.Seq	F	M00032791D:F01	CH08LNL
600	12780	RTA00002891F.e.06.1.P.Seq	F	M00001686D:F06	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
601	182479	RTA00002910F.j.18.1.P.Seq	F	M00022972C:E05	CH03MAH
602	14016	RTA00002923F.n.17.1.P.Seq	F	M00039344C:A11	CH09LNL
603	76075	RTA00002890F.h.23.1.P.Seq	F	M00001620B:A03	CH01COH
604	9806	RTA00002922F.j.05.1.P.Seq	F	M00039078D:C10	CH09LNL
605	9086	RTA00002889F.k.15.1.P.Seq	F	M00001558A:E06	CH01COH
606	2619	RTA00002907F.o.12.1.P.Seq	F	M00022269C:A04	CH03MAH
607	17517	RTA00002907F.h.06.1.P.Seq	F	M00022185A:B03	CH03MAH
608	5089	RTA00002915F.e.22.2.P.Seq	F	M00028777B:G04	CH08LNL
609	6728	RTA00002904F.b.13.1.P.Seq	F	M00007178A:C02	CH02COH
610	41149	RTA00002899F.g.20.1.P.Seq	F	M00004603B:E02	CH01COH
611	35017	RTA00002892F.f.03.2.P.Seq	F	M00003812C:A03	CH01COH
612	7008	RTA00002923F.a.08.1.P.Seq	F	M00039165D:C04	CH09LNL
613	185545	RTA00002912F.k.16.1.P.Seq	F	M00027480C:E09	CH04MAL
614	17840	RTA00002892F.p.15.2.P.Seq	F	M00003854B:F07	CH01COH
615	185914	RTA00002912F.j.24.1.P.Seq	F	M00027467A:C07	CH04MAL
616	6862	RTA00002903F.b.08.1.P.Seq	F	M00006872D:B07	CH02COH
617	20120	RTA00002888F.c.24.1.P.Seq	F	M00001445B:F06	CH01COH
618	20120	RTA00002888F.d.01.1.P.Seq	F	M00001445B:F06	CH01COH
619	13879	RTA00002923F.d.02.1.P.Seq	F	M00039207A:F07	CH09LNL
620	9330	RTA00002915F.g.16.1.P.Seq	F	M00028786B:A04	CH08LNL
621	21572	RTA00002921F.h.19.1.P.Seq	F	M00033441A:B12	CH09LNL
622	2943	RTA00002919F.h.22.1.P.Seq	F	M00033144A:D02	CH08LNL
623	32154	RTA00002905F.b.16.1.P.Seq	F	M00007969D:C01	CH03MAH
624	20875	RTA00002901F.k.16.1.P.Seq	F	M00005603B:H03	CH02COH
625	186324	RTA00002912F.d.17.1.P.Seq	F	M00027274A:A09	CH04MAL
626	10768	RTA00002886F.e.01.1.P.Seq	F	M00001346B:G11	CH01COH
627	16711	RTA00002935F.m.11.1.P.Seq	F	M00055221C:H11	CH17COHLV
628	14688	RTA00002925F.n.14.1.P.Seq	F	M00040023B:B10	CH09LNL
629	44419	RTA00002907F.b.19.1.P.Seq	F	M00022118A:E06	CH03MAH
630	12614	RTA00002896F.p.03.1.P.Seq	F	M00004201D:C01	CH01COH
631	21658	RTA00002902F.c.23.1.P.Seq	F	M00006576D:C02	CH02COH
632	10150	RTA00002901F.i.16.1.P.Seq	F	M00005540A:F09	CH02COH
633	185909	RTA00002912F.c.20.1.P.Seq	F	M00027262A:A07	CH04MAL
634	14893	RTA00002890F.f.08.1.P.Seq	F	M00001607D:H09	CH01COH
635	32125	RTA00002903F.c.08.1.P.Seq	F	M00006884D:A08	CH02COH
636	11909	RTA00002902F.a.11.1.P.Seq	F	M00005766D:D12	CH02COH
637	17237	RTA00002901F.l.12.1.P.Seq	F	M00005616B:F07	CH02COH
638	11148	RTA00002900F.j.18.1.P.Seq	F	M00005346D:A03	CH02COH
639	14837	RTA00002925F.n.20.1.P.Seq	F	M00040025A:B04	CH09LNL
640	4343	RTA00002897F.l.13.1.P.Seq	F	M00004282B:D07	CH01COH
641	18686	RTA00002898F.j.16.1.P.Seq	F	M00004366D:C11	CH01COH
642	10090	RTA00002892F.n.10.2.P.Seq	F	M00003842D:H09	CH01COH
643	612	RTA00002889F.d.13.2.P.Seq	F	M00001535B:E02	CH01COH
644	10752	RTA00002892F.n.06.2.P.Seq	F	M00003842D:D11	CH01COH
645	167203	RTA00002914F.c.14.1.P.Seq	F	M00028070A:H09	CH08LNL
646	21269	RTA00002901F.j.15.1.P.Seq	F	M00005570A:B08	CH02COH
647	186250	RTA00002910F.a.21.1.P.Seq	F	M00022797D:A06	CH03MAH
648	24633	RTA00002907F.i.19.2.P.Seq	F	M00022208B:D03	CH03MAH
649	12295	RTA00002918F.c.02.1.P.Seq	F	M00032836B:A07	CH08LNL
650	7870	RTA00002905F.b.22.1.P.Seq	F	M00007973B:D11	CH03MAH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
651	12225	RTA00002902F.d.08.1.P.Seq	F	M00006585A:D07	CH02COH
652	7775	RTA00002892F.o.12.2.P.Seq	F	M00003847A:H04	CH01COH
653	14901	RTA00002929F.f.21.1.P.Seq	F	M00040349D:D07	CH14EDT
654	6831	RTA00002927F.b.21.1.P.Seq	F	M00039483A:D10	CH12EDT
655	10738	RTA00002930F.b.08.1.P.Seq	F	M00042724A:G06	CH15CON
656	17986	RTA00002932F.a.20.1.P.Seq	F	M00042972C:F04	CH18CON
657	23163	RTA00002895F.h.03.1.P.Seq	F	M00004085A:H01	CH01COH
658	4838	RTA00002923F.i.15.1.P.Seq	F	M00039284D:H07	CH09LNL
659	25386	RTA00002905F.e.05.1.P.Seq	F	M00008007B:E03	CH03MAH
660	13217	RTA00002887F.n.01.1.P.Seq	F	M00001422B:D06	CH01COH
661	30656	RTA00002906F.l.03.1.P.Seq	F	M00022032A:G05	CH03MAH
662	7852	RTA00002889F.e.14.1.P.Seq	F	M00001538B:A07	CH01COH
663	13217	RTA00002887F.m.24.1.P.Seq	F	M00001422B:D06	CH01COH
664	15152	RTA00002925F.f.24.1.P.Seq	F	M00039873B:H04	CH09LNL
665	24143	RTA00002922F.o.18.1.P.Seq	F	M00039143D:C10	CH09LNL
666	23872	RTA00002892F.i.13.1.P.Seq	F	M00003823B:A06	CH01COH
667	13940	RTA00002906F.g.23.1.P.Seq	F	M00021967D:H06	CH03MAH
668	25759	RTA00002907F.m.10.1.P.Seq	F	M00022249D:C01	CH03MAH
669	5761	RTA00002924F.p.05.1.P.Seq	F	M00039786D:A10	CH09LNL
670	41703	RTA00002901F.g.23.1.P.Seq	F	M00005506D:E11	CH02COH
671	7165	RTA00002909F.i.06.1.P.Seq	F	M00022648A:D08	CH03MAH
672	41492	RTA00002889F.m.18.1.P.Seq	F	M00001565A:H05	CH01COH
673	9331	RTA00002906F.g.10.1.P.Seq	F	M00021958B:E08	CH03MAH
674	7961	RTA00002887F.g.24.1.P.Seq	F	M00001399B:B01	CH01COH
675	15367	RTA00002893F.n.17.1.P.Seq	F	M00003958C:H08	CH01COH
676	185628	RTA00002912F.f.17.1.P.Seq	F	M00027319C:C03	CH04MAL
677	7386	RTA00002891F.l.14.1.P.Seq	F	M00003768D:D08	CH01COH
678	67391	RTA00002893F.p.07.1.P.Seq	F	M00003968C:G03	CH01COH
679	46380	RTA00002906F.f.10.1.P.Seq	F	M00021933B:F02	CH03MAH
680	14265	RTA00002892F.e.05.2.P.Seq	F	M00003808A:F11	CH01COH
681	186478	RTA00002912F.f.07.1.P.Seq	F	M00027313C:E01	CH04MAL
682	8192	RTA00002916F.m.07.1.P.Seq	F	M00032634B:D09	CH08LNL
683	13776	RTA00002925F.l.10.1.P.Seq	F	M00039976C:F11	CH09LNL
684	11796	RTA00002912F.e.02.1.P.Seq	F	M00027291A:G08	CH04MAL
685	10827	RTA00002919F.i.10.1.P.Seq	F	M00033147C:B08	CH08LNL
686	1482	RTA00002925F.l.12.1.P.Seq	F	M00039977B:D12	CH09LNL
687	30300	RTA00002906F.f.16.1.P.Seq	F	M00021941A:D09	CH03MAH
688	10454	RTA00002890F.i.15.1.P.Seq	F	M00001623D:A10	CH01COH
689	16649	RTA00002907F.l.01.1.P.Seq	F	M00022229D:E01	CH03MAH
690	7026	RTA00002887F.b.10.1.P.Seq	F	M00001387B:A11	CH01COH
691	5691	RTA00002895F.n.13.1.P.Seq	F	M00004114C:D11	CH01COH
692	13797	RTA00002918F.i.21.1.P.Seq	F	M00032918D:B04	CH08LNL
693	5187	RTA00002923F.n.03.1.P.Seq	F	M00039338B:F07	CH09LNL
694	186115	RTA00002912F.i.01.1.P.Seq	F	M00027376C:A02	CH04MAL
695	4826	RTA00002917F.g.24.1.P.Seq	F	M00032729A:F10	CH08LNL
696	6733	RTA00002917F.m.11.1.P.Seq	F	M00032774C:C04	CH08LNL
697	7604	RTA00002923F.j.05.1.P.Seq	F	M00039291D:F02	CH09LNL
698	46459	RTA00002905F.f.01.1.P.Seq	F	M00008020D:F02	CH03MAH
699	23385	RTA00002889F.i.23.1.P.Seq	F	M00001551D:D01	CH01COH
700	7516	RTA00002891F.h.11.1.P.Seq	F	M00003749C:C08	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
701	45048	RTA00002906F.b.04.1.P.Seq	F	M00021855D:F10	CH03MAH
702	14845	RTA00002903F.o.02.1.P.Seq	F	M00007103C:C12	CH02COH
703	16479	RTA00002887F.i.15.1.P.Seq	F	M00001403D:C12	CH01COH
704	186729	RTA00002911F.d.19.2.P.Seq	F	M00026850B:C09	CH04MAL
705	33658	RTA00002886F.j.07.1.P.Seq	F	M00001361B:A12	CH01COH
706	186755	RTA00002912F.i.18.1.P.Seq	F	M00027400D:H02	CH04MAL
707	4262	RTA00002897F.a.04.1.P.Seq	F	M00004208A:D08	CH01COH
708	14039	RTA00002897F.k.01.1.P.Seq	F	M00004276C:A08	CH01COH
709	11948	RTA00002895F.n.24.1.P.Seq	F	M00004118C:D12	CH01COH
710	14865	RTA00002908F.l.14.1.P.Seq	F	M00022481B:A04	CH03MAH
711	10779	RTA00002915F.i.01.1.P.Seq	F	M00031370B:C01	CH08LNH
712	7503	RTA00002902F.k.16.1.P.Seq	F	M00006738A:F12	CH02COH
713	48130	RTA00002902F.e.04.1.P.Seq	F	M00006595B:C10	CH02COH
714	7858	RTA00002907F.m.12.1.P.Seq	F	M00022250A:B04	CH03MAH
715	4682	RTA00002924F.n.02.1.P.Seq	F	M00039710B:E01	CH09LNL
716	20650	RTA00002888F.p.10.1.P.Seq	F	M00001503B:H10	CH01COH
717	25320	RTA00002910F.e.19.1.P.Seq	F	M00022857B:A09	CH03MAH
718	4924	RTA00002930F.g.01.2.P.Seq	F	M00055805A:H02	CH15CON
719	21170	RTA00002900F.l.13.1.P.Seq	F	M00005365A:F05	CH02COH
720	9258	RTA00002890F.h.17.1.P.Seq	F	M00001618C:D01	CH01COH
721	14039	RTA00002897F.j.24.1.P.Seq	F	M00004276C:A08	CH01COH
722	3483	RTA00002899F.b.07.1.P.Seq	F	M00004430A:A05	CH01COH
723	3877	RTA00002897F.k.10.1.P.Seq	F	M00004278A:G06	CH01COH
724	7483	RTA00002923F.f.19.1.P.Seq	F	M00039246B:A08	CH09LNL
725	99750	RTA00002900F.l.17.1.P.Seq	F	M00005366D:F08	CH02COH
726	46459	RTA00002905F.e.24.1.P.Seq	F	M00008020D:F02	CH03MAH
727	3591	RTA00002886F.o.09.1.P.Seq	F	M00001378C:E10	CH01COH
728	11277	RTA00002923F.g.11.1.P.Seq	F	M00039251D:B08	CH09LNL
729	10292	RTA00002898F.n.11.1.P.Seq	F	M00004393C:D06	CH01COH
730	23211	RTA00002922F.k.13.1.P.Seq	F	M00039105D:A08	CH09LNL
731	185698	RTA00002911F.d.03.2.P.Seq	F	M00026836B:H03	CH04MAL
732	24702	RTA00002898F.i.17.1.P.Seq	F	M00004360C:D09	CH01COH
733	12595	RTA00002904F.c.06.1.P.Seq	F	M00007197B:B05	CH02COH
734	177444	RTA00002910F.o.06.1.P.Seq	F	M00023097D:B08	CH03MAH
735	38147	RTA00002886F.o.11.1.P.Seq	F	M00001379A:F09	CH01COH
736	17909	RTA00002908F.d.09.1.P.Seq	F	M00022386D:F10	CH03MAH
737	13399	RTA00002900F.n.07.1.P.Seq	F	M00005385A:B12	CH02COH
738	17720	RTA00002905F.g.22.1.P.Seq	F	M00008065D:A07	CH03MAH
739	45974	RTA00002909F.l.08.1.P.Seq	F	M00022681D:E10	CH03MAH
740	10779	RTA00002915F.h.24.2.P.Seq	F	M00031370B:C01	CH08LNH
741	195	RTA00002914F.a.14.1.P.Seq	F	M00028055B:G07	CH08LNH
742	1712	RTA00002915F.j.07.1.P.Seq	F	M00031484A:D03	CH08LNH
743	185726	RTA00002912F.a.21.1.P.Seq	F	M00027215B:B12	CH04MAL
744	150298	RTA00002907F.d.20.1.P.Seq	F	M00022140D:A07	CH03MAH
745	358	RTA00002898F.i.02.1.P.Seq	F	M00004358B:G02	CH01COH
746	42920	RTA00002900F.l.16.1.P.Seq	F	M00005309B:A11	CH02COH
747	25681	RTA00002894F.k.18.1.P.Seq	F	M00004038A:A04	CH01COH
748	18005	RTA00002903F.c.18.1.P.Seq	F	M00006890C:F10	CH02COH
749	16143	RTA00002892F.m.04.2.P.Seq	F	M00003839C:H10	CH01COH
750	9306	RTA00002902F.d.09.1.P.Seq	F	M00006585A:F09	CH02COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
751	32293	RTA00002901F.i.13.1.P.Seq	F	M00005535B:B01	CH02COH
752	8913	RTA00002901F.j.07.1.P.Seq	F	M00005557D:H10	CH02COH
753	185819	RTA00002912F.a.20.1.P.Seq	F	M00027215A:F06	CH04MAL
754	10559	RTA00002898F.o.12.1.P.Seq	F	M00004406A:G09	CH01COH
755	8740	RTA00002923F.o.11.1.P.Seq	F	M00039383A:H07	CH09LNL
756	160257	RTA00002907F.l.12.2.P.Seq	F	M00022237C:E04	CH03MAH
757	6078	RTA00002930F.c.11.1.P.Seq	F	M00055433D:G03	CH15CON
758	12543	RTA00002927F.b.14.1.P.Seq	F	M00039377B:E05	CH12EDT
759	9686	RTA00002930F.f.19.1.P.Seq	F	M00055794A:E10	CH15CON
760	3369	RTA00002930F.b.12.1.P.Seq	F	M00042732B:H06	CH15CON
761	6891	RTA00002895F.i.03.1.P.Seq	F	M00004087C:E02	CH01COH
762	13666	RTA00002892F.i.05.1.P.Seq	F	M00003822C:A09	CH01COH
763	6925	RTA00002930F.k.24.1.P.Seq	F	M00056458C:E01	CH15CON
764	11351	RTA00002901F.g.15.1.P.Seq	F	M00005504D:F06	CH02COH
765	11497	RTA00002889F.a.21.1.P.Seq	F	M00001512D:F08	CH01COH
766	1596	RTA00002922F.m.18.1.P.Seq	F	M00039125D:H12	CH09LNL
767	186519	RTA00002924F.a.22.1.P.Seq	F	M00039411D:D09	CH09LNL
768	24429	RTA00002903F.j.04.1.P.Seq	F	M00006989B:G05	CH02COH
769	33795	RTA00002902F.k.18.1.P.Seq	F	M00006739B:A04	CH02COH
770	24267	RTA00002889F.l.17.1.P.Seq	F	M00001561D:H04	CH01COH
771	12536	RTA00002891F.j.20.1.P.Seq	F	M00003760C:G10	CH01COH
772	22627	RTA00002887F.k.07.1.P.Seq	F	M00001410A:G10	CH01COH
773	24430	RTA00002901F.h.20.1.P.Seq	F	M00005520B:E01	CH02COH
774	16151	RTA00002897F.l.22.1.P.Seq	F	M00004284A:F08	CH01COH
775	6148	RTA00002890F.i.16.1.P.Seq	F	M00001623D:E12	CH01COH
776	106064	RTA00002908F.l.19.1.P.Seq	F	M00022485B:E07	CH03MAH
777	9573	RTA00002893F.p.13.1.P.Seq	F	M00003970D:H07	CH01COH
778	19542	RTA00002902F.l.20.1.P.Seq	F	M00006756B:G06	CH02COH
779	16672	RTA00002889F.b.21.1.P.Seq	F	M00001528C:C03	CH01COH
780	8573	RTA00002891F.p.07.1.P.Seq	F	M00003785D:F07	CH01COH
781	15746	RTA00002896F.h.10.1.P.Seq	F	M00004163C:A03	CH01COH
782	4500	RTA00002887F.b.08.1.P.Seq	F	M00001387A:C12	CH01COH
783	16003	RTA00002910F.c.08.1.P.Seq	F	M00022820A:F07	CH03MAH
784	18723	RTA00002916F.g.18.1.P.Seq	F	M00032580D:A09	CH08LNL
785	4270	RTA00002922F.b.01.1.P.Seq	F	M00038616C:C09	CH09LNL
786	30095	RTA00002907F.i.20.1.P.Seq	F	M00022208C:E04	CH03MAH
787	42916	RTA00002924F.c.08.1.P.Seq	F	M00039433B:D06	CH09LNL
788	13652	RTA00002902F.j.09.1.P.Seq	F	M00006714C:D06	CH02COH
789	6972	RTA00002902F.j.06.1.P.Seq	F	M00006712C:H01	CH02COH
790	4519	RTA00002910F.i.06.1.P.Seq	F	M00022947B:D02	CH03MAH
791	13106	RTA00002928F.f.09.1.P.Seq	F	M00040224C:F06	CH13EDT
792	98186	RTA00002909F.m.08.1.P.Seq	F	M00022696B:C11	CH03MAH
793	3167	RTA00002898F.g.09.1.P.Seq	F	M00004344D:C12	CH01COH
794	3272	RTA00002897F.a.18.1.P.Seq	F	M00004212D:C03	CH01COH
795	14446	RTA00002899F.d.05.1.P.Seq	F	M00004462D:D12	CH01COH
796	17865	RTA00002918F.a.13.1.P.Seq	F	M00032825B:F08	CH08LNL
797	5834	RTA00002898F.h.12.1.P.Seq	F	M00004352A:D08	CH01COH
798	14533	RTA00002896F.k.24.1.P.Seq	F	M00004179C:B06	CH01COH
799	15222	RTA00002900F.j.05.1.P.Seq	F	M00005532A:C06	CH02COH
800	22594	RTA00002898F.h.21.1.P.Seq	F	M00004357B:B06	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
801	9204	RTA00002890F.h.20.1.P.Seq	F	M00001619C:H09	CH01COH
802	186464	RTA00002911F.d.09.2.P.Seq	F	M00026842D:C02	CH04MAL
803	5441	RTA00002900F.a.11.1.P.Seq	F	M00004824D:H05	CH02COH
804	32544	RTA00002893F.l.21.1.P.Seq	F	M00003935B:B01	CH01COH
805	15351	RTA00002915F.j.15.1.P.Seq	F	M00032471D:A05	CH08LNH
806	13129	RTA00002898F.a.12.1.P.Seq	F	M00004310B:E02	CH01COH
807	186376	RTA00002912F.k.21.1.P.Seq	F	M00027485C:F07	CH04MAL
808	17816	RTA00002901F.o.04.1.P.Seq	F	M00005674C:F04	CH02COH
809	8434	RTA00002923F.l.22.1.P.Seq	F	M00039326C:B08	CH09LNL
810	22146	RTA00002922F.i.08.1.P.Seq	F	M00039067B:F07	CH09LNL
811	31912	RTA00002904F.a.14.1.P.Seq	F	M00007154A:E06	CH02COH
812	1487	RTA00002925F.n.03.1.P.Seq	F	M00040016C:E07	CH09LNL
813	24777	RTA00002900F.n.02.1.P.Seq	F	M00005380B:H10	CH02COH
814	144483	RTA00002902F.d.01.1.P.Seq	F	M00006577A:H10	CH02COH
815	6546	RTA00002935F.p.16.1.P.Seq	F	M00055425C:A04	CH17COHLV
816	5984	RTA00002935F.p.09.1.P.Seq	F	M00055420A:E06	CH17COHLV
817	24441	RTA00002900F.a.22.1.P.Seq	F	M00004832D:G04	CH02COH
818	20889	RTA00002935F.h.09.1.P.Seq	F	M00054807D:C11	CH17COHLV
819	127721	RTA00002915F.c.18.1.P.Seq	F	M00028763A:G11	CH08LNH
820	20684	RTA00002900F.c.03.1.P.Seq	F	M00004843A:G12	CH02COH
821	30095	RTA00002907F.i.20.2.P.Seq	F	M00022208C:E04	CH03MAH
822	6763	RTA00002892F.o.01.2.P.Seq	F	M00003845D:G03	CH01COH
823	6763	RTA00002892F.n.24.2.P.Seq	F	M00003845D:G03	CH01COH
824	48725	RTA00002907F.l.22.2.P.Seq	F	M00022240B:C12	CH03MAH
825	21260	RTA00002935F.c.22.1.P.Seq	F	M00054499A:C08	CH17COHLV
826	42572	RTA00002930F.c.21.1.P.Seq	F	M00055454A:D02	CH15CON
827	3441	RTA00002935F.i.13.1.P.Seq	F	M00054890C:D05	CH17COHLV
828	21419	RTA00002930F.b.13.1.P.Seq	F	M00042734A:F05	CH15CON
829	8004	RTA00002910F.b.08.1.P.Seq	F	M00022805B:A10	CH03MAH
830	185870	RTA00002912F.c.06.1.P.Seq	F	M00027247C:D02	CH04MAL
831	24580	RTA00002930F.d.01.1.P.Seq	F	M00055466A:F06	CH15CON
832	5153	RTA00002930F.b.16.1.P.Seq	F	M00042743D:G10	CH15CON
833	8653	RTA00002895F.f.17.1.P.Seq	F	M00004080C:C04	CH01COH
834	23799	RTA00002924F.l.23.1.P.Seq	F	M00039698C:B03	CH09LNL
835	11012	RTA00002930F.j.09.1.P.Seq	F	M00056215D:F02	CH15CON
836	46592	RTA00002900F.b.19.1.P.Seq	F	M00004839B:C12	CH02COH
837	6650	RTA00002908F.m.12.1.P.Seq	F	M00022491D:A10	CH03MAH
838	16618	RTA00002889F.n.18.1.P.Seq	F	M00001568C:A03	CH01COH
839	18274	RTA00002889F.g.05.1.P.Seq	F	M00001543C:A08	CH01COH
840	20694	RTA00002908F.h.08.1.P.Seq	F	M00022442B:G03	CH03MAH
841	9493	RTA00002909F.m.11.1.P.Seq	F	M00022698C:D10	CH03MAH
842	6132	RTA00002897F.c.04.1.P.Seq	F	M00004220D:C11	CH01COH
843	186259	RTA00002912F.m.13.1.P.Seq	F	M00027527B:C05	CH04MAL
844	3769	RTA00002916F.g.22.1.P.Seq	F	M00032581B:A09	CH08LNH
845	36584	RTA00002935F.f.12.1.P.Seq	F	M00054683D:G11	CH17COHLV
846	38077	RTA00002890F.e.06.1.P.Seq	F	M00001605B:B05	CH01COH
847	3927	RTA00002935F.a.12.1.P.Seq	F	M00042516B:D01	CH17COHLV
848	4275	RTA00002914F.b.16.1.P.Seq	F	M00028063C:H01	CH08LNH
849	12554	RTA00002921F.a.23.1.P.Seq	F	M00033302A:E11	CH09LNL
850	13761	RTA00002901F.f.22.1.P.Seq	F	M00005489B:C08	CH02COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
851	19059	RTA00002897F.e.22.1.P.Seq	F	M00004237C:D10	CH01COH
852	22944	RTA00002935F.b.17.1.P.Seq	F	M00043355A:D07	CH17COHLV
853	2189	RTA00002925F.j.06.1.P.Seq	F	M00039921A:B10	CH09LNL
854	19153	RTA00002892F.h.04.2.P.Seq	F	M00003819B:B01	CH01COH
855	1833	RTA00002890F.e.13.1.P.Seq	F	M00001606B:A10	CH01COH
856	18447	RTA00002935F.d.23.1.P.Seq	F	M00054569A:B07	CH17COHLV
857	2461	RTA00002922F.b.08.1.P.Seq	F	M00038619B:F09	CH09LNL
858	15917	RTA00002896F.j.06.1.P.Seq	F	M00004172C:A08	CH01COH
859	9379	RTA00002935F.a.15.1.P.Seq	F	M00043299A:B10	CH17COHLV
860	5511	RTA00002931F.b.06.1.P.Seq	F	M00042796A:A10	CH16COP
861	10540	RTA00002891F.k.16.1.P.Seq	F	M00003764B:H11	CH01COH
862	12117	RTA00002899F.a.09.1.P.Seq	F	M00004419A:G02	CH01COH
863	8777	RTA00002919F.a.23.1.P.Seq	F	M00033028D:C10	CH08LNL
864	23972	RTA00002900F.o.18.1.P.Seq	F	M00005403C:A01	CH02COH
865	17005	RTA00002896F.m.10.1.P.Seq	F	M00004187B:C02	CH01COH
866	1085	RTA00002924F.l.20.1.P.Seq	F	M00039694C:H01	CH09LNL
867	4270	RTA00002922F.a.24.1.P.Seq	F	M00038616C:C09	CH09LNL
868	4609	RTA00002935F.e.15.1.P.Seq	F	M00054599D:B03	CH17COHLV
869	6889	RTA00002919F.c.07.1.P.Seq	F	M00033037B:F04	CH08LNL
870	15228	RTA00002919F.e.06.1.P.Seq	F	M00033055D:D02	CH08LNL
871	20971	RTA00002904F.a.22.1.P.Seq	F	M00007158D:D03	CH02COH
872	5174	RTA00002935F.a.23.1.P.Seq	F	M00043313D:E09	CH17COHLV
873	15236	RTA00002928F.e.16.1.P.Seq	F	M00040198A:F12	CH13EDT
874	9223	RTA00002896F.b.15.1.P.Seq	F	M00004141A:D01	CH01COH
875	24591	RTA00002923F.g.10.1.P.Seq	F	M00039251C:H12	CH09LNL
876	36306	RTA00002888F.l.11.1.P.Seq	F	M00001485C:F06	CH01COH
877	3309	RTA00002893F.j.21.1.P.Seq	F	M00003916A:E04	CH01COH
878	186712	RTA00002911F.c.11.2.P.Seq	F	M00026809A:H08	CH04MAL
879	9090	RTA00002891F.g.23.1.P.Seq	F	M00003746C:E11	CH01COH
880	11510	RTA00002888F.i.07.1.P.Seq	F	M00001467C:D04	CH01COH
881	9784	RTA00002889F.j.15.1.P.Seq	F	M00001554C:G10	CH01COH
882	25618	RTA00002930F.a.11.1.P.Seq	F	M00042554A:D01	CH15CON
883	12493	RTA00002928F.i.11.1.P.Seq	F	M00040289D:C06	CH13EDT
884	24361	RTA00002933F.b.08.1.P.Seq	F	M00043134A:F05	CH19COP
885	12449	RTA00002930F.d.02.1.P.Seq	F	M00055468A:A08	CH15CON
886	17894	RTA00002929F.a.04.1.P.Seq	F	M00039747B:B06	CH14EDT
887	13204	RTA00002930F.f.09.1.P.Seq	F	M00055745B:A08	CH15CON
888	32119	RTA00002930F.c.19.1.P.Seq	F	M00055448B:E05	CH15CON
889	5909	RTA00002935F.i.23.1.P.Seq	F	M00054931D:E10	CH17COHLV
890	24453	RTA00002927F.d.15.1.P.Seq	F	M00039526A:A08	CH12EDT
891	46982	RTA00002935F.k.22.1.P.Seq	F	M00055093B:A03	CH17COHLV
892	43888	RTA00002932F.b.23.1.P.Seq	F	M00043070A:C03	CH18CON
893	24580	RTA00002930F.c.24.1.P.Seq	F	M00055406A:F06	CH15CON
894	186495	RTA00002927F.a.21.1.P.Seq	F	M00039304D:E05	CH12EDT
895	12420	RTA00002932F.b.21.1.P.Seq	F	M00043063C:H05	CH18CON
896	3833	RTA00002916F.e.14.1.P.Seq	F	M00032562C:F01	CH08LNL
897	10438	RTA00002930F.j.13.1.P.Seq	F	M00056230D:E07	CH15CON
898	12367	RTA00002922F.n.10.1.P.Seq	F	M00039133B:D06	CH09LNL
899	5012	RTA00002930F.k.16.1.P.Seq	F	M00056342A:C03	CH15CON
900	6458	RTA00002929F.c.21.1.P.Seq	F	M00040291A:G10	CH14EDT

126

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
901	16507	RTA00002929F.d.08.1.P.Seq	F	M00040298B:B09	CH14EDT
902	13914	RTA00002922F.h.18.1.P.Seq	F	M00039063C:H09	CH09LNL
903	11590	RTA00002930F.k.18.1.P.Seq	F	M00056436C:F01	CH15CON
904	15380	RTA00002928F.l.06.1.P.Seq	F	M00040287A:C11	CH13EDT
905	10190	RTA00002895F.k.07.1.P.Seq	F	M00004096D:F02	CH01COH
906	12593	RTA00002934F.a.12.1.P.Seq	F	M00043485C:C03	CH20COHLV
907	112813	RTA00002905F.o.14.1.P.Seq	F	M00021677A:D09	CH03MAH
908	15929	RTA00002930F.j.18.1.P.Seq	F	M00056244C:H05	CH15CON
909	16670	RTA00002935F.o.16.1.P.Seq	F	M00055387C:C12	CH17COHLV
910	10924	RTA00002907F.k.12.2.P.Seq	F	M00022224A:C07	CH03MAH
911	6233	RTA00002896F.b.17.1.P.Seq	F	M00004141B:B01	CH01COH
912	14777	RTA00002897F.k.09.1.P.Seq	F	M00004277D:B02	CH01COH
913	12797	RTA00002935F.h.01.1.P.Seq	F	M00054781D:A11	CH17COHLV
914	186041	RTA00002912F.c.01.1.P.Seq	F	M00027244C:B06	CH04MAL
915	8182	RTA00002931F.a.22.1.P.Seq	F	M00042766C:D05	CH16COP
916	23088	RTA00002888F.p.20.1.P.Seq	F	M00001506B:D11	CH01COH
917	24298	RTA00002935F.p.18.1.P.Seq	F	M00055473C:F02	CH17COHLV
918	40621	RTA00002896F.k.12.1.P.Seq	F	M00004176C:A09	CH01COH
919	7124	RTA00002935F.b.07.1.P.Seq	F	M00043328C:E04	CH17COHLV
920	21107	RTA00002901F.i.02.1.P.Seq	F	M00005524C:H04	CH02COH
921	10807	RTA00002928F.c.15.1.P.Seq	F	M00040162A:E02	CH13EDT
922	12162	RTA00002915F.j.23.1.P.Seq	F	M00032475A:A06	CH08LNL
923	14747	RTA00002931F.a.18.1.P.Seq	F	M00042512D:D10	CH16COP
924	6824	RTA00002931F.b.23.1.P.Seq	F	M00042857C:E01	CH16COP
925	39115	RTA00002932F.a.17.1.P.Seq	F	M00042967D:C01	CH18CON
926	9484	RTA00002934F.a.13.1.P.Seq	F	M00043490C:F02	CH20COHLV
927	77981	RTA00002890F.j.21.1.P.Seq	F	M00001633D:C11	CH01COH
928	16061	RTA00002932F.b.24.1.P.Seq	F	M00043113C:G09	CH18CON
929	4834	RTA00002930F.d.12.1.P.Seq	F	M00055527B:E01	CH15CON
930	9427	RTA00002935F.e.21.1.P.Seq	F	M00054623C:F05	CH17COHLV
931	167736	RTA00002935F.l.11.1.P.Seq	F	M00055117A:E02	CH17COHLV
932	16524	RTA00002935F.b.19.1.P.Seq	F	M00043358C:A02	CH17COHLV
933	23496	RTA00002932F.a.21.1.P.Seq	F	M00042976D:C01	CH18CON
934	163647	RTA00002901F.m.17.1.P.Seq	F	M00005634A:F07	CH02COH
935	14239	RTA00002931F.b.07.1.P.Seq	F	M00042801C:D01	CH16COP
936	25574	RTA00002886F.g.20.1.P.Seq	F	M00001353C:A05	CH01COH
937	2737	RTA00002932F.a.08.1.P.Seq	F	M00042588C:E02	CH18CON
938	6925	RTA00002930F.l.01.1.P.Seq	F	M00056458C:E01	CH15CON
939	21106	RTA00002925F.p.16.1.P.Seq	F	M00040045B:H07	CH09LNL
940	28134	RTA00002917F.k.23.1.P.Seq	F	M00032765A:C05	CH08LNL
941	186496	RTA00002917F.l.16.1.P.Seq	F	M00032770C:G11	CH08LNL
942	21625	RTA00002893F.j.18.1.P.Seq	F	M00003915C:G08	CH01COH
943	12537	RTA00002930F.g.23.1.P.Seq	F	M00055919B:C10	CH15CON
944	15577	RTA00002902F.f.15.1.P.Seq	F	M00006636B:E04	CH02COH
945	6106	RTA00002935F.f.11.1.P.Seq	F	M00054632B:H02	CH17COHLV
946	17136	RTA00002935F.h.14.1.P.Seq	F	M00054818B:F10	CH17COHLV
947	2582	RTA00002921F.f.14.1.P.Seq	F	M00033413A:A08	CH09LNL
948	16638	RTA00002899F.a.15.1.P.Seq	F	M00004420D:E05	CH01COH
949	8869	RTA00002929F.a.05.1.P.Seq	F	M00039748C:G09	CH14EDT
950	14426	RTA00002914F.c.12.1.P.Seq	F	M00028069D:H02	CH08LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
951	11994	RTA00002890F.h.14.1.P.Seq	F	M00001617C:F10	CH01COH
952	186664	RTA00002932F.a.05.1.P.Seq	F	M00042585D:D03	CH18CON
953	162235	RTA00002907F.j.06.2.P.Seq	F	M00022212D:G02	CH03MAH
954	2127	RTA00002912F.o.14.1.P.Seq	F	M00027605B:D09	CH04MAL
955	41014	RTA00002901F.n.04.1.P.Seq	F	M00005641B:E09	CH02COH
956	17636	RTA00002933F.c.19.1.P.Seq	F	M00043222C:B06	CH19COP
957	2328	RTA00002935F.e.05.1.P.Seq	F	M00054579A:C02	CH17COHLV
958	15414	RTA00002935F.p.13.1.P.Seq	F	M00055423C:H10	CH17COHLV
959	11948	RTA00002895F.o.01.1.P.Seq	F	M00004118C:D12	CH01COH
960	24759	RTA00002903F.n.05.1.P.Seq	F	M00007082D:E05	CH02COH
961	15152	RTA00002925F.g.01.1.P.Seq	F	M00039873B:H04	CH09LNL
962	14917	RTA00002922F.b.02.1.P.Seq	F	M00038616D:B07	CH09LNL
963	12941	RTA00002889F.c.15.1.P.Seq	F	M00001532A:G08	CH01COH
964	29676	RTA00002931F.b.03.1.P.Seq	F	M00042788A:F04	CH16COP
965	17789	RTA00002891F.a.21.1.P.Seq	F	M00001671A:H10	CH01COH
966	45097	RTA00002928F.g.06.1.P.Seq	F	M00040247D:D02	CH13EDT
967	18407	RTA00002909F.b.11.1.P.Seq	F	M00022546B:E05	CH03MAH
968	22309	RTA00002900F.n.19.1.P.Seq	F	M00005392A:G06	CH02COH
969	109382	RTA00002907F.k.13.1.P.Seq	F	M00022224A:G07	CH03MAH
970	92273	RTA00002909F.j.17.1.P.Seq	F	M00022662D:H03	CH03MAH
971	8403	RTA00002915F.j.22.1.P.Seq	F	M00032474A:G03	CH08LNL
972	7763	RTA00002928F.h.10.1.P.Seq	F	M00040267D:A12	CH13EDT
973	13470	RTA00002930F.k.09.1.P.Seq	F	M00056304A:H05	CH15CON
974	1484	RTA00002921F.k.10.1.P.Seq	F	M00033556D:C10	CH09LNL
975	10345	RTA00002892F.o.19.2.P.Seq	F	M00003848C:G09	CH01COH
976	17242	RTA00002931F.a.05.1.P.Seq	F	M00042433A:E11	CH16COP
977	171180	RTA00002909F.f.24.1.P.Seq	F	M00022618B:D09	CH03MAH
978	16790	RTA00002914F.c.03.1.P.Seq	F	M00028067A:C11	CH08LNL
979	139516	RTA00002903F.l.02.1.P.Seq	F	M00007032C:A12	CH02COH
980	4825	RTA00002930F.b.15.1.P.Seq	F	M00042742B:E04	CH15CON
981	8830	RTA00002930F.a.05.1.P.Seq	F	M00042528C:H01	CH15CON
982	12398	RTA00002935F.o.19.1.P.Seq	F	M00055391B:C07	CH17COHLV
983	17867	RTA00002900F.c.14.1.P.Seq	F	M00004850A:B02	CH02COH
984	15796	RTA00002935F.b.12.1.P.Seq	F	M00043339C:F11	CH17COHLV
985	185669	RTA00002935F.f.13.1.P.Seq	F	M00054686A:A09	CH17COHLV
986	13638	RTA00002935F.j.20.1.P.Seq	F	M00055002B:E08	CH17COHLV
987	8280	RTA00002930F.e.12.1.P.Seq	F	M00055653C:B07	CH15CON
988	12632	RTA00002931F.c.03.1.P.Seq	F	M00042860B:C07	CH16COP
989	7620	RTA00002935F.m.18.1.P.Seq	F	M00055240A:A08	CH17COHLV
990	23922	RTA00002935F.m.20.1.P.Seq	F	M00055244B:F07	CH17COHLV
991	43864	RTA00002931F.b.05.1.P.Seq	F	M00042794A:F01	CH16COP
992	34478	RTA00002929F.g.13.1.P.Seq	F	M00040367A:C08	CH14EDT
993	6861	RTA00002933F.c.17.1.P.Seq	F	M00043221D:C12	CH19COP
994	13971	RTA00002933F.b.01.1.P.Seq	F	M00043099A:H04	CH19COP
995	13971	RTA00002933F.a.24.1.P.Seq	F	M00043099A:H04	CH19COP
996	13244	RTA00002927F.e.08.1.P.Seq	F	M00039537A:F08	CH12EDT
997	7455	RTA00002935F.d.11.1.P.Seq	F	M00054528B:E05	CH17COHLV
998	18915	RTA00002929F.b.21.1.P.Seq	F	M00040201A:H01	CH14EDT
999	4023	RTA00002935F.h.03.1.P.Seq	F	M00054786C:D08	CH17COHLV
1000	10785	RTA00002933F.a.11.1.P.Seq	F	M00043074C:D07	CH19COP

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1001	14851	RTA00002928F.i.07.1.P.Seq	F	M00040287C:F10	CH13EDT
1002	109382	RTA00002907F.k.13.2.P.Seq	F	M00022224A:G07	CH03MAH
1003	23878	RTA00002933F.b.03.1.P.Seq	F	M00043101D:G11	CH19COP
1004	27516	RTA00002927F.f.17.1.P.Seq	F	M00039598A:E04	CH12EDT
1005	9652	RTA00002931F.c.04.1.P.Seq	F	M00042863D:F09	CH16COP
1006	24729	RTA00002931F.a.12.1.P.Seq	F	M00042462B:C02	CH16COP
1007	186041	RTA00002912F.b.24.1.P.Seq	F	M00027244C:B06	CH04MAL
1008	12282	RTA00002935F.i.18.1.P.Seq	F	M00054908C:A01	CH17COHLV
1009	10704	RTA00002930F.f.12.1.P.Seq	F	M00055757A:B01	CH15CON
1010	3397	RTA00002930F.h.08.1.P.Seq	F	M00055975B:F09	CH15CON
1011	35256	RTA00002886F.m.16.1.P.Seq	F	M00001374A:B02	CH01COH
1012	1448	RTA00002900F.g.05.1.P.Seq	F	M00005002A:C03	CH02COH
1013	1259	RTA00002922F.n.08.1.P.Seq	F	M00039131C:B09	CH09LNL
1014	16903	RTA00002935F.a.01.1.P.Seq	F	M00042352B:A04	CH17COHLV
1015	7884	RTA00002922F.a.13.1.P.Seq	F	M00038390B:F02	CH09LNL
1016	5976	RTA00002930F.j.11.1.P.Seq	F	M00056220D:G02	CH15CON
1017	16832	RTA00002888F.h.20.1.P.Seq	F	M00001466B:F03	CH01COH
1018	10490	RTA00002886F.k.07.1.P.Seq	F	M00001364C:H10	CH01COH
1019	6317	RTA00002928F.g.10.1.P.Seq	F	M00040252C:G05	CH13EDT
1020	41215	RTA00002897F.l.11.1.P.Seq	F	M00004282A:D01	CH01COH
1021	6844	RTA00002889F.l.21.1.P.Seq	F	M00001562B:B02	CH01COH
1022	10456	RTA00002897F.f.20.1.P.Seq	F	M00004242D:H01	CH01COH
1023	2720	RTA00002891F.i.07.1.P.Seq	F	M00003753A:C11	CH01COH
1024	12473	RTA00002888F.o.07.1.P.Seq	F	M00001497C:F10	CH01COH
1025	15840	RTA00002919F.n.17.1.P.Seq	F	M00033230C:G10	CH08LNL
1026	6554	RTA00002895F.b.16.1.P.Seq	F	M00004062D:A02	CH01COH
1027	7330	RTA00002918F.n.17.1.P.Seq	F	M00032987B:F01	CH08LNL
1028	2206	RTA00002919F.f.12.1.P.Seq	F	M00033071C:G05	CH08LNL
1029	42705	RTA00002935F.f.02.1.P.Seq	F	M00054643D:F07	CH17COHLV
1030	33865	RTA00002930F.b.07.1.P.Seq	F	M00042722C:C09	CH15CON
1031	5196	RTA00002925F.o.19.1.P.Seq	F	M00040034B:G02	CH09LNL
1032	8087	RTA00002935F.o.10.1.P.Seq	F	M00055375C:F12	CH17COHLV
1033	20072	RTA00002935F.g.06.1.P.Seq	F	M00054744C:F12	CH17COHLV
1034	12797	RTA00002935F.g.24.1.P.Seq	F	M00054781D:A11	CH17COHLV
1035	3207	RTA00002930F.c.04.1.P.Seq	F	M00054793B:A06	CH15CON
1036	19600	RTA00002929F.f.24.1.P.Seq	F	M00040351D:G07	CH14EDT
1037	6278	RTA00002935F.j.18.1.P.Seq	F	M00055001C:G10	CH17COHLV
1038	19363	RTA00002927F.e.12.1.P.Seq	F	M00039564D:D04	CH12EDT
1039	15447	RTA00002929F.g.12.1.P.Seq	F	M00040366B:H10	CH14EDT
1040	9676	RTA00002932F.a.14.1.P.Seq	F	M00042960B:C06	CH18CON
1041	12560	RTA00002929F.h.06.1.P.Seq	F	M00040381A:B06	CH14EDT
1042	12727	RTA00002933F.c.15.1.P.Seq	F	M00043219C:C02	CH19COP
1043	27475	RTA00002914F.c.16.1.P.Seq	F	M00028070D:C03	CH08LNL
1044	30646	RTA00002908F.f.11.1.P.Seq	F	M00022416D:D01	CH03MAH
1045	45585	RTA00002925F.h.20.1.P.Seq	F	M00039894C:D09	CH09LNL
1046	25025	RTA00002925F.e.18.1.P.Seq	F	M00039860B:E01	CH09LNL
1047	15715	RTA00002919F.p.05.1.P.Seq	F	M00033274D:F03	CH08LNL
1048	38185	RTA00002926F.c.07.2.P.Seq	F	M00040078A:C07	CH09LNL
1049	8384	RTA00002903F.o.13.1.P.Seq	F	M00007112D:D03	CH02COH
1050	8843	RTA00002917F.h.17.1.P.Seq	F	M00032733B:F12	CH08LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1051	21401	RTA00002930F.e.20.2.P.Seq	F	M00055676A:G02	CH15CON
1052	14434	RTA00002903F.l.01.1.P.Seq	F	M00007032A:B05	CH02COH
1053	40045	RTA00002891F.k.14.1.P.Seq	F	M00003764A:H09	CH01COH
1054	21853	RTA00002896F.g.12.1.P.Seq	F	M00004159C:D10	CH01COH
1055	23439	RTA00002935F.p.01.1.P.Seq	F	M00055402A:H01	CH17COHLV
1056	13060	RTA00002934F.a.19.1.P.Seq	F	M00043529A:B08	CH20COHLV
1057	23439	RTA00002935F.o.24.1.P.Seq	F	M00055402A:H01	CH17COHLV
1058	20547	RTA00002931F.b.12.1.P.Seq	F	M00042822A:H04	CH16COP
1059	4319	RTA00002930F.a.03.1.P.Seq	F	M00042525B:H01	CH15CON
1060	21430	RTA00002901F.c.18.1.P.Seq	F	M00005452B:G03	CH02COH
1061	7668	RTA00002935F.g.23.1.P.Seq	F	M00054781B:H04	CH17COHLV
1062	16239	RTA00002935F.k.19.1.P.Seq	F	M00055081A:A05	CH17COHLV
1063	5631	RTA00002929F.e.16.1.P.Seq	F	M00040326B:G09	CH14EDT
1064	18362	RTA00002928F.a.04.1.P.Seq	F	M00039739B:H12	CH13EDT
1065	8034	RTA00002932F.a.22.1.P.Seq	F	M00042982D:A10	CH18CON
1066	12497	RTA00002928F.a.19.1.P.Seq	F	M00040132A:H09	CH13EDT
1067	21001	RTA00002932F.b.07.1.P.Seq	F	M00042996B:H08	CH18CON
1068	471	RTA00002927F.a.11.1.P.Seq	F	M00039184D:H09	CH12EDT
1069	10003	RTA00002897F.b.13.1.P.Seq	F	M00004215B:C05	CH01COH
1070	16074	RTA00002935F.f.18.1.P.Seq	F	M00054708C:B06	CH17COHLV
1071	13698	RTA00002902F.l.01.1.P.Seq	F	M00006743A:H11	CH02COH
1072	24819	RTA00002922F.j.03.1.P.Seq	F	M00039078B:B03	CH09LNL
1073	21511	RTA00002892F.i.01.1.P.Seq	F	M00003821C:E12	CH01COH
1074	12402	RTA00002929F.d.15.1.P.Seq	F	M00040314B:D07	CH14EDT
1075	142755	RTA00002903F.p.06.1.P.Seq	F	M00007126A:A02	CH02COH
1076	3010	RTA00002935F.p.12.1.P.Seq	F	M00055423C:G12	CH17COHLV
1077	17173	RTA00002935F.k.09.1.P.Seq	F	M00055043B:H08	CH17COHLV
1078	2969	RTA00002933F.a.12.1.P.Seq	F	M00043076D:A02	CH19COP
1079	19600	RTA00002929F.g.01.1.P.Seq	F	M00040351D:G07	CH14EDT
1080	8542	RTA00002927F.h.24.1.P.Seq	F	M00039647A:A02	CH12EDT
1081	24795	RTA00002927F.f.10.1.P.Seq	F	M00039594C:B06	CH12EDT
1082	19695	RTA00002927F.i.03.1.P.Seq	F	M00039647B:A02	CH12EDT
1083	8542	RTA00002927F.i.01.1.P.Seq	F	M00039647A:A02	CH12EDT
1084	21409	RTA00002902F.e.09.1.P.Seq	F	M00006601D:G05	CH02COH
1085	186318	RTA00002912F.h.07.1.P.Seq	F	M00027363D:G04	CH04MAL
1086	7379	RTA00002901F.e.10.1.P.Seq	F	M00005468D:C01	CH02COH
1087	91285	RTA00002909F.l.12.1.P.Seq	F	M00022682D:A10	CH03MAH
1088	3285	RTA00002903F.m.18.1.P.Seq	F	M00007064D:D12	CH02COH
1089	6284	RTA00002896F.g.22.1.P.Seq	F	M00004160D:G05	CH01COH
1090	15676	RTA00002935F.h.21.1.P.Seq	F	M00054843A:C01	CH17COHLV
1091	34112	RTA00002894F.o.19.1.P.Seq	F	M00004053D:F09	CH01COH
1092	16407	RTA00002892F.o.24.2.P.Seq	F	M00003851B:A01	CH01COH
1093	919	RTA00002890F.f.18.1.P.Seq	F	M00001609D:C11	CH01COH
1094	59069	RTA00002896F.k.07.1.P.Seq	F	M00004175D:E06	CH01COH
1095	31167	RTA00002900F.f.05.1.P.Seq	F	M00004876B:A06	CH02COH
1096	23873	RTA00002930F.i.03.1.P.Seq	F	M00056035D:A08	CH15CON
1097	15679	RTA00002900F.h.12.1.P.Seq	F	M00005016C:E04	CH02COH
1098	31852	RTA00002911F.o.22.1.P.Seq	F	M00027170D:C07	CH04MAL
1099	39030	RTA00002891F.f.07.1.P.Seq	F	M00001692C:C04	CH01COH
1100	16407	RTA00002892F.p.01.2.P.Seq	F	M00003851B:A01	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1101	4118	RTA00002935F.a.17.1.P.Seq	F	M00043306D:C01	CH17COHLV
1102	11054	RTA00002915F.n.07.2.P.Seq	F	M00032504B:B10	CH08LNH
1103	186640	RTA00002918F.d.03.1.P.Seq	F	M00032848D:B10	CH08LNH
1104	9301	RTA00002887F.f.22.1.P.Seq	F	M00001396D:H02	CH01COH
1105	13438	RTA00002901F.a.11.1.P.Seq	F	M00005422D:H10	CH02COH
1106	23691	RTA00002901F.g.21.1.P.Seq	F	M00005506C:E09	CH02COH
1107	32788	RTA00002909F.m.04.1.P.Seq	F	M00022694A:F05	CH03MAH
1108	34364	RTA00002915F.o.09.2.P.Seq	F	M00032515A:B12	CH08LNH
1109	24840	RTA00002908F.i.01.1.P.Seq	F	M00022452B:E06	CH03MAH
1110	3416	RTA00002911F.j.17.1.P.Seq	F	M00027036A:B06	CH04MAL
1111	16889	RTA00002930F.f.04.1.P.Seq	F	M00055724B:E04	CH15CON
1112	2159	RTA00002929F.f.15.1.P.Seq	F	M00040344C:D05	CH14EDT
1113	8880	RTA00002929F.f.02.1.P.Seq	F	M00040338A:B10	CH14EDT
1114	10722	RTA00002921F.o.22.1.P.Seq	F	M00038304B:E02	CH09LNL
1115	15046	RTA00002887F.c.08.1.P.Seq	F	M00001389B:E10	CH01COH
1116	13868	RTA00002898F.g.18.1.P.Seq	F	M00004347B:E04	CH01COH
1117	4226	RTA00002925F.f.15.1.P.Seq	F	M00039869A:H01	CH09LNL
1118	90435	RTA00002909F.l.06.1.P.Seq	F	M00022678B:C08	CH03MAH
1119	25686	RTA00002900F.l.02.1.P.Seq	F	M00005359B:D09	CH02COH
1120	7296	RTA00002900F.d.08.1.P.Seq	F	M00004856D:F09	CH02COH
1121	11546	RTA00002905F.o.16.1.P.Seq	F	M00021678A:H03	CH03MAH
1122	15748	RTA00002901F.h.12.1.P.Seq	F	M00005515D:F02	CH02COH
1123	5591	RTA00002903F.p.20.1.P.Seq	F	M00007141C:B05	CH02COH
1124	9433	RTA00002935F.p.14.1.P.Seq	F	M00055424B:H06	CH17COHLV
1125	9654	RTA00002924F.i.09.1.P.Seq	F	M00039654C:C11	CH09LNL
1126	21914	RTA00002889F.i.06.1.P.Seq	F	M00001550A:H06	CH01COH
1127	4277	RTA00002927F.h.13.1.P.Seq	F	M00039642A:A08	CH12EDT
1128	12362	RTA00002929F.h.24.1.P.Seq	F	M00040391A:G05	CH14EDT
1129	449	RTA00002924F.e.22.1.P.Seq	F	M00039471D:G10	CH09LNL
1130	1820	RTA00002922F.n.11.1.P.Seq	F	M00039133C:F12	CH09LNL
1131	12159	RTA00002930F.b.24.1.P.Seq	F	M00042894C:A11	CH15CON
1132	25106	RTA00002903F.d.21.1.P.Seq	F	M00006907B:C06	CH02COH
1133	2245	RTA00002917F.b.20.1.P.Seq	F	M00032676C:C10	CH08LNH
1134	14388	RTA00002894F.h.09.1.P.Seq	F	M00003998B:G10	CH01COH
1135	12219	RTA00002898F.d.22.1.P.Seq	F	M00004328A:D01	CH01COH
1136	4726	RTA00002935F.d.16.1.P.Seq	F	M00054538D:C12	CH17COHLV
1137	19479	RTA00002891F.e.15.1.P.Seq	F	M00001688B:B11	CH01COH
1138	13280	RTA00002888F.h.08.1.P.Seq	F	M00001465C:A02	CH01COH
1139	42708	RTA00002901F.h.07.1.P.Seq	F	M00005511A:F05	CH02COH
1140	2022	RTA00002896F.f.09.1.P.Seq	F	M00004155C:A10	CH01COH
1141	7281	RTA00002929F.f.22.1.P.Seq	F	M00040351A:C08	CH14EDT
1142	3241	RTA00002919F.n.09.1.P.Seq	F	M00033223C:G04	CH08LNH
1143	16161	RTA00002930F.h.02.1.P.Seq	F	M00055925D:B07	CH15CON
1144	2766	RTA00002935F.p.21.1.P.Seq	F	M00055477D:B01	CH17COHLV
1145	11175	RTA00002886F.b.05.1.P.Seq	F	M00001340D:F07	CH01COH
1146	7223	RTA00002923F.i.06.1.P.Seq	F	M00039278C:D03	CH09LNL
1147	6786	RTA00002917F.o.05.1.P.Seq	F	M00032792C:B01	CH08LNH
1148	186651	RTA00002923F.d.21.1.P.Seq	F	M00039219B:C08	CH09LNL
1149	7878	RTA00002930F.f.05.1.P.Seq	F	M00055724D:C07	CH15CON
1150	12624	RTA00002935F.p.11.1.P.Seq	F	M00055423A:B08	CH17COHLV

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1151	23018	RTA00002886F.f.21.1.P.Seq	F	M00001351B:E11	CH01COH
1152	186756	RTA00002911F.g.23.1.P.Seq	F	M00026961A:B06	CH04MAL
1153	4177	RTA00002902F.h.07.1.P.Seq	F	M00006673A:A03	CH02COH
1154	10430	RTA00002894F.g.21.1.P.Seq	F	M00003996B:H07	CH01COH
1155	31280	RTA00002903F.k.08.1.P.Seq	F	M00007007A:E04	CH02COH
1156	19098	RTA00002925F.e.23.1.P.Seq	F	M00039861C:B12	CH09LNL
1157	24105	RTA00002932F.a.06.1.P.Seq	F	M00042585D:E10	CH18CON
1158	7750	RTA00002935F.i.02.1.P.Seq	F	M00054856C:D03	CH17COHLV
1159	14582	RTA00002898F.d.07.1.P.Seq	F	M00004324A:D05	CH01COH
1160	21356	RTA00002917F.j.19.1.P.Seq	F	M00032753A:C07	CH08LNL
1161	16210	RTA00002930F.k.17.1.P.Seq	F	M00056345D:A04	CH15CON
1162	2012	RTA00002911F.o.10.1.P.Seq	F	M00027159C:F07	CH04MAL
1163	5391	RTA00002909F.p.21.1.P.Seq	F	M00022738D:G08	CH03MAH
1164	10172	RTA00002886F.a.05.1.P.Seq	F	M00001333C:B02	CH01COH
1165	16403	RTA00002935F.p.15.1.P.Seq	F	M00055424D:G05	CH17COHLV
1166	21920	RTA00002886F.j.05.1.P.Seq	F	M00001361A:C12	CH01COH
1167	7070	RTA00002921F.e.06.1.P.Seq	F	M00033374D:C07	CH09LNL
1168	45734	RTA00002901F.j.14.1.P.Seq	F	M00005569D:G09	CH02COH
1169	12362	RTA00002929F.i.01.1.P.Seq	F	M00040391A:G05	CH14EDT
1170	9405	RTA00002892F.k.04.1.P.Seq	F	M00003830C:D02	CH01COH
1171	6507	RTA00002922F.o.05.1.P.Seq	F	M00039140A:F05	CH09LNL
1172	10735	RTA00002925F.b.24.1.P.Seq	F	M00039822A:H02	CH09LNL
1173	21177	RTA00002935F.d.18.1.P.Seq	F	M00054542B:A10	CH17COHLV
1174	14950	RTA00002894F.m.18.1.P.Seq	F	M00004047D:F12	CH01COH
1175	10762	RTA00002917F.o.08.1.P.Seq	F	M00032793A:G06	CH08LNL
1176	23170	RTA00002887F.f.15.1.P.Seq	F	M00001396B:B01	CH01COH
1177	8487	RTA00002887F.f.16.1.P.Seq	F	M00001396B:B12	CH01COH
1178	185798	RTA00002911F.k.06.1.P.Seq	F	M00027050A:B02	CH04MAL
1179	8976	RTA00002896F.h.03.1.P.Seq	F	M00004161B:G07	CH01COH
1180	12159	RTA00002930F.c.01.1.P.Seq	F	M00042894C:A11	CH15CON
1181	7788	RTA00002932F.b.13.1.P.Seq	F	M00043017C:D08	CH18CON
1182	43336	RTA00002917F.d.09.1.P.Seq	F	M00032688C:A03	CH08LNL
1183	10313	RTA00002902F.k.19.1.P.Seq	F	M00006740B:A09	CH02COH
1184	4588	RTA00002891F.o.11.1.P.Seq	F	M00003782A:B02	CH01COH
1185	18090	RTA00002925F.l.17.1.P.Seq	F	M00039981D:B01	CH09LNL
1186	185994	RTA00002911F.p.07.1.P.Seq	F	M00027177B:D04	CH04MAL
1187	166276	RTA00002908F.h.03.1.P.Seq	F	M00022438C:H09	CH03MAH
1188	15984	RTA00002932F.a.10.1.P.Seq	F	M00042621C:C04	CH18CON
1189	13242	RTA00002889F.i.11.1.P.Seq	F	M00001550D:B11	CH01COH
1190	6840	RTA00002935F.i.06.1.P.Seq	F	M00054866B:C08	CH17COHLV
1191	17265	RTA00002935F.l.04.1.P.Seq	F	M00055105B:A02	CH17COHLV
1192	12542	RTA00002933F.b.17.1.P.Seq	F	M00043152C:B10	CH19COP
1193	1568	RTA00002928F.d.10.1.P.Seq	F	M00040174D:G06	CH13EDT
1194	8721	RTA00002901F.k.23.1.P.Seq	F	M00005606D:B12	CH02COH
1195	13519	RTA00002898F.j.19.1.P.Seq	F	M00004365A:B11	CH01COH
1196	4471	RTA00002890F.d.14.1.P.Seq	F	M00001600B:G01	CH01COH
1197	11357	RTA00002931F.c.06.1.P.Seq	F	M00042873D:F05	CH16COP
1198	11804	RTA00002935F.m.17.1.P.Seq	F	M00055239D:F11	CH17COHLV
1199	6999	RTA00002896F.c.21.1.P.Seq	F	M00004146A:C11	CH01COH
1200	4408	RTA00002897F.a.02.1.P.Seq	F	M00004207C:A04	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1201	4618	RTA00002935F.j.21.1.P.Seq	F	M00055004C:H05	CH17COHLV
1202	185841	RTA00002912F.o.08.1.P.Seq	F	M00027600B:C07	CH04MAL
1203	1278	RTA00002912F.j.15.1.P.Seq	F	M00027459C:B10	CH04MAL
1204	19677	RTA00002929F.h.16.1.P.Seq	F	M00040384B:E04	CH14EDT
1205	17539	RTA00002909F.c.06.1.P.Seq	F	M00022563B:C08	CH03MAH
1206	11390	RTA00002892F.k.03.1.P.Seq	F	M00003830B:C06	CH01COH
1207	10735	RTA00002925F.c.01.1.P.Seq	F	M00039822A:H02	CH09LNL
1208	3239	RTA00002887F.j.07.1.P.Seq	F	M00001406D:F06	CH01COH
1209	181718	RTA00002905F.n.20.1.P.Seq	F	M00021668D:A03	CH03MAH
1210	6957	RTA00002917F.n.18.1.P.Seq	F	M00032787D:C05	CH08LNH
1211	23673	RTA00002930F.a.14.1.P.Seq	F	M00042557D:B06	CH15CON
1212	11405	RTA00002918F.b.13.1.P.Seq	F	M00032831A:E09	CH08LNH
1213	10256	RTA00002888F.d.16.1.P.Seq	F	M00001449B:H10	CH01COH
1214	25563	RTA00002891F.b.23.1.P.Seq	F	M00001675B:D06	CH01COH
1215	2669	RTA00002886F.l.03.1.P.Seq	F	M00001368A:B07	CH01COH
1216	185877	RTA00002911F.b.11.2.P.Seq	F	M00023389A:G04	CH04MAL
1217	1314	RTA00002930F.c.08.1.P.Seq	F	M00054911D:E06	CH15CON
1218	25843	RTA00002908F.o.05.1.P.Seq	F	M00022509A:H02	CH03MAH
1219	1794	RTA00002924F.g.06.1.P.Seq	F	M00039560C:G06	CH09LNL
1220	22038	RTA00002896F.a.20.1.P.Seq	F	M00004136C:B12	CH01COH
1221	6011	RTA00002924F.f.12.1.P.Seq	F	M00039478C:B02	CH09LNL
1222	41087	RTA00002901F.o.06.1.P.Seq	F	M00005675D:D09	CH02COH
1223	18534	RTA00002908F.o.16.1.P.Seq	F	M00022512B:A09	CH03MAH
1224	1444	RTA00002922F.a.12.1.P.Seq	F	M00038389D:D10	CH09LNL
1225	1078	RTA00002893F.p.24.1.P.Seq	F	M00003972C:F07	CH01COH
1226	8632	RTA00002896F.h.09.1.P.Seq	F	M00004163B:C03	CH01COH
1227	105042	RTA00002917F.o.11.1.P.Seq	F	M00032795C:A03	CH08LNH
1228	6878	RTA00002912F.l.11.1.P.Seq	F	M00027513D:F06	CH04MAL
1229	23639	RTA00002912F.i.05.1.P.Seq	F	M00027381B:B04	CH04MAL
1230	19635	RTA00002896F.c.15.1.P.Seq	F	M00004144D:B02	CH01COH
1231	7217	RTA00002926F.d.18.2.P.Seq	F	M00040094B:C08	CH09LNL
1232	4930	RTA00002930F.g.04.1.P.Seq	F	M00055810C:D03	CH15CON
1233	16945	RTA00002921F.o.01.1.P.Seq	F	M00038290A:D12	CH09LNL
1234	24790	RTA00002890F.e.21.1.P.Seq	F	M00001606D:D06	CH01COH
1235	22721	RTA00002932F.a.07.1.P.Seq	F	M00042586A:B01	CH18CON
1236	14861	RTA00002901F.g.18.1.P.Seq	F	M00005505B:E01	CH02COH
1237	2452	RTA00002921F.b.02.1.P.Seq	F	M00033302B:F10	CH09LNL
1238	19269	RTA00002887F.p.11.1.P.Seq	F	M00001430B:C01	CH01COH
1239	16029	RTA00002930F.j.17.1.P.Seq	F	M00056244A:B06	CH15CON
1240	3038	RTA00002922F.m.04.1.P.Seq	F	M00039121D:E07	CH09LNL
1241	2933	RTA00002922F.g.20.1.P.Seq	F	M00039056B:G01	CH09LNL
1242	15956	RTA00002891F.j.23.1.P.Seq	F	M00003761B:B02	CH01COH
1243	15524	RTA00002930F.g.09.1.P.Seq	F	M00055818B:D01	CH15CON
1244	21550	RTA00002935F.f.21.1.P.Seq	F	M00054725C:D09	CH17COHLV
1245	17567	RTA00002918F.p.11.1.P.Seq	F	M00033006A:F10	CH08LNH
1246	20293	RTA00002888F.j.20.1.P.Seq	F	M00001477D:G09	CH01COH
1247	9520	RTA00002927F.h.15.1.P.Seq	F	M00039642C:F08	CH12EDT
1248	2700	RTA00002889F.e.21.1.P.Seq	F	M00001539C:F12	CH01COH
1249	25891	RTA00002909F.p.23.1.P.Seq	F	M00022740C:H11	CH03MAH
1250	4298	RTA00002908F.c.22.1.P.Seq	F	M00022383C:A12	CH03MAH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1251	20412	RTA00002909F.e.02.1.P.Seq	F	M00022590B:E05	CH03MAH
1252	29413	RTA00002906F.m.23.1.P.Seq	F	M00022069D:C12	CH03MAH
1253	12315	RTA00002907F.l.24.2.P.Seq	F	M00022240D:B11	CH03MAH
1254	4930	RTA00002930F.g.04.2.P.Seq	F	M00055810C:D03	CH15CON
1255	12018	RTA00002924F.c.16.1.P.Seq	F	M00039438B:D08	CH09LNL
1256	10501	RTA00002930F.h.23.1.P.Seq	F	M00056024B:F09	CH15CON
1257	11314	RTA00002935F.k.03.1.P.Seq	F	M00055023A:E11	CH17COHLV
1258	6426	RTA00002927F.b.15.1.P.Seq	F	M00039377B:H09	CH12EDT
1259	2205	RTA00002904F.c.03.1.P.Seq	F	M00007195C:E11	CH02COH
1260	6991	RTA00002922F.j.12.1.P.Seq	F	M00039081B:C04	CH09LNL
1261	11928	RTA00002906F.h.05.1.P.Seq	F	M00021971C:B11	CH03MAH
1262	28226	RTA00002907F.n.20.1.P.Seq	F	M00022262B:B06	CH03MAH
1263	16059	RTA00002935F.j.13.1.P.Seq	F	M00054975C:F01	CH17COHLV
1264	2252	RTA00002886F.k.24.1.P.Seq	F	M00001368A:A08	CH01COH
1265	4059	RTA00002935F.f.19.1.P.Seq	F	M00054714B:G10	CH17COHLV
1266	21795	RTA00002901F.b.16.1.P.Seq	F	M00005442A:B10	CH02COH
1267	15049	RTA00002935F.j.10.1.P.Seq	F	M00054973B:E12	CH17COHLV
1268	5565	RTA00002930F.c.02.1.P.Seq	F	M00042908A:F09	CH15CON
1269	20493	RTA00002933F.a.14.1.P.Seq	F	M00043077C:D12	CH19COP
1270	20257	RTA00002934F.a.14.1.P.Seq	F	M00043495C:H05	CH20COHLV
1271	16392	RTA00002899F.a.05.1.P.Seq	F	M00004418B:A11	CH01COH
1272	15797	RTA00002930F.c.23.1.P.Seq	F	M00055456C:H06	CH15CON
1273	1811	RTA00002891F.d.21.1.P.Seq	F	M00001684D:E04	CH01COH
1274	17503	RTA00002935F.f.08.1.P.Seq	F	M00054675D:G03	CH17COHLV
1275	14639	RTA00002905F.h.12.1.P.Seq	F	M00008073D:D01	CH03MAH
1276	9146	RTA00002934F.a.10.1.P.Seq	F	M00043465C:H11	CH20COHLV
1277	10689	RTA00002930F.h.19.1.P.Seq	F	M00056004B:C05	CH15CON
1278	11596	RTA00002890F.e.23.1.P.Seq	F	M00001607A:E04	CH01COH
1279	23731	RTA00002930F.g.18.1.P.Seq	F	M00055873D:C02	CH15CON
1280	25429	RTA00002930F.h.10.1.P.Seq	F	M00055980C:B04	CH15CON
1281	1610	RTA00002931F.b.24.1.P.Seq	F	M00042855C:G11	CH16COP
1282	1176	RTA00002935F.a.10.1.P.Seq	F	M00042457C:B06	CH17COHLV
1283	23578	RTA00002930F.a.22.1.P.Seq	F	M00042579A:D09	CH15CON
1284	17238	RTA00002932F.a.18.1.P.Seq	F	M00042970C:B01	CH18CON
1285	1610	RTA00002931F.c.01.1.P.Seq	F	M00042855C:G11	CH16COP
1286	16366	RTA00002932F.a.04.1.P.Seq	F	M00042585A:H11	CH18CON
1287	19709	RTA00002932F.a.12.1.P.Seq	F	M00042951D:G12	CH18CON
1288	11027	RTA00002932F.b.10.1.P.Seq	F	M00043013B:E03	CH18CON
1289	23451	RTA00002933F.a.09.1.P.Seq	F	M00042617B:E01	CH19COP
1290	23731	RTA00002930F.g.18.2.P.Seq	F	M00055873D:C02	CH15CON
1291	47898	RTA00002911F.k.07.1.P.Seq	F	M00027052A:E10	CH04MAL
1292	32581	RTA00002932F.b.02.1.P.Seq	F	M00042982D:E03	CH18CON
1293	42	RTA00002934F.a.11.1.P.Seq	F	M00043470A:C10	CH20COHLV
1294	1447	RTA00002935F.d.14.1.P.Seq	F	M00054532B:B01	CH17COHLV
1295	10449	RTA00002935F.o.20.1.P.Seq	F	M00055395D:D11	CH17COHLV
1296	35359	RTA00002935F.h.11.1.P.Seq	F	M00054817D:A11	CH17COHLV
1297	19657	RTA00002935F.l.20.1.P.Seq	F	M00055162C:D10	CH17COHLV
1298	12659	RTA00002930F.i.21.1.P.Seq	F	M00056133A:E11	CH15CON
1299	9081	RTA00002934F.a.22.1.P.Seq	F	M00043640A:B01	CH20COHLV
1300	17084	RTA00002935F.a.14.1.P.Seq	F	M00042520B:H04	CH17COHLV

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1301	11972	RTA00002935F.b.10.1.P.Seq	F	M00043336D:B03	CH17COHLV
1302	11077	RTA00002935F.c.12.1.P.Seq	F	M00043402B:G07	CH17COHLV
1303	126414	RTA00002885F.a.01.1.P.Seq	F	M00042350A:A05	CH16COP
1304	113291	RTA00002935F.m.15.1.P.Seq	F	M00055232A:E08	CH17COHLV
1305	13224	RTA00002935F.f.15.1.P.Seq	F	M00054693A:E11	CH17COHLV
1306	14883	RTA00002930F.k.14.1.P.Seq	F	M00056320B:A03	CH15CON
1307	13363	RTA00002935F.a.02.1.P.Seq	F	M00042352D:B03	CH17COHLV
1308	16869	RTA00002889F.c.21.1.P.Seq	F	M00001533C:G11	CH01COH
1309	16	RTA00002935F.a.06.1.P.Seq	F	M00042449B:F05	CH17COHLV
1310	4359	RTA00002903F.j.16.1.P.Seq	F	M00006994C:F06	CH02COH
1311	20726	RTA00002908F.a.17.1.P.Seq	F	M00022363C:D05	CH03MAH
1312	13713	RTA00002924F.l.09.1.P.Seq	F	M00039686C:C01	CH09LNL
1313	29271	RTA00002935F.d.20.1.P.Seq	F	M00054548C:H06	CH17COHLV
1314	6237	RTA00002935F.f.14.1.P.Seq	F	M00054686A:F10	CH17COHLV
1315	3472	RTA00002922F.n.12.1.P.Seq	F	M00039134D:F08	CH09LNL
1316	186798	RTA00002911F.f.11.1.P.Seq	F	M00026914C:H09	CH04MAL
1317	13193	RTA00002886F.l.16.1.P.Seq	F	M00001369A:G06	CH01COH
1318	3554	RTA00002919F.i.14.1.P.Seq	F	M00033149B:E10	CH08LNH
1319	19991	RTA00002908F.h.11.1.P.Seq	F	M00022446C:H06	CH03MAH
1320	173046	RTA00002901F.o.19.1.P.Seq	F	M00005703D:G10	CH02COH
1321	21798	RTA00002932F.b.12.1.P.Seq	F	M00043016B:F09	CH18CON
1322	11303	RTA00002898F.i.11.1.P.Seq	F	M00004359A:E01	CH01COH
1323	4026	RTA00002915F.m.02.2.P.Seq	F	M00032494C:H08	CH08LNH
1324	94859	RTA00002909F.i.23.1.P.Seq	F	M00022656D:D07	CH03MAH
1325	12315	RTA00002907F.m.01.1.P.Seq	F	M00022240D:B11	CH03MAH
1326	4822	RTA00002909F.l.16.1.P.Seq	F	M00022690A:A07	CH03MAH
1327	97129	RTA00002909F.l.13.1.P.Seq	F	M00022684A:E06	CH03MAH
1328	15996	RTA00002897F.l.09.1.P.Seq	F	M00004281A:C04	CH01COH
1329	7209	RTA00002918F.c.01.1.P.Seq	F	M00032835D:G04	CH08LNH
1330	111888	RTA00002902F.h.08.1.P.Seq	F	M00006678C:C02	CH02COH
1331	15642	RTA00002902F.g.06.1.P.Seq	F	M00006646A:A07	CH02COH
1332	20016	RTA00002916F.f.05.1.P.Seq	F	M00032567B:G05	CH08LNH
1333	21603	RTA00002902F.a.05.1.P.Seq	F	M00005763D:A01	CH02COH
1334	156903	RTA00002907F.i.09.2.P.Seq	F	M00022200B:B05	CH03MAH
1335	1425	RTA00002916F.b.19.1.P.Seq	F	M00032541C:G03	CH08LNH
1336	186061	RTA00002911F.e.24.1.P.Seq	F	M00026900A:H07	CH04MAL
1337	20717	RTA00002907F.o.19.1.P.Seq	F	M00022273A:E03	CH03MAH
1338	12586	RTA00002887F.a.09.1.P.Seq	F	M00001385A:E07	CH01COH
1339	19719	RTA00002914F.h.23.1.P.Seq	F	M00028212D:C05	CH08LNH
1340	474	RTA00002917F.g.15.1.P.Seq	F	M00032727A:E04	CH08LNH
1341	11907	RTA00002923F.o.07.1.P.Seq	F	M00039381C:C07	CH09LNL
1342	6806	RTA00002928F.d.02.1.P.Seq	F	M00040169A:G06	CH13EDT
1343	13146	RTA00002892F.f.10.2.P.Seq	F	M00003814A:G05	CH01COH
1344	16686	RTA00002919F.f.14.1.P.Seq	F	M00033072A:A09	CH08LNH
1345	6823	RTA00002888F.a.04.1.P.Seq	F	M00001433B:E02	CH01COH
1346	43029	RTA00002897F.d.03.1.P.Seq	F	M00004225D:E03	CH01COH
1347	14789	RTA00002935F.k.11.1.P.Seq	F	M00055055C:F01	CH17COHLV
1348	186061	RTA00002911F.f.01.1.P.Seq	F	M00026900A:H07	CH04MAL
1349	12823	RTA00002921F.g.24.1.P.Seq	F	M00033434D:F05	CH09LNL
1350	25844	RTA00002908F.k.23.1.P.Seq	F	M00022474B:C08	CH03MAH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1351	47793	RTA00002930F.g.03.2.P.Seq	F	M00055809A:B09	CH15CON
1352	7695	RTA00002892F.n.18.2.P.Seq	F	M00003845A:C07	CH01COH
1353	16997	RTA00002922F.k.15.1.P.Seq	F	M00039107A:E12	CH09LNL
1354	25441	RTA00002906F.i.08.1.P.Seq	F	M00021931A:C02	CH03MAH
1355	4303	RTA00002897F.o.20.1.P.Seq	F	M00004295D:C07	CH01COH
1356	5741	RTA00002887F.c.19.1.P.Seq	F	M00001390D:E02	CH01COH
1357	17264	RTA00002900F.a.18.1.P.Seq	F	M00004831C:G11	CH02COH
1358	11766	RTA00002925F.f.20.1.P.Seq	F	M00039871C:G05	CH09LNL
1359	13618	RTA00002893F.o.15.1.P.Seq	F	M00003963D:F01	CH01COH
1360	13903	RTA00002923F.c.18.1.P.Seq	F	M00039204A:E09	CH09LNL
1361	10673	RTA00002927F.h.23.1.P.Seq	F	M00039646A:E06	CH12EDT
1362	17412	RTA00002932F.b.11.1.P.Seq	F	M00043015D:D05	CH18CON
1363	2218	RTA00002919F.a.20.1.P.Seq	F	M0003302SC:A02	CH08LNL
1364	5858	RTA00002923F.i.01.1.P.Seq	F	M00039275B:E02	CH09LNL
1365	2510	RTA00002898F.b.14.1.P.Seq	F	M00004316A:B03	CH01COH
1366	8050	RTA00002900F.n.04.1.P.Seq	F	M00005383A:C11	CH02COH
1367	186538	RTA00002929F.e.18.1.P.Seq	F	M00040329A:H05	CH14EDT
1368	25427	RTA00002935F.n.20.1.P.Seq	F	M00055337B:C04	CH17COHLV
1369	24098	RTA00002901F.a.10.1.P.Seq	F	M00005422D:H02	CH02COH
1370	123823	RTA00002905F.h.08.1.P.Seq	F	M00008071D:H03	CH03MAH
1371	3644	RTA00002901F.c.03.1.P.Seq	F	M00005445D:D04	CH02COH
1372	27783	RTA00002917F.a.17.1.P.Seq	F	M00032666A:C02	CH08LNL
1373	1682	RTA00002910F.b.03.1.P.Seq	F	M00022801D:D09	CH03MAH
1374	3200	RTA00002887F.e.07.1.P.Seq	F	M00001393C:F04	CH01COH
1375	8442	RTA00002917F.h.23.1.P.Seq	F	M00032734B:E12	CH08LNL
1376	15353	RTA00002910F.e.11.1.P.Seq	F	M00022854C:G07	CH03MAH
1377	6314	RTA00002922F.b.06.1.P.Seq	F	M0003861SD:D08	CH09LNL
1378	93549	RTA00002909F.j.14.1.P.Seq	F	M00022662C:H04	CH03MAH
1379	15496	RTA00002906F.p.03.1.P.Seq	F	M00022088B:H02	CH03MAH
1380	16572	RTA00002886F.k.03.1.P.Seq	F	M00001364A:C09	CH01COH
1381	74821	RTA00002890F.p.21.1.P.Seq	F	M00001663A:A12	CH01COH
1382	11315	RTA00002889F.d.12.1.P.Seq	F	M00001535B:B10	CH01COH
1383	10859	RTA00002894F.c.18.1.P.Seq	F	M00003980D:C06	CH01COH
1384	15391	RTA00002914F.f.04.1.P.Seq	F	M00028193B:E07	CH08LNL
1385	23172	RTA00002896F.b.18.1.P.Seq	F	M00004141B:F08	CH01COH
1386	22510	RTA00002886F.l.05.1.P.Seq	F	M00001368A:C02	CH01COH
1387	17156	RTA00002934F.a.08.1.P.Seq	F	M00043455B:C08	CH20COHLV
1388	4593	RTA00002896F.o.18.1.P.Seq	F	M00004200C:A04	CH01COH
1389	2178	RTA00002901F.m.08.1.P.Seq	F	M00005626D:G11	CH02COH
1390	1015	RTA00002933F.c.11.1.P.Seq	F	M00043213A:D05	CH19COP
1391	26792	RTA00002907F.a.18.1.P.Seq	F	M00022103C:D05	CH03MAH
1392	27830	RTA00002921F.c.07.1.P.Seq	F	M00033344A:B06	CH09LNL
1393	14648	RTA00002898F.j.11.1.P.Seq	F	M00004365C:G11	CH01COH
1394	12585	RTA00002897F.i.20.1.P.Seq	F	M00004269A:F11	CH01COH
1395	15825	RTA00002916F.d.12.1.P.Seq	F	M00032553A:A07	CH08LNL
1396	7043	RTA00002900F.h.07.1.P.Seq	F	M00005014B:F02	CH02COH
1397	29354	RTA00002905F.c.13.1.P.Seq	F	M00007981C:F07	CH03MAH
1398	29703	RTA00002907F.d.24.1.P.Seq	F	M00022144C:E12	CH03MAH
1399	6811	RTA00002913F.b.07.1.P.Seq	F	M00027724D:D04	CH04MAL
1400	12657	RTA00002906F.b.20.1.P.Seq	F	M00021866C:H08	CH03MAH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1401	2033	RTA00002922F.e.08.2.P.Seq	F	M00039024D:E12	CH09LNL
1402	24229	RTA00002920F.b.04.1.P.Seq	F	M00033329C:C02	CH08LNLH
1403	20664	RTA00002886F.a.07.1.P.Seq	F	M00001338C:F05	CH01COH
1404	3656	RTA00002902F.f.20.1.P.Seq	F	M00006641B:F05	CH02COH
1405	10998	RTA00002931F.c.07.1.P.Seq	F	M00042878D:G06	CH16COP
1406	1150	RTA00002922F.j.14.1.P.Seq	F	M00039081B:G07	CH09LNL
1407	45221	RTA00002900F.h.06.1.P.Seq	F	M00005013D:H05	CH02COH
1408	34505	RTA00002901F.a.16.1.P.Seq	F	M00005423C:A10	CH02COH
1409	8175	RTA00002924F.f.01.1.P.Seq	F	M00039472B:E05	CH09LNL
1410	8175	RTA00002924F.e.24.1.P.Seq	F	M00039472B:E05	CH09LNL
1411	19375	RTA00002903F.n.02.1.P.Seq	F	M00007081B:C08	CH02COH
1412	10866	RTA00002929F.c.15.1.P.Seq	F	M00040219B:B07	CH14EDT
1413	24166	RTA00002891F.k.07.1.P.Seq	F	M00003763A:B02	CH01COH
1414	15333	RTA00002888F.c.12.1.P.Seq	F	M00001442C:G12	CH01COH
1415	44436	RTA00002907F.b.17.1.P.Seq	F	M00022117C:A02	CH03MAH
1416	9247	RTA00002930F.a.16.1.P.Seq	F	M00042560C:G06	CH15CON
1417	12317	RTA00002908F.g.13.1.P.Seq	F	M00022430C:C06	CH03MAH
1418	11968	RTA00002890F.i.24.1.P.Seq	F	M00001625D:B04	CH01COH
1419	14181	RTA00002908F.n.09.2.P.Seq	F	M00022499D:D08	CH03MAH
1420	15359	RTA00002909F.l.02.1.P.Seq	F	M00022677C:C01	CH03MAH
1421	46675	RTA00002916F.h.03.1.P.Seq	F	M00032584A:D06	CH08LNLH
1422	24898	RTA00002903F.k.17.1.P.Seq	F	M00007019B:E01	CH02COH
1423	156424	RTA00002905F.m.22.1.P.Seq	F	M00021653A:B02	CH03MAH
1424	11996	RTA00002901F.b.24.1.P.Seq	F	M00005445A:E07	CH02COH
1425	11996	RTA00002901F.c.01.1.P.Seq	F	M00005445A:E07	CH02COH
1426	4784	RTA00002894F.e.20.1.P.Seq	F	M00003988D:B01	CH01COH
1427	9120	RTA00002914F.h.10.1.P.Seq	F	M00028210B:H03	CH08LNLH
1428	11295	RTA00002890F.j.15.1.P.Seq	F	M00001632C:A10	CH01COH
1429	3991	RTA00002896F.h.05.1.P.Seq	F	M00004162D:F02	CH01COH
1430	20358	RTA00002908F.b.06.1.P.Seq	F	M00022367D:G11	CH03MAH
1431	12823	RTA00002921F.h.01.1.P.Seq	F	M00033434D:F05	CH09LNL
1432	147419	RTA00002906F.g.05.1.P.Seq	F	M00021952B:G06	CH03MAH
1433	12174	RTA00002919F.f.13.1.P.Seq	F	M00033071D:E08	CH08LNLH
1434	35608	RTA00002897F.o.24.1.P.Seq	F	M00004296B:D03	CH01COH
1435	2325	RTA00002894F.g.07.1.P.Seq	F	M00003994A:B10	CH01COH
1436	166261	RTA00002908F.l.05.1.P.Seq	F	M00022475D:C07	CH03MAH
1437	5713	RTA00002920F.a.09.1.P.Seq	F	M00033324B:F04	CH08LNLH
1438	3624	RTA00002910F.g.06.1.P.Seq	F	M00022901A:C05	CH03MAH
1439	10305	RTA00002909F.a.07.1.P.Seq	F	M00022530B:C04	CH03MAH
1440	7768	RTA00002910F.k.22.1.P.Seq	F	M00022992B:G12	CH03MAH
1441	9847	RTA00002908F.p.07.1.P.Seq	F	M00022516B:C05	CH03MAH
1442	8583	RTA00002887F.o.06.1.P.Seq	F	M00001426C:F06	CH01COH
1443	24376	RTA00002900F.b.07.1.P.Seq	F	M00004836B:C02	CH02COH
1444	8743	RTA00002907F.n.19.1.P.Seq	F	M00022262A:F06	CH03MAH
1445	22251	RTA00002926F.c.10.2.P.Seq	F	M00040079B:F06	CH09LNL
1446	12337	RTA00002928F.d.07.1.P.Seq	F	M00040173D:A04	CH13EDT
1447	13623	RTA00002911F.d.08.2.P.Seq	F	M00026842B:A01	CH04MAL
1448	5521	RTA00002887F.j.06.1.P.Seq	F	M00001406B:H09	CH01COH
1449	2193	RTA00002933F.a.13.1.P.Seq	F	M00043077B:F11	CH19COP
1450	773	RTA00002889F.j.02.1.P.Seq	F	M00001551D:H09	CH01COH

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1451	142367	RTA00002927F.h.11.1.P.Seq	F	M00039630D:B07	CH12EDT
1452	19284	RTA00002889F.e.10.1.P.Seq	F	M00001537B:H10	CH01COH
1453	24011	RTA00002924F.c.17.1.P.Seq	F	M00039440C:G06	CH09LNL
1454	5930	RTA00002911F.f.08.1.P.Seq	F	M00026910B:G06	CH04MAL
1455	21581	RTA00002902F.c.05.1.P.Seq	F	M00005822C:A04	CH02COH
1456	3662	RTA00002925F.c.07.1.P.Seq	F	M00039826D:E04	CH09LNL
1457	4873	RTA00002930F.b.05.1.P.Seq	F	M00042719A:G08	CH15CON
1458	11214	RTA00002896F.h.01.1.P.Seq	F	M00004161A:E08	CH01COH
1459	22888	RTA00002892F.l.09.1.P.Seq	F	M00003837C:D10	CH01COH
1460	15490	RTA00002925F.k.08.1.P.Seq	F	M00039932B:A07	CH09LNL
1461	112819	RTA00002905F.o.13.1.P.Seq	F	M00021676C:G03	CH03MAH
1462	19688	RTA00002896F.l.02.1.P.Seq	F	M00004179D:A12	CH01COH
1463	15132	RTA00002922F.n.20.1.P.Seq	F	M00039138B:G05	CH09LNL
1464	25022	RTA00002914F.i.21.1.P.Seq	F	M00028219B:H05	CH08LNH
1465	16303	RTA00002888F.b.12.1.P.Seq	F	M00001438A:E01	CH01COH
1466	16828	RTA00002897F.b.04.1.P.Seq	F	M00004214A:E05	CH01COH
1467	14295	RTA00002921F.a.18.1.P.Seq	F	M00033296C:C11	CH09LNL
1468	1979	RTA00002930F.f.06.1.P.Seq	F	M00055725D:D09	CH15CON
1469	36248	RTA00002888F.g.05.1.P.Seq	F	M00001460C:E10	CH01COH
1470	5676	RTA00002926F.b.22.2.P.Seq	F	M00040075B:A05	CH09LNL
1471	1239	RTA00002887F.o.21.1.P.Seq	F	M00001428B:C10	CH01COH
1472	7937	RTA00002917F.g.22.1.P.Seq	F	M0003272SD:F01	CH08LNH
1473	4483	RTA00002911F.d.22.2.P.Seq	F	M00026856B:G03	CH04MAL
1474	7796	RTA00002925F.c.05.1.P.Seq	F	M00039826B:F09	CH09LNL
1475	17330	RTA00002915F.a.03.1.P.Seq	F	M00028616C:D09	CH08LNH
1476	25620	RTA00002902F.f.09.1.P.Seq	F	M00006631C:A04	CH02COH
1477	20601	RTA00002923F.l.20.1.P.Seq	F	M00039326A:G07	CH09LNL
1478	6205	RTA00002923F.g.21.1.P.Seq	F	M00039258C:C01	CH09LNL
1479	726	RTA00002913F.b.16.1.P.Seq	F	M00027734D:C03	CH04MAL
1480	104999	RTA00002908F.g.17.1.P.Seq	F	M00022435B:G12	CH03MAH
1481	30321	RTA00002919F.o.17.1.P.Seq	F	M00033264B:E06	CH08LNH
1482	5878	RTA00002913F.a.16.1.P.Seq	F	M00027688C:C01	CH04MAL
1483	5944	RTA00002905F.m.07.1.P.Seq	F	M00021649B:A02	CH03MAH
1484	5796	RTA00002908F.i.21.1.P.Seq	F	M00022457A:G05	CH03MAH
1485	3804	RTA00002935F.m.24.1.P.Seq	F	M00055254A:H03	CH17COHLV
1486	2728	RTA00002918F.a.22.1.P.Seq	F	M00032828A:A06	CH08LNH
1487	3804	RTA00002935F.n.01.1.P.Seq	F	M00055254A:H03	CH17COHLV
1488	3932	RTA00002915F.o.19.2.P.Seq	F	M00032517C:E10	CH08LNH
1489	16691	RTA00002891F.o.03.1.P.Seq	F	M00003780A:G01	CH01COH
1490	15430	RTA00002900F.g.10.1.P.Seq	F	M00005003D:C02	CH02COH
1491	5637	RTA00002925F.b.18.1.P.Seq	F	M00039820B:F06	CH09LNL
1492	16633	RTA00002897F.g.15.1.P.Seq	F	M00004246B:H07	CH01COH
1493	21826	RTA00002898F.g.06.1.P.Seq	F	M00004344A:G11	CH01COH
1494	22193	RTA00002919F.i.09.1.P.Seq	F	M00033146D:A03	CH08LNH
1495	10720	RTA00002898F.c.14.1.P.Seq	F	M00004320C:E07	CH01COH
1496	22491	RTA00002925F.m.06.1.P.Seq	F	M00040003A:G10	CH09LNL
1497	10423	RTA00002915F.n.13.2.P.Seq	F	M00032507D:G08	CH08LNH
1498	4953	RTA00002916F.h.11.1.P.Seq	F	M00032586C:B04	CH08LNH
1499	185567	RTA00002911F.p.08.1.P.Seq	F	M00027178B:A11	CH04MAL
1500	25605	RTA00002924F.m.22.1.P.Seq	F	M00039710B:A01	CH09LNL

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
1501	29446	RTA00002906F.m.24.1.P.Seq	F	M00022070B:B04	CH03MAH
1502	9668	RTA00002908F.g.02.1.P.Seq	F	M00022421A:F12	CH03MAH
1503	29446	RTA00002906F.n.01.1.P.Seq	F	M00022070B:B04	CH03MAH
1504	7171	RTA00002887F.m.22.1.P.Seq	F	M00001421B:E07	CH01COH

Table 3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
6	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
7	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
8	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
9	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
10	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
11	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
12	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
13	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
14	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
15	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
16	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
17	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
18	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
19	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
20	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
21	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
22	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
23	<NONE>	<NONE>	<NONE>	548562	GENOME POLYPROTEIN [CONTAINS: RNA REPLICASE ; HELICASE: COAT PROTEIN] 2.7.7.48) - apple stem grooving virus (strain P-209)	9.2
24	<NONE>	<NONE>	<NONE>	416959	EXCISION REPAIR PROTEIN ERCC-6 DNA repair helicase ERCC6 - human >gi 182181 (L04791) excision repair protein [Homo sapiens]	8.9
25	<NONE>	<NONE>	<NONE>	3327096	(AB014541) KIAA0641 protein [Homo sapiens]	8.7
26	<NONE>	<NONE>	<NONE>	861293	(U28741) F35D2.1 gene product [Caenorhabditis elegans]	7.9
27	<NONE>	<NONE>	<NONE>	3297821	(AL031032) extensin-like protein	5.5
28	<NONE>	<NONE>	<NONE>	2119692	transforming growth factor-beta type III receptor - chicken >gi 511843 (L01121)	5.1
29	<NONE>	<NONE>	<NONE>	2136028	transforming growth factor-beta type III receptor [Gallus gallus] protein kinase PRK1 - human	5.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
30	<NONE>	<NONE>	<NONE>	2746912	(AF040659) No definition line found [Caenorhabditis elegans]	4.6
31	<NONE>	<NONE>	<NONE>	2358287	(AF010404) ALR [Homo sapiens]	4.5
32	<NONE>	<NONE>	<NONE>	3877816	(Z96048) predicted using Genefinder; cDNA EST EMBL:D65516 comes from this gene; cDNA EST yk191a5.5 comes from this gene [Caenorhabditis elegans]	4.4
33	<NONE>	<NONE>	<NONE>	4140268	(Y14953) SRCR domain, membrane form 2	4.1
34	<NONE>	<NONE>	<NONE>	1708663	(U51183) transposase [Hydra vulgaris]	4.0
35	<NONE>	<NONE>	<NONE>	1184100	(U45958) pistil extensin-like protein [Nicotiana glauca]	3.9
36	<NONE>	<NONE>	<NONE>	121073	GLUCOCORTICOID RECEPTOR (GR)	3.9
37	<NONE>	<NONE>	<NONE>	1718298	(U75698) ORF 45; contains an extended acidic domain; EBV BKRF4 homolog [Kaposi's sarcoma-associated herpesvirus] homolog, conserved in other gamma-herpesviruses	2.6
38	<NONE>	<NONE>	<NONE>	2352538	(AF006564) alcohol dehydrogenase [Drosophila persimilis] persimilis]	1.4
39	<NONE>	<NONE>	<NONE>	3192897	(AF066071) SP85; PsB [Dictyostelium discoideum]	1.4
40	<NONE>	<NONE>	<NONE>	561645	(L33421) This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal	1.0
41	<NONE>	<NONE>	<NONE>	3878857	(Z83120) predicted using Genefinder; cDNA EST EMBL:D35016 comes from this gene; cDNA EST EMBL:D32583 comes from this gene; cDNA EST EMBL:D35258 comes from this gene; cDNA EST EMBL:C11471 comes from this gene; cDNA EST EMBL:C...	1.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
42	<NONE>	<NONE>	<NONE>	1658571	(U75903) UGT1A7 [Rattus norvegicus]	1.0
43	<NONE>	<NONE>	<NONE>	2338034	(AF005370) putative immediate early protein [Alcelaphine herpesvirus 1]	0.86
44	<NONE>	<NONE>	<NONE>	3043714	(AB011167) KIAA0595 protein [Homo sapiens]	0.42
45	<NONE>	<NONE>	<NONE>	1723710	HYPOTHETICAL 92.7 KD PROTEIN IN ASN2-PHB1 INTERGENIC REGION >gi 2131678 pir S64439 hypothetical protein YGR130c - yeast (Saccharomyces cerevisiae) >gi 1323215 gnl PID e243523 (Z72915) ORF YGR130c [Saccharomyces cerevisiae]	0.40
46	<NONE>	<NONE>	<NONE>	1723710	HYPOTHETICAL 92.7 KD PROTEIN IN ASN2-PHB1 INTERGENIC REGION >gi 2131678 pir S64439 hypothetical protein YGR130c - yeast (Saccharomyces cerevisiae) >gi 1323215 gnl PID e243523 (Z72915) ORF YGR130c [Saccharomyces cerevisiae]	0.38
47	<NONE>	<NONE>	<NONE>	2996117	(AF046125) immediate early 2 [Rat cytomegalovirus]	0.26
48	<NONE>	<NONE>	<NONE>	4151809	(AF102855) synaptic SAPAP-interacting protein Synamon	0.024
49	<NONE>	<NONE>	<NONE>	2773341	(AF040954) putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]	0.017
50	<NONE>	<NONE>	<NONE>	1653522	(D90914) hypothetical protein	3e-04
51	<NONE>	<NONE>	<NONE>	3219965	HYPOTHETICAL 100.6 KD TRP-ASP REPEATS CONTAINING PROTEIN C2C6.04C IN CHROMOSOME I	3e-06
52	<NONE>	<NONE>	<NONE>	4185567	(AF115480) cAMP-dependent Rap1 guanine-nucleotide exchange factor [Mus musculus]	7e-07

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
53	<NONE>	<NONE>	<NONE>	1176527	HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III >gi 500724 (U10402) C34E10.1 gene product [Caenorhabditis elegans]	3e-20
54	X85444	G.pallida repetitive DNA element	5.0	2118936	beta-globin - chimpanzee (fragment)	8.6
55	X72961	Synechococcus sp. cpeB, cpeA genes and ORF3	5.0	462569	MICROTUBULE-ASSOCIATED PROTEIN 1A microtubule-associated protein MAP1A - rat >gi 205538 norvegicus]	2.2
56	U94747	Human WD repeat protein HAN11 mRNA. complete cds	5.0	3875538	(Z67990) similar to cuticle collagen	1.3
57	AF032108	Homo sapiens integrin alpha-7 mRNA. complete cds	5.0	2147194	collagen - Paralvinella grasslei	0.002
58	Z50798	G.gallus mRNA for p52	5.0	3122885	ASPARTYL-TRNA SYNTHETASE synthetase [Bacillus subtilis]	3e-11
59	AB002384	Human mRNA for KIAA0386 gene, complete cds	5.0	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	9e-12
60	X14835	Thermofilum pendens DNA for 16S and 23S ribosomal RNA, tRNA-Met, and tRNA Gly	4.9	<NONE>	<NONE>	<NONE>
61	U87149	Hordeum vulgare nucellin gene, complete cds	4.9	128578	NONSTRUCTURAL PROTEIN NS-S spotted wilt virus (strain CPNH1) non-structural protein [Tomato spotted wilt virus]	2.8
62	D87541	Mus musculus gene for integrin alpha v subunit, promoter region	4.9	136956	HYPOTHETICAL PROTEIN UL61 cytomegalovirus (strain AD169) cytomegalovirus]	0.038
63	U72520	Mus musculus mena protein (Mena) mRNA. complete cds	4.9	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	6e-07

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
64	S79797	enzymatic glycosylation-regulating gene [rats, Sprague-Dawley, streptozotocin diabetic, heart, mRNA, 5010 nt]	4.8	<NONE>	<NONE>	<NONE>
65	AB011102	Homo sapiens mRNA for KIAA0530 protein, partial cds	4.8	138022	RECEPTOR RECOGNIZING PROTEIN gp38 - phage Ox2 >gi 15126 (X05675) gene 38 (AA 1-266); pid:gi15126 [Bacteriophage Ox2]	3.6
66	AF100985	Penaeus monodon phosphopyruvate hydratase mRNA, complete cds	4.8	500615	(D16221) endochitinase [Oryza sativa]	2.8
67	U31756	Bacillus subtilis gamma-aminobutyrate permease cds	4.8	3880699	(AL021471) similar to Eukaryotic aspartyl proteases [Caenorhabditis elegans] Eukaryotic aspartyl proteases [Caenorhabditis elegans]	2.8
68	U25111	Pisum sativum chloroplast processing enzyme mRNA, nuclear gene encoding chloroplast protein, complete cds.	4.8	1800145	(U83658) FH1/FH2 protein homolog [Emericella nidulans]	1.6
69	U00454	Mus musculus Cdx-2 homeobox protein gene, complete cds.	4.7	<NONE>	<NONE>	<NONE>
70	M84166	Hamster c-Ha-ras protein gene, complete cds.	4.7	1710606	RENIN-BINDING PROTEIN (RNBP) protein [Rattus norvegicus]	0.88
71	AF087516	Mus musculus major sperm fibrous sheath protein Pro-mAKAP82 gene, alternative splice exons I' and I"	4.6	<NONE>	<NONE>	<NONE>
72	X74160	M.esculenta mRNA for granule-bound starch synthase	4.6	<NONE>	<NONE>	<NONE>
73	M97487	Haloferax volcanii superoxide dismutase (sod2) gene, complete cds.	4.6	2623307	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]	3.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Drosophila melanogaster suppressor of sable gene, complete cds.	4.5	<NONE>	<NONE>	<NONE>
74	M57889					
75	D49708	Rattus norvegicus mRNA for RNA binding protein	4.5	<NONE>	<NONE>	<NONE>
76	D31853	Yeast GTS1 gene for glycyl-threonin/serine repeat protein, complete cds	4.5	2447195	(U42580) NETTF (7x), DETTS (4x) [Paramecium bursaria Chlorella virus 1]	3.3
77	Z47036	Human partial cDNA sequence, clone bs613;	2.9	<NONE>	<NONE>	<NONE>
78	L19660	Rattus norvegicus gastric inhibitory peptide receptor mRNA, complete cds	2.7	2358279	(AF007871) torsinA [Homo sapiens]	2e-07
79	X82841	A.thaliana Aco gene	2.6	483212	immediate-early protein IE110 - human herpesvirus 1 (strain HFEM) (fragment)	8.4
80	X61931	S.purpurascens famA and famB genes for FAS domain and acyl-CoA-dehydrogenases, respectively	2.6	2290534	(U95031) sublingual gland mucin [Homo sapiens]	0.47
81	U13680	Human lactate dehydrogenase-C (LDH-C) mRNA, complete cds.	2.5	2887449	(AB007874) KIAA0414 [Homo sapiens]	3.1
82	AB007869	Homo sapiens KIAA0409 mRNA, partial cds	2.4	3130157	(AB008859) pheromone receptor [Fugu rubripes]	5.4
83	X97479	H.sapiens mas proto-oncogene, 5' region	2.1	<NONE>	<NONE>	<NONE>
84	X98374	R.norvegicus mRNA for KIS protein	1.9	<NONE>	<NONE>	<NONE>
85	AE000710	Aquifex aeolicus section 42 of 109 of the complete genome	1.9	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens mRNA				
86	D30612	for repressor protein, partial cds	1.9	<NONE>	<NONE>	<NONE>
87	Y14321	Homo sapiens PMP69 gene, exons 8,9,10 & 11	1.9	<NONE>	<NONE>	<NONE>
88	D90773	E.coli genomic DNA, Kohara clone #262(30.3-30.5 min.)	1.9	1536816	(D78305) DNA binding protein [Chlorella virus]	7.9
89	AE000991	Archaeoglobus fulgidus section 116 of 172 of the complete genome	1.9	520645	(X79095) pyruvate,orthophosphate dikinase [Flaveria trinervia]	2.7
90	U39476	Rattus norvegicus p95 Vav (Vav) proto-oncogene mRNA, complete cds.	1.9	4158178	(AL023496) hypothetical protein	1.6
91	U28838	Human transcription factor TFIIIB 90 kDa subunit	1.9	2495730	HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269 >gi 1665805 gnl PID d1014089 (D87459) Similar to Volbox carteri extensin (S22697) [Homo sapiens]	0.23
92	U20106	Rattus norvegicus synaptotagmin VII mRNA, complete cds.	1.9	478380	UL47h protein - Marek's disease virus	0.23
93	AF071010	Mouse mammary tumor virus putative integrase, env polyprotein, and superantigen mRNA, complete cds	1.9	2781386	(AC004010) similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	4e-33
94	AF061881	Mesocricetus auratus c-fos proto-oncogene protein (c-fos) gene, complete cds	1.8	<NONE>	<NONE>	<NONE>
95	AE001397	Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence	1.8	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Horseshoe crab				
96	D14701	mRNA for coagulation factor B, complete cds	1.8	<NONE>	<NONE>	<NONE>
97	M29154	P.falciparum multidrug resistance (MDR) gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
98	L16532	Rattus norvegicus (clone pCNPII) 2',3'-cyclic nucleotide 3'-phosphodiesterase (CNPII) mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE>
99	AE001434	Plasmodium falciparum chromosome 2, section 71 of 73 of the complete sequence	1.8	<NONE>	<NONE>	<NONE>
100	Z46785	D.melanogaster gene for protamine (mst35Bb).	1.8	<NONE>	<NONE>	<NONE>
101	X69822	P.sylvestris mRNA for glutamine synthetase	1.8	219896	(D90452) I-caldesmon I [Homo sapiens]	9.7
102	U49055	Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds	1.8	2497252	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 (IGFBP-4) (IBP-4) (IGF-BINDING PROTEIN 4) factor-binding protein-4 - sheep (fragment) factor-binding protein-4, IGFBP-4 [sheep, liver, Peptide, 237 aa] [Ovis aries]	2.5
103	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	1.8	4204267	(AC005223) 55585 [Arabidopsis thaliana]	2.4
104	U66987	Pandorina morum internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence	1.8	2635909	(Z99121) permease [Bacillus subtilis]	1.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human polymorphic				
105	X58033	MspI site DNA (D3S3 locus)	1.8	2136878	keratin KAP5.5 - sheep (fragment) >gi 313722	0.65
106	U15780	Human p82 (ST5) mRNA, alternatively spliced, complete cds	1.8	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	0.64
107	AF038535	Homo sapiens synaptotagmin VII mRNA, partial cds	1.8	457927	(U00690) calcium channel alpha-1 subunit [Drosophila melanogaster]	0.51
108	AF052134	Homo sapiens clone 23585 mRNA sequence	1.8	232263	HOMEBOX PROTEIN HOX-D1 (HOX-4.9)	0.28
109	X75208	H.sapiens HEK2 mRNA for protein tyrosine kinase receptor.	1.8	1730198	GROWTH-ARREST-SPECIFIC PROTEIN 1 gene product [Homo sapiens]	0.22
110	AB013896	Xenopus laevis mRNA for SOX-D, complete cds	1.8	2494501	TRANSCRIPTION FACTOR FKH-4 factor [Mus musculus]	0.17
111	D16947	Human HepG2 3' region cDNA, clone hmd6b10	1.8	3413870	(AB007923) KIAA0454 protein [Homo sapiens]	0.002
112	D13547	Mouse DNA, T early alpha (TEA) region	1.8	3393018	(AL031174) hypothetical protein	5e-08
113	M35498	Woodchuck c-myc protein gene, exon 1.	1.8	3183405	HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I >gi 2370504 gnl PID e339194 pombe] >gi 3451305 gnl PID e1316730 (AL031324) very hypothetical protein [Schizosaccharomyces pombe]	8e-10
114	M84166	Hamster c-Ha-ras protein gene, complete cds.	1.8	3386622	(AC004665) unknown protein [Arabidopsis thaliana]	2e-10
115	U33135	Mychodea carnosia 18S ribosomal RNA gene, complete sequence	1.8	3334982	(AC005306) R27216_1 [Homo sapiens]	3e-22
116	U84003	Homo sapiens putative tumor suppressor (BIN1) gene, exons 7-12	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
117	AE001121	Borrelia burgdorferi (section 7 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
118	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
119	U82064	Angiostrongylus cantonensis adult-specific muscle protein-1 gene, partial cds	1.7	<NONE>	<NONE>	<NONE>
120	AF041836	Buchnera aphidicola plasmid pLeu-Sg, complete plasmid sequence	1.7	<NONE>	<NONE>	<NONE>
121	M87479	Lymnaea stagnalis FMRFamide gene, mature peptides.	1.7	<NONE>	<NONE>	<NONE>
122	M55163	Xenopus laevis fibroblast growth factor receptor mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
123	S57565	histamine H2-receptor [rats, Genomic, 1928 nt]	1.7	<NONE>	<NONE>	<NONE>
124	M27256	Simian immunodeficiency virus (SIV) pol region.	1.7	<NONE>	<NONE>	<NONE>
125	U31516	Human chromosome 8 anonymous clone pBS8-165	1.7	<NONE>	<NONE>	<NONE>
126	X12671	Human gene for heterogeneous nuclear ribonucleoprotein (hnRNP) core protein A1	1.7	<NONE>	<NONE>	<NONE>
127	AF009054	Paeonia suffruticosa ssp. spontanea alcohol dehydrogenase 1B (Adh1B) gene, partial cds	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
128	AF046917	Mus musculus transketolase gene, exon 6 and partial cds	1.7	<NONE>	<NONE>	<NONE>
129	D89053	Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds	1.7	<NONE>	<NONE>	<NONE>
130	U57968	Staphylothermus marinus surface layer-associated STABLE protease gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
131	L39072	Bovine herpesvirus 1 (clone p95) UL24 homologue gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
132	X04980	Drosophila simulans retrotransposon 297 5'-LTR and flanks (pWK1020)	1.7	<NONE>	<NONE>	<NONE>
133	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
134	X04434	Human mRNA for insulin-like growth factor I receptor	1.7	<NONE>	<NONE>	<NONE>
135	U07890	Mus musculus C57BL/6J epidermal surface antigen (mesa) mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
136	D26163	Human tyrosinase gene, 5'-flanking region cell-specific transcription)	1.7	<NONE>	<NONE>	<NONE>
137	AF093818	Panorpa nipponensis NADH dehydrogenase subunit 5 gene, mitochondrial gene encoding mitochondrial protein, partial cds	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis				
138	D50560	mRNA for cytochrome P-450, complete cds	1.7	<NONE>	<NONE>	<NONE>
139	AF083488	Mus musculus phospholipase D1 (PLD1) gene, exons 18 and 19, complete sequence	1.7	<NONE>	<NONE>	<NONE>
140	AF100694	Mus musculus Pontin52 mRNA, complete cds	1.7	<NONE>	<NONE>	<NONE>
141	M73749	Streptococcus salivarius thermophilus beta-D-galactose (lacZ) gene, complete cds. > :: gb M63636 STRLAC ZZ Streptococcus thermophilus beta-D-galactosidase (lacZ) gene, complete cds.	1.7	<NONE>	<NONE>	<NONE>
142	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	2183023	(U84971) unknown [Homo sapiens]	9.2
143	L01983	Human type IV sodium channel alpha polypeptide	1.7	130504	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR ... virus (strain D)]	9.2
144	L19731	Plecotus rafinesquii mitochondrial cytochrome b gene, 5' end.	1.7	3327096	(AB014541) KIAA0641 protein [Homo sapiens]	9.1
145	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.7	2183023	(U84971) unknown [Homo sapiens]	8.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
146	L27218	Bos taurus serum amine oxidase mRNA, complete cds. > oxidase=amiloride-binding protein homolog [cattle, liver, mRNA, 2664 nt]	1.7	1174459	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 6 (IL-4 STAT) >gi 559855 (U16031) IL-4 Stat [Homo sapiens]	7.1
147	Z49868	Caenorhabditis elegans cosmid W07E11, complete sequence [Caenorhabditis elegans]	1.7	4204263	(AC005223) 40409 [Arabidopsis thaliana]	6.7
148	AL022271	Caenorhabditis elegans cosmid F32F2, complete sequence [Caenorhabditis elegans]	1.7	2497969	PERIPLASMIC NITRATE REDUCTASE PRECURSOR >gi 1086107 pir S50163 nitrate reductase large chain precursor, periplasmic - Thiosphaera pantotropha >gi 600093 (Z36773) periplasmic nitrate reductase large subunit [Paracoccus denitrificans]	6.7
149	U43844	Mus musculus cyclin D3 gene, complete cds	1.7	3861490	(AF062037) capsid protein precursor [Thosea asigna virus]	5.1
150	Z25464	S.cerevisiae UNF1, LTV1, MRP8, CYB3 and TGL1 genes, complete CDS's	1.7	1255404	(U53151) weak similarity to cytochrome b [Caenorhabditis elegans]	4.1
151	U77846	Human elastin gene, partial cds and partial 3'UTR	1.7	3355682	(AL031124) putative secreted lyase	4.0
152	X62880	S.scrofa mRNA for calcium release channel (CRC)	1.7	3327080	(AB014533) KIAA0633 protein [Homo sapiens]	4.0
153	Y00067	Human gene for neurofilament subunit M (NF-M)	1.7	479829	heterogeneous ribonuclear particle protein homolog - Caenorhabditis elegans similarity to RNA recognition motifs [Caenorhabditis elegans]	3.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
154	X68393	D.melanogaster gene for Beta-tubulin, exons 1 and 2	1.7	2342682	(AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb X95577). [Arabidopsis thaliana]	3.8
155	AB012284	Shuttle vector pAUR123 gene for Aur1-C, complete cds	1.7	417704	POL POLYPROTEIN (ORF1A/1B) [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; HELICASE; PROTEASE]	3.8
156	M96633	Rattus norvegicus mitochondrial intermediate peptidase (MIP) mRNA, complete cds.	1.7	2314209	(AE000613) H. pylori predicted coding region HP1054	3.1
157	U49055	Rattus norvegicus CTD-binding SR-like protein rA8 mRNA, complete cds	1.7	2497252	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 (IGFBP-4) (IBP-4) (IGF-BINDING PROTEIN 4) factor-binding protein-4 - sheep (fragment) factor-binding protein-4, IGFBP-4 [sheep, liver, Peptide, 237 aa] [Ovis aries]	3.0
158	Y15907	Mus musculus mRNA for myc-intron-binding protein-1	1.7	912776	iduronate-2-sulfatase, IDS {EC 3.1.6.13} Peptide Mutant, 550 aa]	3.0
159	U67600	Methanococcus jannaschii section 142 of 150 of the complete genome	1.7	2982355	(AF052252) fork head domain protein FKD9 [Danio rerio]	3.0
160	AF013759	Homo sapiens calumein (Calu) mRNA, complete cds	1.7	2982355	(AF052252) fork head domain protein FKD9 [Danio rerio]	2.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
161	AF062915	Arabidopsis thaliana putative transcription factor (MYB90) mRNA, complete cds	1.7	3878065	(AF021066) Similarity to Human mRNA product KIAA0077 (TR:Q14997); cDNA EST yk243h8.5 comes from this gene; cDNA EST yk243h8.3 comes from this gene; cDNA EST yk359h4.5 comes from this gene [Caenorhabditis elegans] >gi 3880318 gnl PID e1349839 (Z81133) Similarity to Human mRNA product KIAA0077 (TR:Q14997); cDNA EST yk243h8.5 comes from this gene; cDNA EST yk243h8.3 comes from this gene; cDNA EST yk359h4.5 comes from this gene	2.3
162	X87526	H.sapiens genomic DNA (chromosome 3; clone NL3003R)	1.7	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	2.3
163	AC005573	Homo sapiens chromosome 5, PAC clone 202e13	1.7	2465540	(AF005632) phosphodiesterase I/nucleotide pyrophosphatase beta [Homo sapiens]	1.8
164	D83402	Homo sapiens gene for prostacyclin synthase, exon 10 and complete cds	1.7	627608	steroid hormone receptor TR3 - human sapiens]	1.7
165	AF053700	Homo sapiens deltex (Dx) mRNA, complete cds	1.7	2662089	(AB007864) KIAA0404 [Homo sapiens]	1.7
166	AF043225	Mus musculus 6-pyruvoyl-tetrahydropterin synthase (Pts) mRNA, complete cds	1.7	2352538	(AF006564) alcohol dehydrogenase [Drosophila persimilis] persimilis]	1.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
167	U52917	<i>Thermus aquaticus</i> thermophilus NADH dehydrogenase I subunits NQO7, NQO6, NQO5, NQO4, NQO2, NQO1, NQO3, NQO8, NQO9, NQO10, NQO11, NQO12, NQO13, and NQO14, complete cds.	1.7	2564334	(AB006631) The human homolog of mouse Cux-2 [Homo sapiens]	1.0
168	X72222	<i>M. musculus</i> gene for serotonin 2 receptor	1.7	3875796	(Z73425) Similarity to Yeast hypothetical YIK9 protein (SW:YIK9_YEAST); cDNA EST EMBL:T01252 comes from this gene; cDNA EST EMBL:D33205 comes from this gene; cDNA EST EMBL:D33955 comes from this gene; cDNA EST EMBL:D35484 co...	1.0
169	U23186	<i>Crotalus scutulatus</i> PLA2-like pseudogene	1.7	853971	(X83413) DR5 [Human herpesvirus 6] >gi 853972 (X83413) DR5 [Human herpesvirus 6]	0.99
170	M83118	<i>Mus musculus</i> factor VIII-associated protein (f8a) mRNA, complete cds.	1.7	3201617	(AC004669) hypothetical protein [Arabidopsis thaliana] (AL031282) dJ283E3.3.2 (Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase)) (isoform beta 2-2) [Homo sapiens]	0.80
171	M38347	<i>E. coli</i> ATP-dependent proteinase (lon) gene, complete cds.	1.7	4140322	HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269 >gi 1665805 gnl PID d1014089 (D87459) Similar to Volbox carteri extensin (S22697) [Homo sapiens]	0.78
172	U28838	Human transcription factor TFIIIB 90 kDa subunit	1.7	2495730		0.62

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
173	U72487	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds	1.7	544411	GLYCOPROTEIN GP100 PRECURSOR (P29F8) [discoideum]	0.35
174	AE000718	Aquifex aeolicus section 50 of 109 of the complete genome	1.7	2497569	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3) (HEPARIN-BINDING GROWTH FACTOR RECEPTOR) >gi 2117851 pir I55363 fibroblast growth factor receptor 3 - mouse >gi 199145 (M81342) fibroblast growth factor receptor 3 [Mus musculus]	0.34
175	AF016897	Oryza sativa GDP dissociation inhibitor protein OsGDI2 (OsGDI2) mRNA, complete cds	1.7	125362	MACROPHAGE COLONY STIMULATING FACTOR I RECEPTOR PRECURSOR (CSF-1-R) (FMS PROTO-ONCOGENE) (C-FMS) factor 1 receptor - cat >gi 163855 (J03149) M-CSF receptor [Felis domesticus]	0.34
176	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.7	85058	muscarinic acetylcholine receptor - fruit fly acetylcholine receptor [Drosophila melanogaster]	0.20
177	AF077352	Chlamydomonas reinhardtii myosin heavy chain	1.7	728901	ACROSOMAL PROTEIN SP-10 PRECURSOR SP-10 - western baboon >gi 298488 bbs 127113 (S56458) SP-10=intraacrosomal protein [Papio papio=baboons, Peptide, 285 aa] [Papio hamadryas]	0.20
178	Z92788	Caenorhabditis elegans cosmid F53B8, complete sequence [Caenorhabditis elegans]	1.7	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.068

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
179	AF002217	Ralstonia eutropha megaplasmid pHG1 nitric oxide reductase (norB) gene, complete cds	1.7	1143538	(X87883) mitochondrial capsule selenoprotein [Rattus norvegicus] >gi 1354135 (U48702) mitochondria associated cysteine-rich protein SMCP	0.039
180	D30749	Rat mRNA for protein tyrosine phosphatase	1.7	1228035	(D83776) The KIAA0191 gene is expressed ubiquitously.; The KIAA0191 protein retains the C2H2 zinc-finger at its N-terminal region. [Homo sapiens]	0.008
181	M15202	Rat fast skeletal TnT gene encoding troponin T isoforms, complete cds.	1.7	731172	SKIN SECRETORY PROTEIN XP2 PRECURSOR	4e-04
182	L07592	Human peroxisome proliferator activated receptor mRNA, complete cds.	1.7	4033414	PUTATIVE IMPORTIN BETA-4 SUBUNIT	2e-06
183	U64031	Dendrobium crumenatum ACC synthase gene, complete cds	1.7	3122885	ASPARTYL-TRNA SYNTHETASE synthetase [Bacillus subtilis]	2e-11
184	AF034970	Homo sapiens docking protein (DOK-2) mRNA, complete cds	1.7	2289097	(U78737) alpha(1,3)fucosyltransferase [Cricetulus griseus]	8e-12
185	Z12839	L.longiflorum mRNA encoding calmodulin. > :: gb L18912 LILCALM ODU Lilium longiflorum calmodulin mRNA, complete cds.	1.7	2511747	(AF023270) probable transcriptional regulator dre4	4e-12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
186	X53459	Equine arteritis virus (EAV) RNA genome > :: emb A45589 A45589 Sequence 1 from Patent WO9519438 > :: emb A58849 A58849 Sequence 1 from Patent WO9700963 > :: gb AR013959 AR013959 Sequence 1 from patent US 5773235	1.7	3979817	(Z70683) Weak similarity to Human tyrosine-protein kinase CSK (SW:CSK_HUMAN); cDNA EST EMBL:C10908 comes from this gene; cDNA EST EMBL:C12822 comes from this gene; cDNA EST yk408c.3 comes from this gene; cDNA EST yk408c.2.5 ... Human tyrosine-protein kinase CSK (SW:CSK_HUMAN); cDNA EST EMBL:C10908 comes from this gene; cDNA EST EMBL:C12822 comes from this gene; cDNA EST yk408c.3 comes from this gene; cDNA EST yk408c.2.5 ...	1e-14
187	K02668	E. coli ddl gene encoding D-alanine:D-alanine ligase and ftsQ and ftsA genes, complete cds, and ftsZ gene, 5' end.	1.7	3879121	(Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES...	2e-19
188	AB008375	Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds	1.7	2496945	HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II >gi 733603 (U23484) No definition line found [Caenorhabditis elegans]	1e-19
189	L36603	Pseudomonas cepacia (clone Psudom70-1) heat shock protein 70 (hsp70) gene, complete cds	1.7	2661842	(Y15732) DNA polymerase beta [Xenopus laevis]	6e-20

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
190	Z49760	P.blakesleeanus mRNA GTP cyclohydrolase I	1.7	1731181	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi 3874230 gnl PID e1351618 protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans] (AF125443) contains similarity to S. pombe phosphatidyl synthase (GB:Z28295) [Caenorhabditis elegans]	3e-21
191	U52428	Human fatty acid synthase gene, partial cds	1.7	4226073		6e-25
192	U12767	Human mitogen induced nuclear orphan receptor	1.6	<NONE>	<NONE>	<NONE>
193	Z63478	H.sapiens CpG DNA, clone 85a12, forward read cpg85a12.ft1a.	1.6	<NONE>	<NONE>	<NONE>
194	AF084375	Homo sapiens inversin protein, exons 8 and 9	1.6	<NONE>	<NONE>	<NONE>
195	AE001114	Archaeoglobus fulgidus section 165 of 172 of the complete genome	1.6	<NONE>	<NONE>	<NONE>
196	AF084375	Homo sapiens inversin protein, exons 8 and 9	1.6	<NONE>	<NONE>	<NONE>
197	U24217	Kluyveromyces lactis RNA polymerase II largest subunit gene, partial cds	1.6	<NONE>	<NONE>	<NONE>
198	AE000580	Helicobacter pylori 26695 section 58 of 134 of the complete genome	1.6	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
199	X62083	H.sapiens mRNA for Drosophila female sterile homeotic (FSH) homologue > :: gb M80613 HUMFS HG Human homolog of Drosophila female sterile homeotic mRNA, complete cds.	1.6	<NONE>	<NONE>	<NONE>
200	M28064	Plasmodium brasilianum DNA homologous to the histidine-rich knob protein region of Plasmodium falciparum.	1.6	457495	(M26647) ORF X [Saccharomyces cerevisiae]	8.4
201	U03114	Streptomyces albus lipase precursor (lip) gene, complete cds, and unidentified 5' ORF and 3' ORF, partial cds.	1.6	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	7.8
202	U88422	Strix varia oocyte maturation factor Mos (c-mos) proto-oncogene, partial cds	1.6	137618	VITAMIN D3 RECEPTOR (VDR) receptor [Rattus norvegicus]	6.4
203	M68519	Human pulmonary surfactant-associated protein SP-A (SFTP1) gene, complete cds.	1.6	3875423	(Z38112) E03A3.6 [Caenorhabditis elegans]	4.9
204	AF044575	Homo sapiens transcription factor POU4F3	1.6	2133625	GABA transport protein - tobacco hornworm	4.7
205	L48476	Homo sapiens (subclone 3_e10 from P1 H21) DNA sequence.	1.6	3687297	(AJ005588) 5-epi-aristolochene synthase	4.6
206	M18630	Rat CNS 2',3'-cyclic nucleotide 3-phosphodiesterase	1.6	3880315	(Z81133) Similarity to Human mRNA product KIAA0077 (TR:Q14997) [Caenorhabditis elegans]	3.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
207	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1.6	267068	TUMOR-ASSOCIATED ANTIGEN L6	3.6
208	U53448	Babesia microti heat shock protein 70 (hsp70) gene, complete cds	1.6	1255429	(U53155) strong similarity to the carboxyl two-thirds of valyl-tRNA synthetases [Caenorhabditis elegans]	2.2
209	AF084367	Homo sapiens inversin protein mRNA, complete cds	1.6	1730076	PROBABLE SERINE/THREONINE-PROTEIN KINASE CY49.28 >gi 1370255 gnl PID e247094 (Z73966) pknJ	1.2
210	D55635	Yeast dis1+ gene for p93dis1, complete cds	1.6	3128353	(AF010496) maltose transport inner membrane protein	1.2
211	AF035756	Streptomyces sp. 2-dehydro-3-deoxyphosphoheptonate aldolase gene, partial cds	1.6	853971	(X83413) DR5 [Human herpesvirus 6] >gi 853972 (X83413) DR5 [Human herpesvirus 6]	0.97
212	X73479	O.cuniculus rPTPA mRNA	1.6	3413810	(Y17034) Bassoon [Mus musculus]	0.94
213	X98330	H.sapiens mRNA for ryanodine receptor 2	1.6	2072986	(U95142) putative G-protein-coupled receptor G-protein-coupled receptor [Arabidopsis thaliana]	0.73
214	X64194	P.anserina FMR1 gene exons 1 and 2	1.6	128014	NECDIN >gi 91129 pir JN0148 necdin, brain - mouse >gi 200020 (M80840) necdin [Mus musculus]	0.42
215	Z92788	Caenorhabditis elegans cosmid F53B8, complete sequence [Caenorhabditis elegans]	1.6	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.19
216	AE000888	Methanobacterium thermoautotrophicum from bases 1098908 to 1112186 (section 94 of 148) of the complete genome	1.6	462415	INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC) >gi 346520 pir S27387 interferon alpha receptor type 1 - bovine >gi 432	0.001

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
217	AB008375	Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds	1.6	2496945	HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME II >gi 733603 (U23484) No definition line found [Caenorhabditis elegans] (Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	1e-18
218	M25312	Orang-utan involucrin gene, complete cds.	1.6	3875131		3e-26
219	AB012882	Cyprinus carpio mRNA for MyoD, complete cds	1.5	<NONE>	<NONE>	<NONE>
220	U29487	Caenorhabditis elegans cosmid C09C7	1.5	<NONE>	<NONE>	<NONE>
221	X74760	M.musculus mRNA for Notch 3	1.5	1364094	integral membrane protein - Streptomyces pristinaespiralis >gi 872306 (X84072) integral membrane protein [Streptomyces pristinaespiralis]	4.3
222	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	1.5	121855	EXOGLUCANASE II PRECURSOR cellulose 1,4-beta cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus cellobiohydrolase II [Trichoderma reesei]	4.3
223	U42391	Human myosin-IXb mRNA, complete cds	1.5	3688428	(AJ011534) sucrose synthase	4.2
224	M92296	Pongo pygmaeus gamma-1 and gamma-2 globin genes, complete cds.	1.5	186413	(M13144) inhibin A [Homo sapiens]	0.22
225	X94144	C.japonica mRNA for QNR-71 protein	1.5	2745737	(AF029791) UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase-II [Mus musculus]	3e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
226	AB014557	Homo sapiens mRNA for KIAA0657 protein, partial cds	1.5	1212992	(X90568) Protein sequence and annotation available soon via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE [Homo sapiens]	4e-13
227	AF000948	Borrelia burgdorferi oligopeptide permease homolog OppAIV (oppAIV) gene, complete cds	1.3	<NONE>	<NONE>	<NONE>
228	AF057287	Mus musculus RAB/Rip protein mRNA, partial cds	1.3	2498005	MYC PROTO-ONCOGENE PROTEIN (C-MYC) proto-oncogene [Sus scrofa]	2.6
229	U38951	Drosophila melanogaster vacuolar ATPase subunit E	1.1	<NONE>	<NONE>	<NONE>
230	AF027148	Homo sapiens myogenic determining factor 3	1.1	3172134	(U90209) RNA polymerase II largest subunit [Bonnemaisonia hamifera]	2.3
231	AF079310	Mus musculus histone deacetylase 3 (Hdac3) gene, exons 4 through 15 and complete cds	1.0	1657601	(U66220) unknown [Nannocystis exedens]	0.25
232	X52134	P.radiata lac gene for laccase	0.95	996020	(X91638) BRM protein [Gallus gallus]	0.31
233	D89016	Human mRNA for Neuroblastoma, complete cds	0.93	<NONE>	<NONE>	<NONE>
234	X76392	C.familiaris VIP36 (vesicular integral-membrane protein of 36 kDa) mRNA	0.93	4176446	(AL022238) dJ1042K10.2.1 (novel protein with probable rabGAP domains and Src homology domain 3)	7e-81
235	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.90	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
236	AE000991	Archaeoglobus fulgidus section 116 of 172 of the complete genome	0.90	1176579	EGT2 PROTEIN PRECURSOR (EARLY G1 TRANSCRIPT 2) >gi 1362345 pir S55862 probable membrane protein YNL327w - yeast (Saccharomyces cerevisiae) cerevisiae] >gi 1302445 gnl PID e239572 (Z71603) ORF YNL327w [Saccharomyces cerevisiae]	6.9
237	Z35922	S.cerevisiae chromosome II reading frame ORF YBR053c	0.86	<NONE>	<NONE>	<NONE>
238	U47331	Rattus norvegicus metabotropic glutamate receptor 4b mRNA, complete cds.	0.82	1550703	(Z80225) hypothetical protein Rv2662	4.1
239	X72810	H.sapiens Ig germline kappa-chain gene variable region (L3)	0.69	3023063	(AF052587) F14 [Xylella fastidiosa]	6.7
240	Z11700	Escherichia coli genes faeG, faeH, faeI, faeJ and IS629-like insertion sequence. >:: emb Z11710 ECFAE HIJ E.coli faeH, faeI and faeJ genes encoding FaeH, FaeI and FaeJ proteins	0.69	2347188	(AC002338) laccase isolog [Arabidopsis thaliana] thaliana]	3.9
241	U71597	Phrynosoma douglassii NADH dehydrogenase subunit 4 (ND4) gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.65	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
242	Z77798	Ammonia species LSU rRNA gene (partial; isolate Tr S 5; clone 16)	0.64	1174506	GLUTAMYL-tRNA SYNTHETASE glutamate--tRNA ligase (EC 6.1.1.17) - Haemophilus influenzae (strain Rd KW20) >gi 1573240 (U32713) glutamyl-tRNA synthetase (gltX) [Haemophilus influenzae Rd]	1.2
243	D25542	Human mRNA for golgi antigen gcp372, complete cds	0.64	111230	ultra-high-sulfur keratin 1 - mouse	1e-05
244	M80234	Cow dopamine transporter mRNA, putative cds.	0.64	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	8e-06
245	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.64	2833239	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi 530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	2e-14
246	X51754	Human U266 rearranged DNA for lambda-immunoglobulin light chain	0.63	2072301	(U95102) mitotic phosphoprotein 90 [Xenopus laevis]	1.5
247	AE001554	Helicobacter pylori, strain J99 section 115 of 132 of the complete genome	0.62	<NONE>	<NONE>	<NONE>
248	Z64067	H.sapiens CpG DNA, clone 96e7, reverse read cpg96e7.rt1a .	0.62	<NONE>	<NONE>	<NONE>
249	AJ223768	Pinus sylvestris microsatellite DNA, clone SPAC11.5	0.62	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
250	AJ011592	Bacteriophage P1 ban gene	0.62	2493689	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN [deltoides] >gi 2143326 gnl PID e319090 (Y13328) 10kDa phosphoprotein [Populus deltoides]	7.9
251	AF027151	Xenopus laevis survival of motor neuron protein interacting protein 1 (SIP1) mRNA, complete cds	0.62	4007790	(AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]	2.0
252	AJ000376	Helobdella triserialis mRNA for actin	0.62	1117968	(U40763) CARS-Cyp [Homo sapiens] sapiens]	0.90
253	M69231	Rat thymosin beta 4 gene (pTB4G).intron.	0.62	4176370	(AC005058) similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	6e-51
254	AB021638	Homo sapiens X11L2 mRNA for X11-like protein 2, complete cds	0.61	<NONE>	<NONE>	<NONE>
255	D26470	Bacteroides gingivalis DNA for arginyl endopeptidase, complete cds	0.61	<NONE>	<NONE>	<NONE>
256	J04737	A.thaliana ATPase gene, complete cds.	0.61	<NONE>	<NONE>	<NONE>
257	U06756	Bos taurus clone bm1308 microsatellite and are-1p repeat region.	0.61	1922280	(Y09905) snail like protein [Gallus gallus]	0.51
258	S75756	p15=cyclin D-dependent kinases 4 and 6-binding protein/p15 product {exon/intron 1} [human, brain tumors, Genomic, 753 nt]	0.61	484938	hypothetical protein 253 - Streptomyces griseus plasmid pSG1 (fragment)	0.13
259	L39837	Drosophila melanogaster tumor suppressor (warts) mRNA exons 1-8, complete cds.	0.61	3875131	(Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	1e-09

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
260	U52428	Human fatty acid synthase gene, partial cds	0.61	4226073	(AF125443) contains similarity to <i>S. pombe</i> phosphatidyl synthase (GB:Z28295) [<i>Caenorhabditis elegans</i>]	2e-26
261	X15292	<i>Plasmodium falciparum</i> gene for heat-shock protein pPf203	0.60	<NONE>	<NONE>	<NONE>
262	AB020663	Homo sapiens mRNA for KIAA0856 protein, partial cds	0.60	470341	(U00043) No definition line found [<i>Caenorhabditis elegans</i>]	5.7
263	U68723	Human checkpoint suppressor 1 mRNA, complete cds	0.60	544375	GALACTOSE-BINDING PROTEIN REGULATOR glucose/galactose binding protein regulator - <i>Agrobacterium tumefaciens</i> >gi 142228 (L10424) glucose/galactose binding protein regulator	5.7
264	M32687	<i>S. griseus</i> sporulation protein genes 1590 and 1422.	0.60	2582017	(AF012871) Mergla' [<i>Mus musculus</i>]	3.3
265	AJ005331	Homo sapiens NKCC2 gene, exon 4, isoform B	0.60	3128353	(AF010496) maltose transport inner membrane protein	1.5
266	U14103	<i>Mus musculus</i> RGL protein mRNA, complete cds.	0.60	4099845	(U90533) serine protease inhibitor [<i>Streptomyces fradiae</i>]	0.098
267	U95094	<i>Xenopus laevis</i> XL-INCENP (XL-INCENP) mRNA, complete cds	0.59	3282851	(AF047897) ankyrin-like protein HGE-ANK [<i>Ehrlichia sp.</i> BDS]	5.5
268	AE000872	<i>Methanobacterium thermoautotrophicum</i> from bases 896604 to 912784 (section 78 of 148) of the complete genome	0.59	401553	HYPOTHETICAL 24.5 KD PROTEIN IN NADB-SRMB INTERGENIC REGION	4.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
269	L11871	Gallus gallus achaete-scute homologue (ASH) mRNA, complete cds.	0.59	628110	hypothetical protein - human herpesvirus 4 reading frame 1 [Human herpesvirus 4] 2 [Human herpesvirus 4] >gi 1334838 gnl PID e25079 4 [Human herpesvirus 4] >gi 1334840 gnl PID e25081 6 [Human herpesvirus 4] >gi 1334842 gnl PID e25067 8 [Human herpesvirus 4] >gi 1334844 gnl PID e25069 10 [Human herpesvirus 4] >gi 1334846 gnl PID e25071 12 [Human herpesvirus 4]	4.2
270	AF017114	Oryctolagus cuniculus glycogen synthase mRNA, complete cds	0.59	728856	NITROGENASE IRON-IRON PROTEIN ALPHA CHAIN (NITROGENASE COMPONENT I) (DINITROGENASE) capsulatus >gi 312238 (X70033) alternative nitrogenase	2.4
271	AF027807	Homo sapiens beta-casein (CSN2) gene, complete cds	0.59	3252932	(AF067155) truncated rev protein [Human immunodeficiency virus type 1]	1.5
272	U81787	Human Wnt10B mRNA, complete cds	0.59	3875538	(Z67990) similar to cuticle collagen	1.4
273	U76036	Apteryx australis 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.59	4193356	(AF055088) ATP-binding cassette; PsaB [Streptococcus pneumoniae]	0.83
274	AB014564	Homo sapiens mRNA for KIAA0664 protein, partial cds	0.59	1709851	PTB-ASSOCIATED SPLICING FACTOR (PSF) long form - human >gi 38458 (X70944) PTB-associated splicing factor [Homo sapiens]	0.17
275	AF044171	Homo sapiens cyclin-dependent kinase inhibitor 2D (CDKN2D) gene, partial cds	0.59	3925213	(AL032626) Y37D8A.17 [Caenorhabditis elegans]	3e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
276	L19640	Saccharomyces cerevisiae cdc2/cdc28 related protein kinase gene, complete cds.	0.59	3880115	(Z81130) T23G11.9 [Caenorhabditis elegans]	1e-21
277	Z80999	Human DNA sequence from cosmid E140G5 on chromosome 22, complete sequence [Homo sapiens]	0.58	<NONE>	<NONE>	<NONE>
278	Y11108	H.sapiens WNT8B gene	0.58	<NONE>	<NONE>	<NONE>
279	U80001	Sphyrana idiaestes lactate dehydrogenase A	0.58	<NONE>	<NONE>	<NONE>
280	Z49637	S.cerevisiae chromosome X reading frame ORF YJR137c	0.58	<NONE>	<NONE>	<NONE>
281	X64467	H.sapiens ALAD gene for porphobilinogen synthase	0.58	<NONE>	<NONE>	<NONE>
282	X74506	G.gallus hox B3 mRNA	0.58	<NONE>	<NONE>	<NONE>
283	U68040	Cochliobolus heterostrophus polyketide synthase	0.58	<NONE>	<NONE>	<NONE>
284	AF089084	Arabidopsis thaliana putative auxin efflux carrier protein (PIN1) mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
285	U38481	Rattus norvegicus ROK-alpha mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
286	AF017656	Homo sapiens G protein beta 5 subunit mRNA, complete cds	0.58	3236249	(AC004684) hypothetical protein [Arabidopsis thaliana]	9.2
287	M96234	Human glutathione transferase class mu number 4	0.58	1280073	(U55366) Similar to cuticle collagen [Caenorhabditis elegans]	7.1
288	AB002339	Human mRNA for KIAA0341 gene, partial cds	0.58	861293	(U28741) F35D2.1 gene product [Caenorhabditis elegans]	7.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
289	U11295	Neisseria gonorrhoeae carbamoyl phosphate synthetase (glutamine) small subunit (carA) and large subunit (carB) genes, complete cds.	0.58	2425135	(AF020283) DG2044 gene product [Dictyostelium discoideum]	5.3
290	D80001	Human mRNA for KIAA0179 gene, partial cds	0.58	4097223	(U49836) gamma-glutamyl transpeptidase precursor [Brugia malayi]	4.1
291	Z11700	Escherichia coli genes faeG, faeH, faeI, faeJ and IS629-like insertion sequence. > :: emb Z11710 ECFAE HIJ E.coli faeH, faeI and faeJ genes encoding FaeH, FaeI and FaeJ proteins	0.58	2347188	(AC002338) laccase isolog [Arabidopsis thaliana] thaliana]	3.2
292	M77350	Mouse hair keratin A1 (MHKA1) gene, complete cds.	0.58	141165	HYPOTHETICAL 8.3 KD PROTEIN >gi 62179	3.2
293	X63787	T.thermophila gene for snRNA U3-2	0.58	2826900	(AB004461) DNA polymerase alpha catalytic subunit [Oryza sativa]	3.1
294	D63881	Human mRNA for KIAA0160 gene, partial cds	0.58	1934730	(U95036) germin-like protein [Arabidopsis thaliana]	3.1
295	U39378	Gymnocarena mexicana 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial RNA, partial sequence	0.58	2194131	(AC002062) Similar to Synechocystis antiviral protein	3.1
296	X87987	P.pastoris PRC1 gene > :: dbj E12103 E12103 DNA encoding precursor of protease from Pichia pastoris	0.58	3914197	OCCLUDIN >gi 1276983 (U49221) occludin [Canis familiaris] >gi 1589181 prf 2210347D occludin [Canis familiaris]	3.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
297	X75782	A.thaliana (L.Heynh.) chloroplast mRNA for recombinant APS-kinase	0.58	1732444	(D38529) DRPLA protein [Homo sapiens]	2.4
298	M64848	Mouse platelet-derived growth factor B chain musculus platelet-derived growth factor beta-chain (sis) gene, exon 5.	0.58	3025832	(AF055985) pyrrolidone-rich antigen [Onchocerca volvulus]	1.4
299	AE001460	Helicobacter pylori, strain J99 section 21 of 132 of the complete genome	0.58	2827198	(AF037454) ubiquitin protein ligase [Mus musculus]	1.1
300	X65720	M.musculus gene for protein kinase C-gamma (exon1 and exon 2)	0.58	418395	CHDI PROTEIN >gi 320737 pir S30818 hypothetical protein YER164w - yeast (Saccharomyces cerevisiae) >gi 603404 (U18917) Chd1p: transcriptional regulator [Saccharomyces cerevisiae]	1.1
301	AF043130	Arabidopsis thaliana lactate dehydrogenase	0.58	3024637	SEX-DETERMINING REGION Y PROTEIN determining protein [Mus	0.62
302	D28116	Human genes for collagen type IV alpha 5 and 6, exon 1 and exon 1'	0.58	1458250	(U64835) T09D3.3 [Caenorhabditis elegans]	0.36
303	AE001075	Archaeoglobus fulgidus section 32 of 172 of the complete genome	0.58	2276333	(Z97991) hypothetical protein Rv0336	0.36
304	AF003948	Rhodococcus opacus chloromuconate cycloisomerase transposase homolog genes. complete cds	0.58	477072	mucin 7 precursor, salivary - human	0.28
305	U10692	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds.	0.58	3287858	HOMEBOX PROTEIN HOX-C11	0.054

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
306	AF003948	Rhodococcus opacus chloromuconate cycloisomerase transposase homolog genes, complete cds	0.58	3551821	(AF058803) mucin 4 [Homo sapiens]	0.041
307	X99350	H.sapiens HFH4 gene, exon 1 and joined CDS	0.58	137483	VAV PROTO-ONCOGENE >gi 55221 (X64361) proto-oncogene [Mus musculus]	0.024
308	AJ234282	Homo sapiens mRNA for Ig heavy chain variable region, clone C	0.58	3264846	(AC003682) R27945_2 [Homo sapiens]	0.018
309	AF079310	Mus musculus histone deacetylase 3 (Hdac3) gene, exons 4 through 15 and complete cds	0.58	1657601	(U66220) unknown [Nannocystis exedens]	0.014
310	AF019367	Human thiopurine methyltransferase (TPMT) gene, exons 6 and 7	0.58	3283352	(AF063020) lens epithelium-derived growth factor [Homo sapiens]	0.011
311	X65720	M.musculus gene for protein kinase C-gamma (exon1 and exon 2)	0.58	1790878	(U38291) microtubule-associated protein 1a [Homo sapiens]	0.008
312	AB011155	Homo sapiens mRNA for KIAA0583 protein, partial cds	0.58	1351166	SYNAPSINS IA AND IB >gi 163713	0.006
313	X63692	H.sapiens mRNA for DNA	0.58	1817548	(D84307) phosphoethanolamine cytidyltransferase [Homo sapiens]	0.001
314	U53746	Feline immunodeficiency virus isolate FIV-Pco336-8 pol polyprotein (pol) gene, partial cds	0.58	2246532	(U93872) ORF 73, contains large complex repeat CR 73	2e-05
315	K00436	Rattus norvegicus (clone rtl-1) pseudo-Gly-tRNA gene.	0.58	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	1e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
316	S79632	HSF2=heat shock factor 2 {alternatively spliced, splice junction region} [mice, CBA/J, testis, Genomic, 120 nt. segment 2 of 3]	0.58	4038594	(AJ222798) tDET1 protein [Lycopersicon esculentum] (U55376) coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II)	3e-06
317	D43964	Rat liver mRNA for Kan-1, complete cds	0.58	1280135	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi 530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	1e-08
318	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.58	2833239	(D45027) 25 kDa trypsin inhibitor [Homo sapiens]	3e-13
319	AB001466	Homo sapiens mRNA for Efs1, complete cds	0.58	2943716	(Z81130) T23G11.9 [Caenorhabditis elegans]	2e-14
320	Z11701	Saccharomyces cerevisiae IRE1 gene for putative protein kinase.	0.58	3880115	(Z83819) dJ146H21.2 (similar to CYTOCHROME B-245 HEAVY CHAIN) [Homo sapiens]	9e-21
321	Z49535	S.cerevisiae chromosome X reading frame ORF YJR035w	0.58	4106562		3e-33
322	M62506	S.cerevisiae DBF20 gene, complete cds.	0.57	<NONE>	<NONE>	<NONE>
323	X05944	Yeast PSS gene for phosphatidylserine synthetase	0.57	<NONE>	<NONE>	<NONE>
324	D38536	Snail gene for ADP-ribosyl cyclase, complete cds	0.57	<NONE>	<NONE>	<NONE>
325	Z75004	S.cerevisiae chromosome XV reading frame ORF YOR096w	0.57	<NONE>	<NONE>	<NONE>
326	L77034	Homo sapiens (subclone 10_e10 from P1 H16) DNA sequence.	0.57	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cyprinus carpio c-myc gene for c-Myc, complete cds				
327	D37887		0.57	<NONE>	<NONE>	<NONE>
328	AB014562	Homo sapiens mRNA for KIAA0662 protein, partial cds	0.57	197406	(M57576) Ig kappa chain [Mus musculus]	8.9
329	Z69651	Human DNA sequence from cosmid L75B9, Huntington's Disease Region, chromosome 4p16.3	0.57	1079280	chaperonin containing TCP-1 complex gamma chain - African clawed frog >gi 793886 (X84990) Cctg	8.9
330	D89285	Mesocricetus auratus mRNA for inter-alpha trypsin inhibitor heavy chain 1, complete cds	0.57	134132	RYANODINE RECEPTOR, SKELETAL MUSCLE	6.9
331	Z48951	S.cerevisiae chromosome XVI cosmid 9723	0.57	4210432	(AJ130783) APC2 protein [Mus musculus]	5.3
332	X95573	A.thaliana mRNA for salt-tolerance zinc finger protein	0.57	1174828	TYROSINE DECARBOXYLASE 2 4.1.1.25 - parsley >gi 169671 (M96070) tyrosine decarboxylase [Petroselinum	5.2
333	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.57	465646	PROBABLE ABC TRANSPORTER ATP-BINDING PROTEIN IN NTRA/RPON 5'REGION (ORF1) Azorhizobium caulinodans >gi 311388 (X69959) ORF1	4.0
334	AE001116	Borrelia burgdorferi (section 2 of 70) of the complete genome	0.57	2314735	(AE000653) Na+/H+ antiporter (nhaA) [Helicobacter pylori 26695]	4.0
335	Z34291	R.norvegicus mRNA for putative chloride channel.	0.57	1350832	DNA-DIRECTED RNA POLYMERASE I SECOND LARGEST SUBUNIT (RNA POLYMERASE I SUBUNIT 2) chain RPA2 - Euplotes octocarinatus (SGC9) >gi 578407 octocarinatus]	3.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
336	D88255	Homo sapiens A30 Vk germline gene, partial cds	0.57	3875983	(Z81063) similar to Actinin-type actin-binding domain containing proteins [Caenorhabditis elegans]	3.0
337	AF037261	Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds	0.57	1397341	(U61955) Similar to kinesin-like protein; coded for by C. elegans cDNA yk184h5.3; coded for by C. elegans cDNA yk184h5.5; coded for by C. elegans cDNA yk13d7.3; coded for by C. elegans cDNA yk13d7.5; coded for by C. elegans cDNA yk31e1.5; co... >gi 3493541 (AF057567) kinesin-like protein ZEN-4a [Caenorhabditis elegans]	2.3
338	U26595	Rattus norvegicus prostaglandin F2a receptor regulatory protein precursor, mRNA, complete cds	0.57	2773160	(AF039656) neuronal tissue-enriched acidic protein [Homo sapiens]	2.3
339	X69903	R.norvegicus mRNA for interleukin 4 receptor	0.57	2649193	(AE001009) quinone-reactive Ni/Fe-hydrogenase B-type cytochrome subunit (hydC) [Archaeoglobus fulgidus]	1.8
340	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w	0.57	1458319	(U64846) F47D2.5 gene product [Caenorhabditis elegans]	1.4
341	AJ131469	Foot-and-mouth disease virus O vp1 gene, strain O/A/58	0.57	91206	proline-rich protein - mouse (fragment) musculus]	1.4
342	AF011360	Mus musculus regulator of G-protein signaling 7 (RGS7) mRNA, complete cds	0.57	542514	gelsolin - American lobster	0.80
343	AF011360	Mus musculus regulator of G-protein signaling 7 (RGS7) mRNA, complete cds	0.57	1078946	gelsolin - American lobster >gi 452313 gelsolin [Homarus americanus]	0.80

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
344	L39210	Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds	0.57	559526	(X77466) 98.8kD polyprotein [Strawberry latent ringspot virus]	0.79
345	U81523	Human endometrial bleeding associated factor mRNA, complete cds	0.57	211499	(K01702) HMW/LMW collagen subunit precursor [Gallus gallus]	0.79
346	U46561	Tetrahymena thermophila polyubiquitin (TTU3) gene, complete cds, and RNA polymerase II subunit 2 (RPB2) gene, partial cds	0.57	2506493	HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION >gi 882654 (U29579) alternate gene name ygcB; ORF_f888 [Escherichia coli] >gi 1789119	0.60
347	X95543	C.japonica mRNA for legumin (clone CjLeg31)	0.57	1709261	NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M) >gi 1083164 pir S55395 neurofilament protein M - rabbit (fragment) >gi 854353	0.46
348	Y17282	Homo sapiens mRNA for cytokeratin type II	0.57	3044086	(AF055904) unknown [Myxococcus xanthus]	0.45
349	X00716	Frog mRNA fragment for alpha-A2-crystallin	0.57	3406654	(AF079369) transcriptional repressor TUP1 [Dictyostelium discoideum]	0.20
350	X53238	Klebsiella sp. bacteriophage K11 gene 1 for RNA polymerase	0.57	1228093	(Z46913) polyketide synthase (S78897) GOR=antigenic epitope [chimpanzees, Peptide, 427 aa] [Pan]	0.16
351	X99012	H.sapiens FUS gene, exon 12	0.57	243898		0.090
352	AL008711	Human DNA sequence from PAC 390N22 on chromosome Xp22.2	0.57	1469545	(U53585) fibronectin attachment protein [Mycobacterium avium]	0.053
353	S74506	SOX9 [human, fetal brain, Genomic, 1494 nt, segment 3 of 3]	0.57	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	0.017

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
354	D25542	Human mRNA for golgi antigen gcp372, complete cds	0.57	4063399	(AF102575) cell surface protein DTFA [Dictyostelium discoideum]	0.005
355	AB015426	Mus musculus mRNA for alpha1,3-fucosyltransferase IX, complete cds	0.57	2661842	(Y15732) DNA polymerase beta [Xenopus laevis]	7e-11
356	X51394	Xenopus mRNA for APEG protein, containing a highly repetitive amino acid sequence	0.57	1929056	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]	9e-12
357	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.57	2833239	EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 >gi 530823 (U12535) epidermal growth factor receptor kinase substrate [Homo sapiens]	3e-13
358	AB001466	Homo sapiens mRNA for Efs1, complete cds	0.57	2943716	(D45027) 25 kDa trypsin inhibitor [Homo sapiens]	2e-14
359	Y00760	Rabbit mRNA for adult fast skeletal troponin-C	0.57	2576348	(AC002400) Glutamyl tRNA synthetase [Homo sapiens]	2e-28
360	X95153	H.sapiens brca2 gene exon 3 > :: emb A62778 A62778 Sequence 19 from Patent WO9719110	0.57	3419847	(AC004982) similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]	2e-55
361	X85967	B.vulgaris mRNA for betavulgin	0.56	<NONE>	<NONE>	<NONE>
362	U09251	Mycoplasma genitalium DNA gyrase subunit B complete cds, DNA polymerase III beta subunit (dnaN) and seryl-tRNA synthetase (serS) genes, partial cds.	0.56	<NONE>	<NONE>	<NONE>
363	V00158	Chloroplast Euglena gracilis genes coding for transfer RNAs specific for threonine, glycine, methionine, serine and glutamine.	0.56	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Clostridium				
364	D88151	perfringens DNA for D-alanine:D-alanine ligase, cortical fragment-lytic enzyme	0.56	<NONE>	<NONE>	<NONE>
365	U67478	Methanococcus jannaschii section 20 of 150 of the complete genome	0.56	<NONE>	<NONE>	<NONE>
366	L23800	Tachyglossus aculeatus beta-globin homolog (HBB) gene, complete cds	0.56	<NONE>	<NONE>	<NONE>
367	AB011129	Homo sapiens mRNA for KIAA0557 protein, partial cds	0.56	<NONE>	<NONE>	<NONE>
368	L77034	Homo sapiens (subclone 10_e10 from P1 H16) DNA sequence.	0.56	<NONE>	<NONE>	<NONE>
369	Z47202	C.albicans gene for TFIIB (BRF1) subunit.	0.56	<NONE>	<NONE>	<NONE>
370	U53868	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds	0.56	<NONE>	<NONE>	<NONE>
371	AF041259	Homo sapiens breast cancer putative transcription factor (ZABC1) mRNA, complete cds	0.56	<NONE>	<NONE>	<NONE>
372	L42636	Plasmodium falciparum variant-specific surface protein (var-7) mRNA, complete cds.	0.56	2213557	(Z97052) hypothetical protein	8.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
373	U96180	Human protein tyrosine phosphatase (TEP1) mRNA, complete cds	0.56	731016	THIOREDOXIN REDUCTASE thioredoxin reductase (NADPH) [Coxiella burnetii]	8.7
374	L76259	Homo sapiens PTS gene, complete cds	0.56	2369863	(Y12225) Spi-1/PU.1 transcription factor	6.7
375	AF045946	Mus musculus D16Jhu17 YAC 98B3 acentric end, partial sequence	0.56	2130017	hypothetical protein - common sunflower protein [Helianthus annuus]	5.1
376	X97986	M.musculus mRNA for desmocollin type 1	0.56	4038031	(AC005936) hypothetical protein [Arabidopsis thaliana]	3.9
377	X79437	M.musculus whey acidic protein (WAP) gene, exon 1	0.56	549670	SPINDLE POLE BODY COMPONENT SPC42 yeast (Saccharomyces cerevisiae) >gi 486054 (Z28042) ORF YKL042w [Saccharomyces cerevisiae] >gi 666098 (X71621) hypothetical 42.3 kD protein [Saccharomyces cerevisiae]	3.9
378	M27902	Rat cardiac specific sodium channel alpha-subunit mRNA, complete cds.	0.56	585234	ENDOGLUCANASE G PRECURSOR 3.2.1.-) CelCCG precursor - Clostridium cellulolyticum cellulolyticum]	3.9
379	AF036696	Caenorhabditis elegans cosmid F15B10	0.56	546071	gp70=envelope protein [endogenous provirus] host=cat lymphoid tissues, Peptide, 445 aa]	3.6
380	Z99102	Caenorhabditis elegans cosmid B0331, complete sequence [Caenorhabditis elegans]	0.56	603664	(U14101) putative reverse transcriptase; ORF2; encodes aa motifs conserved in reverse transcriptases; most closely related reverse transcriptases are those of non-LTR retrotransposons. The 3' 901 bp of this CDS are identical to the 3' 901 bp ...	3.0
381	L27850	Equus caballus (clone T131) T-cell receptor DNA, V-region.	0.56	1079150	transcription factor shn - fruit fly	1.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 113.1 KD	
382	X97986	M.musculus mRNA for desmocollin type 1	0.56	2497227	PROTEIN IN PRE5-FET4 INTERGENIC REGION >gi 1072409 (Z54141) unknown	1.7
383	AF087455	Didelphis virginiana G protein receptor kinase 2 mRNA, complete cds	0.56	1213453	(U12964) contains ankyrin-like repeats; similar to human desmoplakin repeat region [Caenorhabditis elegans]	1.3
384	D80011	Human mRNA for KIAA0189 gene, complete cds	0.56	226535	protease [Hepatitis B virus]	1.1
385	AJ002272	Mus musculus mRNA for HAP1-A protein, 3' region	0.56	3327158	(AB014572) KIAA0672 protein [Homo sapiens]	1.0
386	L39210	Homo sapiens inosine monophosphate dehydrogenase type II gene, complete cds	0.56	628431	coat protein - strawberry latent ringspot virus	0.77
387	X02770	Mouse Thy-1.2 gene 5' untranslated region and exon 1	0.56	3327046	(AB014516) KIAA0616 protein [Homo sapiens]	0.59
388	AF038575	Schizosaccharomyces pombe Wiskott-Aldrich Syndrome protein homolog (wsp1+) gene, complete cds, and BTF3/beta-NAC gene, partial sequence	0.56	88466	salivary proline-rich phosphoprotein precursor PRH1 (allele PIF) - human >gi 190484 (K03203) prepro salivary proline-rich protein [Homo sapiens] >gi 190512	0.35
389	X56747	Rat mRNA for fetal intestinal lactase-phlorizin hydrolase precursor, partial	0.56	2072742	(Z48674) chitinase homologue [Sesbania rostrata]	0.23
390	Y12072	G.arboreum mRNA for farnesyl pyrophosphate synthase	0.56	296670	(X07882) Po protein [Homo sapiens]	0.20
391	S75756	p15=cyclin D-dependent kinases 4 and 6-binding protein/p15 product {exon/intron 1} [human, brain tumors, Genomic, 753 nt]	0.56	1082743	protein kinase (EC 2.7.1.37) SPRK - human sapiens] >gi 1090771 prf 2019437A protein Tyr kinase I	0.15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Equus caballus type				
392	U62528	II collagen mRNA, complete cds	0.56	461671	[Segment 1 of 2] COLLAGEN ALPHA 1(I) CHAIN	0.030
393	X96877	C.reinhardtii mRNA for unknown luminal polypeptide	0.56	3341678	(AC003672) putative zinc finger protein [Arabidopsis thaliana]	5e-09
394	S78788	cGATA-3 [chickens, liver, Genomic, 979 nt, segment 4 of 4]	0.56	2661590	(AL009196) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=59.41; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA950019; 2-match_description=LD29959.5p rime LD Drosophila melanogas...	2e-11
395	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.56	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	6e-12
396	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.56	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	4e-13
397	AE000716	Aquifex aeolicus section 48 of 109 of the complete genome	0.56	3688350	(AL030996) dJ1189B24.4 (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8) [Homo sapiens]	3e-66
398	Z36079	S.cerevisiae chromosome II reading frame ORF YBR210w	0.55	<NONE>	<NONE>	<NONE>
399	Y17267	Mus musculus mRNA for ubiquitin conjugating enzyme	0.55	<NONE>	<NONE>	<NONE>
400	AC001461	Homo sapiens (subclone 2_g5 from BAC H107) DNA sequence	0.55	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Alouatta seniculus				
401	AF019079	breast and ovarian susceptibility (BRCA1) gene, partial cds	0.55	<NONE>	<NONE>	<NONE>
402	M90058	Human serglycin gene, exons 1,2, and 3.	0.55	<NONE>	<NONE>	<NONE>
403	AB013469	Mus musculus CLM2 gene for cytohesin 2, complete and partial cds, alternative splicing	0.55	1729760	(Z68152) chitinase [Gossypium hirsutum]	8.6
404	AJ011592	Bacteriophage P1 ban gene	0.55	2493689	PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN deltoides] >gi 2143326 gnl PID e319090 (Y13328) 10kDa phosphoprotein [Populus deltoides]	6.6
405	Z15118	T.brucei kinetoplast maxicircle variable region DNA	0.55	2970432	(AF049132) NADH dehydrogenase subunit 5 [Florometra serratissima]	6.5
406	Z48951	S.cerevisiae chromosome XVI cosmid 9723	0.55	4210432	(AJ130783) APC2 protein [Mus musculus]	4.9
407	U78726	Homo sapiens mad protein homolog Smad2 gene, promoter, exon 1a and exon 1b	0.55	3319290	(AF055994) thyroid hormone receptor-associated protein complex component TRAP220 [Homo sapiens]	4.9
408	AG001389	Homo sapiens genomic DNA, 21q region, clone: 9H11Bm42	0.55	125684	KRUEPPEL PROTEIN >gi 72899 pir TWFF Krueppel gap protein - fruit fly (Drosophila sp.) melanogaster] >gi 224875 prf 1202348A Krueppel gene	3.8
409	M27640	Plasmodium vivax major blood stage surface antigen gene, partial cds.	0.55	549453	X-LINKED PEST-CONTAINING TRANSPORTER transporter - human >gi 458255 (U05321) X-linked PEST-containing transporter [Homo sapiens]	3.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Fugu rubripes mRNA				
410	D37977	for sodium channel alpha subunit, partial cds	0.55	1435038	(D38024) ORF [Homo sapiens]	3.7
411	M88505	Ostertagia ostertagi cathepsin B-like cysteine protease gene, partial cds.	0.55	3941277	(AF000900) p45 [Rattus norvegicus]	2.9
412	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.55	2570154	(AB008376) 17-kDa PKC-potentiated inhibitory protein of PP1 [Sus scrofa]	2.8
413	U89241	Human mibp gene, partial cds	0.55	4097465	(U62253) 16kDa secretory protein [Sus scrofa]	2.2
414	AF027151	Xenopus laevis survival of motor neuron protein interacting protein 1 (SIP1) mRNA, complete cds	0.55	4007790	(AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]	1.7
415	AF006821	Bufo marinus natriuretic peptide receptor C mRNA, partial cds	0.55	2245075	(Z97343) GTP-binding RAB2A protein	1.7
416	Y12736	Lactococcus lactis cremoris plasmid pJW565 DNA, llabiiM, llabiiR genes and orfX	0.55	3386334	(AF035120) type I procollagen pro-alpha 2 chain [Canis familiaris]	1.3
417	U38307	Mus musculus collagen alpha-1 type 1 gene, 5' flanking region, partial sequence.	0.55	1362802	gastric mucin - human (fragment) >gi 547517	1.3
418	D13473	Mouse mRNA for Rad51 protein	0.55	1374698	(D83032) nuclear protein, NP220 [Homo sapiens]	1.3
419	AF045238	Bungarus fasciatus acetylcholinesterase gene, alternatively spliced products, partial cds	0.55	3261734	(Z94752) hypothetical protein Rv1004c	0.99
420	AE000795	Methanobacterium thermoautotrophicum from bases 1 to 10208 (section 1 of 148) of the complete genome	0.55	186396	(M94131) mucin [Homo sapiens]	0.97

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Y.lipolytica</i> SEC62 gene	0.55		(Z81068) F25H5.2 [Caenorhabditis elegans]	0.58
421	X99537			3876397		
422	U08147	<i>Aquilegia</i> sp. phytochrome (PHYB/D) gene, partial cds.	0.55	2338024	(AF005370) ribonucleotide-reductase, large subunit	0.57
423	Z56586	<i>H.sapiens</i> CpG DNA, clone 12c8, reverse read cpg12c8.rt1d.	0.55	3320122	(U46007) espin [Rattus norvegicus]	0.44
424	U39442	<i>Mus musculus</i> glutamine:fructose-6-phosphate amidotransferase (GFAT) gene, 5' region and partial cds	0.55	282600	hypothetical protein - <i>Mycoplasma hyorhinis</i>	0.43
425	K02298	Rat chymotrypsin B (chyB) gene, complete cds.	0.55	3413810	(Y17034) Bassoon [Mus musculus]	0.33
426	X84792	<i>M.musculus</i> clusterin gene	0.55	1652475	(D90905) hypothetical protein	0.25
427	U00185	<i>Capra aegagrus</i> Saanen and Weisse Edel breeds DR beta-chain antigen binding domain, MHC class II DRB	0.55	2507136	SUBTILIN BIOSYNTHESIS PROTEIN SPAB	0.19
428	Z54946	<i>H.sapiens</i> CpG DNA, clone 178a12, reverse read cpg178a12.rt1a.	0.55	807646	(M17294) unknown protein [Human herpesvirus 4]	0.065
429	AF031650	<i>Oryctolagus cuniculus</i> anion exchanger 3 brain isoform (AE3) mRNA. complete cds	0.55	1778210	(U68412) fibrillar collagen [Arenicola marina]	0.044
430	M25579	Bovine adenylyl cyclase Type I mRNA. complete cds.	0.55	2649040	(AE000997) conserved hypothetical protein [Archaeoglobus fulgidus]	0.023
431	Z48796	<i>H.sapiens</i> Ski-W mRNA for helicase	0.55	330452	(M14708) DNA polymerase [Human cytomegalovirus]	0.023

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
432	M80234	Cow dopamine transporter mRNA, putative cds.	0.55	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	4e-04
433	U91616	Human I kappa B epsilon (IkBe) mRNA, complete cds	0.55	3875577	(Z68314) similar to G-protein; cDNA EST EMBL:C11959 comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene [Caenorhabditis elegans] >gi 3880364 gnl PID e1349948 (Z83016) similar to G-protein; cDNA EST EMBL:C11959 comes from this gene; cDNA EST EMBL:C10341 comes from this gene; cDNA EST yk494e4.3 comes from this gene; cDNA EST yk448a8.5 comes from this gene [Caenorhabditis elegans]	7e-06
434	D10910	Arabidopsis thaliana Atpk7 gene for serine/threonine protein kinase, complete cds	0.55	3876072	(Z81505) Similarity to Metanococcus hypothetical protein 0682 (TR:Q58095) [Caenorhabditis elegans]	4e-42
435	L22013	Swinepox virus complete ORFS C20L-C1L > :: gb I58297 I58297 Sequence 14 from patent US 5651972	0.54	<NONE>	<NONE>	<NONE>
436	Z92653	Human immunodeficiency virus type 1 env gene	0.54	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
437	K01992	E.coli phosphate-repressible periplasmic phosphate-binding protein (phoS), peripheral membrane proteins (pstC, pstB and phoU) and integral membrane protein (pstA) genes, complete cds.	0.54	<NONE>	<NONE>	<NONE>
438	AE001415	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence	0.54	<NONE>	<NONE>	<NONE>
439	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.54	<NONE>	<NONE>	<NONE>
440	X12591	E.coli plasmid DNA for colicin E9	0.54	<NONE>	<NONE>	<NONE>
441	U73679	Caenorhabditis elegans YNK1-a mRNA, complete cds	0.54	<NONE>	<NONE>	<NONE>
442	Z93990	Unidentified bacterium DNA for 16S ribosomal RNA	0.54	<NONE>	<NONE>	<NONE>
443	X85967	B.vulgaris mRNA for betavulgin	0.54	757836	(Z37980) ORF12 [Escherichia coli]	8.3
444	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.54	151377	(M80653) tetraheme [Pseudomonas stutzeri]	6.2
445	X71800	H.sapiens gene for 5S rRNA (640 bp) > :: emb X71801 HS5SR6-40B H.sapiens gene for 5S rRNA (640 bp)	0.54	3322653	(AE001216) T. pallidum predicted coding region TP0369	2.7
446	U89241	Human mibp gene, partial cds	0.54	4097465	(U62253) 16kDa secretory protein [Sus scrofa]	2.2

186

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
447	L16013	Rattus norvegicus Q-like gene sequence	0.54	3087760	(AJ005583) p75 protein [Cryptocodium cohnii]	0.95
448	U60275	Capra hircus skeletal muscle voltage-gated chloride channel gCIC-1 mRNA, partial cds	0.54	1781344	(Y10438) FK506 polyketide synthase	0.95
449	U36795	Myxococcus xanthus rfbABC O-antigen biosynthesis operon, rfbA, rfbB, and rfbC genes, complete cds.	0.54	3877232	(Z81540) predicted using Genefinder	0.74
450	AF053091	Drosophila melanogaster eyelid (eld) mRNA, complete cds	0.54	2144110	zinc finger protein RIZ - rat >gi 949996	0.14
451	V00602	Genome of the bacteriophage fd (Inoviridae).	0.54	2661620	(AL009197) hypothetical protein	0.11
452	U60800	Human semaphorin (CD100) mRNA, complete cds	0.54	125682	KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN) >gi 109116 pir A36686 ultra-high-sulfur keratin - sheep >gi 1306 (X55294) ultra high-sulphur keratin protein [Ovis aries]	0.003
453	X85969	S.coelicolor secD, secF & apt genes	0.54	3874972	(Z99709) similar to Elongation factor Tu family (contains ATP/GTP binding P-loop); cDNA EST EMBL:D76223 comes from this gene; cDNA EST yk478c5.5 comes from this gene [Caenorhabditis elegans]	7e-06
454	Y08265	H.sapiens mRNA for DAN26 protein, partial	0.54	3875131	(Z70750) similar to vanadate resistance protein transmembranous domains [Caenorhabditis elegans]	5e-12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Hydromantes				
		platycephalus				
		cytochrome b (cytb)				
		gene, mitochondrial				
		gene encoding				
455	U89613	mitochondrial protein, partial cds	0.53	<NONE>	<NONE>	<NONE>
		Habrobracon hebetor				
		cytochrome oxidase				
		II gene, partial cds;				
		and tRNA-Asp, tRNA				
		His, and tRNA-Lys				
		genes, complete				
		sequence,				
		mitochondrial genes				
456	AF034597	for mitochondrial products	0.53	<NONE>	<NONE>	<NONE>
		Yeast (S.cerevisiae)				
		tau repetitive element				
457	K02653	and Cys-tRNA.	0.53	<NONE>	<NONE>	<NONE>
		Human mRNA for				
		actin-binding protein				
458	X53416	(filamin)	0.53	2134839	bullous pemphigoid antigen 2 - human	6.2
		Drosophila				
		subobscura alcohol				
		dehydrogenase (Adh)				
		gene, and alcohol				
		dehydrogenase (Adh-				
		dup) gene, complete				
459	M55545	cds's.	0.53	2136865	hair keratin cysteine rich protein - sheep	2.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
460	U19362	Methanobacterium thermoautotrophicum methylene-tetrahydromethanopterin dehydrogenase (mtd), imidazoleglycerol-phosphate dehydrogenase (hisB), and putative ferredoxin (fdxA) genes, complete cds, orf9 gene, partial cds, orfs ...	0.53	731969	HYPOTHETICAL 91.6 KD PROTEIN IN HXT8-CRT1 INTERGENIC REGION >gi 1078261 pir S50773 probable membrane protein YJL212c - yeast (Saccharomyces cerevisiae) >gi 496950 (Z34098) ORF [Saccharomyces cerevisiae] >gi 1015596 (Z49487) ORF YJL212c	0.54
461	AB011527	Rattus norvegicus mRNA for MEGF1, complete cds	0.53	417037	GERM CELL-LESS PROTEIN fruit fly (Drosophila melanogaster) >gi 157490 (M97933) germ cell-less protein [Drosophila melanogaster]	3e-06
462	U64313	Bacillus firmus MsyB gene, 5' upstream region and partial cds	0.52	<NONE>	<NONE>	<NONE>
463	AF008590	Caenorhabditis elegans paraquat responsive protein (CePqM132) mRNA, complete cds	0.52	<NONE>	<NONE>	<NONE>
464	L10245	Mus saxicola spermidine/spermine N1-acetyltransferase (SSAT) gene, complete cds.	0.52	<NONE>	<NONE>	<NONE>
465	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.52	124263	INSULIN-LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) >gi 69361 pir IGHU1B insulin-like growth factor IB precursor - human prepropeptide [Homo sapiens]	7.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis elegans cosmid H31B20, complete sequence [Caenorhabditis elegans]	0.52	2589162	(D88451) aldehyde oxidase [Zea mays]	6.0
466	AL021066				(U39850) coded for by C. elegans cDNA yk37g1.5; coded for by C. elegans cDNA yk5c9.5; coded for by C. elegans cDNA yk1a9.5; alternatively spliced form of F52C9.8b	4.6
467	AF038588	Porphyra linearis 18S ribosomal RNA gene, 3' partial sequence	0.52	1055055		
468	AE001125	Borrelia burgdorferi (section 11 of 70) of the complete genome	0.52	4115827	(AB021287) polyprotein [Hepatitis G virus]	2.0
469	AF006640	Drosophila melanogaster Ste20-like protein kinase mRNA, complete cds	0.52	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	0.002
470	U90177	Aplysia californica ubiquitin carboxyl-terminal hydrolase (Ap-uch) mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
471	Z28304	S.cerevisiae chromosome XI reading frame ORF YKR079c	0.51	<NONE>	<NONE>	<NONE>
472	Z92837	Caenorhabditis elegans cosmid R03E1, complete sequence [Caenorhabditis elegans]	0.51	123506	HYDROPHOBIC SEED PROTEIN (HPS)	7.6
473	D13803	Mouse mRNA for RecA-like protein MmRad51, complete cds	0.51	3327228	(AB014607) KIAA0707 protein [Homo sapiens]	4.5
474	X07187	Pea hsp21 mRNA	0.51	3328678	(AE001299) hypothetical protein [Chlamydia trachomatis]	4.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
475	S63168	CCAAT/enhancer-binding protein delta=transcription factor CRP3 homolog [human, prostate carcinoma cell line LNCaP, Genomic, 1594 nt]	0.51	1653215	(D90911) apolipoprotein N-acyltransferase [Synechocystis sp.]	1.2
476	U67078	Xenopus laevis C2-HC type zinc finger protein X-MyT1 mRNA, complete cds	0.51	3850320	(AF067520) PITSLRE protein kinase beta SV2 isoform [Homo sapiens]	0.17
477	L38933	Homo sapiens GT198 mRNA, complete ORF	0.51	3219965	HYPOTHETICAL 100.6 KD TRP-ASP REPEATS CONTAINING PROTEIN C2C6.04C IN CHROMOSOME I	0.059
478	AF001000	Lycopersicon esculentum polygalacturonase 1	0.50	<NONE>	<NONE>	<NONE>
479	Z28304	S.cerevisiae chromosome XI reading frame ORF YKR079c	0.50	<NONE>	<NONE>	<NONE>
480	X97225	Oncorhynchus keta IGF-II gene	0.50	<NONE>	<NONE>	<NONE>
481	AJ001388	Homo Sapiens, RP58 cDNA for complete mRNA	0.50	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo Sapiens, RP58				
481	AJ001388	cDNA for complete mRNA	0.50	<NONE>	<NONE>	<NONE>
482	M86626	P.occultum 23S ribosomal RNA, partial cds.	0.50	<NONE>	<NONE>	<NONE>
483	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.50	1722856	CHROMOSOME ASSEMBLY PROTEIN XCAP-E African clawed frog >gi 563814 (U13674) XCAP-E [Xenopus laevis]	3.2
484	AF031663	Mus musculus striatin mRNA, complete cds	0.50	179521	(M63730) BPAG2 [Homo sapiens]	3.2
485	U32729	Haemophilus influenzae Rd section 44 of 163 of the complete genome	0.50	3875699	(Z92829) F10A3.15 [Caenorhabditis elegans]	0.65
486	AF067198	Dictyostelium discoideum clone 9.10 Tdd-3 and RED repetitive elements, partial sequence	0.50	2494740	HYPOTHETICAL 28.3 KD PROTEIN IN GBD 5'REGION (ORF4) >gi 2120954 pir I39562 ORF4 - Alcaligenes eutrophus >gi 695274 (L36817) ORF4	0.008
487	M23442	Human interleukin 4 (IL-4) gene, complete cds.	0.49	<NONE>	<NONE>	<NONE>
488	U16367	Caenorhabditis elegans POU homeobox protein CEH-18 (ceh-18) mRNA, complete cds.	0.47	3786409	(AF098499) contains similarity to Saccharomyces cerevisiae MAF1 protein (GB:U19492) [Caenorhabditis elegans]	8.9
489	AF001000	Lycopersicon esculentum polygalacturonase 1	0.45	<NONE>	<NONE>	<NONE>
490	Z18920	Yersinia enterocolitica wbb gene cluster	0.41	<NONE>	<NONE>	<NONE>
491	D86983	Human mRNA for KIAA0230 gene, partial cds	0.35	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	4e-05
492	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.33	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Vitreoscilla sp. outer				
493	AF067083	membrane protein homolog gene, complete cds; Trp repressor binding protein gene, partial cds; and unknown genes	0.33	401553	HYPOTHETICAL 24.5 KD PROTEIN IN NADB-SRMB INTERGENIC REGION	8.3
494	Y15520	Papio hamadryas anubis gene encoding fertilin alpha-II	0.29	2408049	(Z99164) hypothetical protein	3.1
495	U33475	Alestes sp. ependymin mRNA, partial cds	0.28	3913078	ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR HOMOLOG (DARNT) (TANGO PROTEIN) transcription factor [Drosophila melanogaster]	1.4
496	D88356	Mouse DNA for 8-oxodGTPase, complete cds	0.22	<NONE>	<NONE>	<NONE>
497	U67603	Methanococcus jannaschii section 145 of 150 of the complete genome	0.22	2209261	(U51222) p40 [Streptomyces halstedii]	8.3
498	U82386	Malurus cyaneus microsatellite McyU2	0.22	992631	(U29131) Mg-chelatase subunit [Synechocystis sp.]	0.56
499	Z49625	S.cerevisiae chromosome X reading frame ORF YJR125c	0.21	<NONE>	<NONE>	<NONE>
500	U64830	Dictyostelium discoideum AX2 protein tyrosine kinase gene, complete cds.	0.21	<NONE>	<NONE>	<NONE>
501	M24543	Human prostate-specific antigen (PA) gene, complete cds.	0.21	2764859	(X97918) gene 12.1 [Bacteriophage SPPI]	6.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					u0002b protein -	
502	X87618	B.taurus mRNA for thrombospondin (partial) 2162 bp	0.21	2146000	Mycobacterium tuberculosis tuberculosis >gi 1694863 gnl PID e283373 (Z83018) hypothetical protein Rv2968c [Mycobacterium tuberculosis]	3.5
503	X71591	B.taurus microsatellite sequence INRA048	0.21	1354453	(U52830) orf [Homo sapiens]	2.7
504	X57808	Human germline immunoglobulin lambda light chain gene	0.21	2119158	procollagen type V alpha 2 - mouse >gi 309181	2.7
505	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.21	2497139	HYPOTHETICAL 78.8 KD PROTEIN IN ABF2-CHL12 INTERGENIC REGION >gi 1078003 pir S52835 hypothetical protein YMR075w - yeast (Saccharomyces cerevisiae) >gi 763022 (Z48952) unknown [Saccharomyces cerevisiae]	2.0
506	U84216	Mycobacterium fortuitum plasmid pJAZ38 replication protein Rep (rep) gene, complete cds	0.21	2499087	UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) glucosyltransferase - fruit fly (Drosophila sp.) glucosyltransferase precursor [Drosophila melanogaster]	0.003
507	U31463	Rattus norvegicus nonmuscle myosin heavy chain-A mRNA, complete cds.	0.21	3880111	(Z81130) predicted using Genefinder	0.002
508	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.21	630864	LRR47 protein - fruit fly (Drosophila melanogaster) >gi 415947 (X75760) LRR47 [Drosophila melanogaster]	1e-06
509	AF086476	Homo sapiens full length insert cDNA clone ZD88F12	0.20	<NONE>	<NONE>	<NONE>
510	AF077006	Helicobacter pylori plasmid pHPM186, complete sequence	0.20	<NONE>	<NONE>	<NONE>
511	X75480	E.gunnii CAD gene.	0.20	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>T.aestivum</i>				
512	X75036	mitochondrial nad7 gene for NADH dehydrogenase subunit 7	0.20	<NONE>	<NONE>	<NONE>
513	D90875	<i>E.coli</i> genomic DNA, Kohara clone #422(55.5-55.8 min.)	0.20	<NONE>	<NONE>	<NONE>
514	Z68343	<i>Caenorhabditis elegans</i> cosmid F59B8, complete sequence [Caenorhabditis elegans]	0.20	<NONE>	<NONE>	<NONE>
515	X62486	<i>M.musculus</i> V alpha 11.1 gene 5'-region	0.20	<NONE>	<NONE>	<NONE>
516	AF040651	<i>Caenorhabditis elegans</i> cosmid W04H10	0.20	1170683	PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, SKELETAL MUSCLE ISOFORM (PHOSPHORYLASE KINASE ALPHA M SUBUNIT) >gi 2135923 pir I38111 phosphorylase kinase (EC 2.7.1.38) - human >gi 791043	7.4
517	U10470	<i>Pseudomonas fluorescens</i> PHA depolymerase (phaZ) gene, complete cds.	0.20	3721862	(AB016024) Pfj2 [Plasmodium falciparum]	1.9
518	D83778	Human mRNA for KIAA0194 gene, partial cds	0.20	126363	LAMININ ALPHA-1 CHAIN PRECURSOR precursor - human	0.65
519	S43579	c-scr=pp60c-src, sdr=src downstream region	0.20	4159887	(AC004908) similar to ribosomal protein L23a; similar to P29316 (PID:g132848) [Homo sapiens]	0.52
520	U07357	<i>Mus musculus</i> Balb/c brain-specific kinase (Bsk) mRNA, complete cds.	0.20	206712	(M64793) salivary proline-rich protein [Rattus norvegicus]	0.51

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
521	AF034460	Penicillium thomii internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	0.20	114136	AMINO-ACID ACETYLTRANSFERASE Pseudomonas aeruginosa >gi 151036 (M38358) N-acetylglutamate synthase [Pseudomonas aeruginosa]	0.39
522	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.20	2842674	POU DOMAIN CLASS 2, ASSOCIATING FACTOR 1 (B-CELL-SPECIFIC COACTIVATOR OBF-1) (OCT BINDING FACTOR 1) (BOB-1) (OCA-B) Bob1, B-cell-specific - mouse >gi 1881818 bbs 179852 mBob1=B-cell specific transcriptional coactivator line J558L, Peptide, 256 aa] >gi 1353792 (U43788) Oct binding factor 1 [Mus musculus] (AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	0.073
523	X95971	S.lividans groEL2 gene	0.20	3925277		4e-19
524	L41502	Ovis aries vasopressin V1 receptor (V1R) gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
525	J03885	K.pneumoniae oxalacetate decarboxylase alpha subunit gene, complete cds.	0.19	<NONE>	<NONE>	<NONE>
526	AE001451	Helicobacter pylori, strain J99 section 12 of 132 of the complete genome	0.19	<NONE>	<NONE>	<NONE>

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
527	D88084	Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)5'exon	0.19	<NONE>	<NONE>	<NONE>
528	U67599	Methanococcus jannaschii section 141 of 150 of the complete genome	0.19	<NONE>	<NONE>	<NONE>
529	J05500	Human beta-spectrin (SPTB) mRNA, complete cds.	0.19	<NONE>	<NONE>	<NONE>
530	Y10137	M.mycoides ftsY gene homologue and gene encoding hypothetical protein	0.19	<NONE>	<NONE>	<NONE>
531	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
532	D43805	Mouse thymic stromal cell mRNA for TLSF-beta, complete cds	0.19	<NONE>	<NONE>	<NONE>
533	AJ012585	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2	0.19	<NONE>	<NONE>	<NONE>
534	X51475	Brassica napus 5-enolpyruvylshikimate-3-phosphate synthase gene	0.19	<NONE>	<NONE>	<NONE>
535	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
536	Z49625	S.cerevisiae chromosome X reading frame ORF YJR125c	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens pilot				
537	X63741	mRNA	0.19	<NONE>	<NONE>	<NONE>
538	Y11255	O.laticipes mRNA for annexin max4	0.19	<NONE>	<NONE>	<NONE>
539	L63537	Oncorhynchus mykiss (clone Jb-10) beta-2 microglobulin (B2m) mRNA. complete cds.	0.19	<NONE>	<NONE>	<NONE>
540	X70903	N.tobacum T92 gene for auxin-binding protein	0.19	<NONE>	<NONE>	<NONE>
541	U61958	Caenorhabditis elegans cosmid C25A8	0.19	<NONE>	<NONE>	<NONE>
542	U33959	Macaca fascicularis fertilin beta mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
543	Z49835	H.sapiens mRNA for protein disulfide isomerase	0.19	2113940	(Z95556) hypothetical protein Rv2507	9.4
544	AF035458	Spinacia oleracea heat shock 70 protein protein. complete cds	0.19	267293	PROBABLE E4 PROTEIN papillomavirus (type 1) >gi 61015 (X62844) E4 gene product [Pygmy chimpanzee papillomavirus type 1]	9.4
545	U23441	Tetrahymena thermophila B internal deletion sequence.	0.19	3877185	(Z66563) F46C3.2 [Caenorhabditis elegans]	9.3
546	U53921	Pneumocystis carinii major surface glycoprotein	0.19	3548901	(AF052502) DA26 homolog [Epiphyas postvittana nucleopolyhedrovirus]	9.3
547	L11002	Rat ankyrin binding glycoprotein-1 related mRNA sequence.	0.19	3337352	(AC004481) putative chromatin structural protein Supt5hp	9.1
548	U67560	Methanococcus jannaschii section 102 of 150 of the complete genome	0.19	3183689	(Y13585) serotonin receptor 4 [Cavia porcellus]	8.7
549	U18424	Mus musculus bacteria binding macrophage receptor MARCO mRNA. complete cds.	0.19	3659853	(AF089083) complement component C1qB like protein	7.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
550	X66467	C.albicans sec18 gene	0.19	1326385	(U58751) C07G1.7 gene product [Caenorhabditis elegans]	6.9
551	AF003487	Syngaster lepidus 16S ribosomal RNA gene, partial sequence	0.19	3122039	DIHYDROPYRIMIDINASE (DHPASE) dihydropyrimidinase - rat >gi 1378019 gnl PID d1010479	6.9
552	J05087	Rat calmodulin-sensitive plasma membrane Ca ²⁺ -transporting ATPase (PMCA3) mRNA, complete cds.	0.19	422462	hypothetical protein - fruit fly (Drosophila melanogaster) >gi 296434 (X68408) ORF [Drosophila melanogaster]	5.3
553	AF080464	Homo sapiens glutamate oxaloacetate transaminase	0.19	3024834	PROBABLE E4 PROTEIN >gi 790898 position 3286..3288 is first start codon; putative	5.3
554	U78876	Human MEK kinase 3 mRNA, complete cds	0.19	1710445	(U78083) unknown [Emericella nidulans]	5.3
555	AB009077	Vigna radiata mRNA for proton pyrophosphatase, complete cds	0.19	3256922	(AP000002) 256aa long hypothetical protein [Pyrococcus horikoshii]	5.1
556	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.19	4226159	(AF125463) contains similarity to BTB (also known as BR-C/Ttk) domains (Pfam:PF00651, Score=62.8, E=7.6e-15, N=1) [Caenorhabditis elegans]	4.1
557	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome	0.19	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
558	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome	0.19	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.0
559	L81774	Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence	0.19	4001725	(AB015981) MnhA [Staphylococcus aureus]	3.0
560	AL021108	Drosophila melanogaster cosmid clone 137E7	0.19	4001688	(AB015718) protein kinase [Homo sapiens]	3.0
561	AB001510	Carabus leptoplesioides mitochondrial DNA for NADH dehydrogenase subunit 5, partial cds	0.19	3758855	(Z98551) MAL3P6.11 [Plasmodium falciparum]	2.4
562	AF069696	Egernia stokesii clone EST1 microsatellite	0.19	3328994	(AE001326) Amino Acid (Branched) Transport [Chlamydia trachomatis]	2.4
563	X64144	F.pringlei ppcA1 gene for phosphoenolpyruvate carboxylase	0.19	3242974	(AF069555) G protein-coupled receptor p2y3 [Meleagris gallopavo]	2.3
564	U56897	Human immunodeficiency virus type 1 gag polyprotein (gag) gene, partial cds	0.19	2257710	(U73041) resolvase-like protein [Thiobacillus ferrooxidans]	2.3
565	U57975	Danio rerio Notch homologue 3 mRNA, complete cds	0.19	3874971	(Z99709) similar to NAD dependant epimerase/dehydratase family; cDNA EST EMBL:C10103 comes from this gene; cDNA EST EMBL:D66400 comes from this gene; cDNA EST EMBL:D70143 comes from this gene; cDNA EST yk493h11.3 comes from ...	1.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
566	Y12502	R.norvegicus mRNA for factor XIIIa	0.19	2133693	masquerade precursor - fruit fly (Drosophila melanogaster) >gi 665545 (U18130) masquerade [Drosophila melanogaster] >gi 1095942 prf 2110286A masquerade gene	1.8
567	S82470	BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	0.19	2444026	(U77783) N-methyl-D-aspartate receptor 2D subunit precursor [Homo sapiens]	1.8
568	U97408	Caenorhabditis elegans cosmid F48A9	0.19	542433	225K protein - Babesia bovis (fragment)	1.8
569	U10470	Pseudomonas fluorescens PHA depolymerase (phaZ) gene. complete cds.	0.19	3721862	(AB016024) Pfj2 [Plasmodium falciparum]	1.7
570	M88160	Ovis aries MAF214 locus polymorphic dinucleotide repeat .	0.19	1293816	(U56963) T13A10.5 gene product [Caenorhabditis elegans]	1.4
571	AJ131336	Lolium italicum mRNA for pollen allergen (Hol i 2, group II) > :: emb AJ131339 LIT13 1339 Lolium italicum mRNA for pollen allergen (Lol i 2, group II) > allergen (Poa p 2, group II) > :: emb AJ131338 TAE1 31338 Triticum aestivum mRNA for pollen allergen (Tri a 2, group II)	0.19	3880447	(AL032675) predicted using Genefinder	0.82
572	X84036	S.cerevisiae ARG8 and CDC33 genes	0.19	3882041	(AJ010405) hypothetical protein	0.62

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human WD protein			mucin - human >gi 501033	
573	U57058	IR10 pre-mRNA, partial cds	0.19	631302	(U14383) mucin [Homo sapiens]	0.60
574	AF034460	Penicillium thomii internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	0.19	114136	AMINO-ACID ACETYLTRANSFERASE Pseudomonas aeruginosa >gi 151036 (M38358) N-acetylglutamate synthase [Pseudomonas aeruginosa]	0.35
575	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.19	105270	alpha-2-adrenergic receptor - human name 'ADRA2R' [Homo sapiens]	0.27
576	AG001475	Homo sapiens genomic DNA, 21q region, clone: 125H6N2	0.19	94977	hypothetical protein 3 - Pseudomonas sp. (DSM 6898) plasmid pKB740 >gi 45867 (X66604) ORF3	0.16
577	M63284	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 9 and 10, clones lambda-Fc(3.2.93).	0.19	3024681	TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) of RNA polymerase II transcription factor TFIID [Homo sapiens]	0.088
578	U38241	Pseudomonas aeruginosa orotate phosphoribosyl transferase (pyrE), catabolite repression control protein (crc) and RNasePH (rph) genes, complete cds	0.19	3044086	(AF055904) unknown [Myxococcus xanthus]	0.052
579	AF039734	Lontra longicaudis transthyretin intron 1, partial sequence	0.19	322759	pistil extensin-like protein (clone pMG14) - common tobacco (fragment) >gi 19927 (Z14015) pistil extensin like protein [Nicotiana tabacum]	0.030
580	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.19	2147194	collagen - Paralvinella grasslei	0.002

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
581	AB004232	Drosophila melanogaster mRNA for DAD polypeptide, complete cds	0.19	2498765	PEROXISOMAL MEMBRANE PROTEIN PEX16 lipolytica]	0.002
582	AF098919	Gallus gallus alpha-globin gene domain 5' region	0.19	1086863	(U41272) T03G11.6 gene product [Caenorhabditis elegans]	4e-05
583	AE001457	Helicobacter pylori, strain J99 section 18 of 132 of the complete genome	0.19	2924552	(AL022018) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=165.48; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA264666; 2-match_description=LD08351.5p rime LD Drosophila melanoga...	3e-05
584	L10329	Plasmid RP4 traE gene, 3' end; traD gene, complete cds; traF gene, 5' end.	0.19	3878117	(Z49068) mitochondrial carrier protein	8e-07
585	AE001155	Borrelia burgdorferi (section 41 of 70) of the complete genome	0.19	861276	(U28739) similar to TPR domains in e.g. yeast STI1 protein [Caenorhabditis elegans]	2e-12
586	U49979	Orf virus E10R homolog gene, partial cds, and DNA polymerase gene, complete cds	0.19	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	1e-15
587	U88155	Xenopus laevis RanGTPase activating protein	0.19	995714	(X91258) pid:e198503 [Saccharomyces cerevisiae]	4e-16
588	AF061854	Schizosaccharomyces pombe Clr4p (clr4) gene, complete cds	0.19	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	5e-19
589	M23865	S.cerevisiae CHS2 gene encoding chitin synthase.	0.18	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis XL- INCENP (XL- INCENP) mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>
590	U95094	Caenorhabditis elegans cosmid F41A4	0.18	<NONE>	<NONE>	<NONE>
591	AF067610	Homo sapiens gonadotropin- releasing hormone precursor, second form (GnRH-II) gene, complete cds	0.18	<NONE>	<NONE>	<NONE>
592	AF036329	H.sapiens mitoxantrone- resistance associated mRNA	0.18	<NONE>	<NONE>	<NONE>
593	Z49216	Torulopsis glabrata mitochondrial DNA for tRNA-Thr,-His and -Glu upstream of cytochrome b gene	0.18	<NONE>	<NONE>	<NONE>
594	X02167	R.communis (Carmencita) Scr1 mRNA for sucrose carrier	0.18	<NONE>	<NONE>	<NONE>
595	Z31561	Homo sapiens (subclone 2_c9 from P1 H56) DNA sequence	0.18	1346575	55 KD ERYTHROCYTE MEMBRANE PROTEIN	8.4
596	L81692	Nocardia lactamdurans pcbAB and pcbC genes for alpha-aminoadipyl-L- cysteinyl-D-valine synthetase and isopenicillin N synthase	0.18	126404	SEED LIPOXYGENASE-2 (L- 2) soybean >gi 170014 (J03211) lipoxigenase (EC 1.13.11.12)	6.5
597	X57310	Sus scrofa parathyroid receptor (PTH) mRNA, complete cds	0.18	1022323	(X04647) collagen alpha-2(IV) chain [Mus musculus]	3.8
598	U18315					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
599	AL010158	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-85, complete sequence	0.18	2506816	VERSICAN CORE PROTEIN PRECURSOR PROTEOGLYCAN CORE PROTEIN 2) (GLIAL HYALURONATE-BINDING PROTEIN) (GHAP) >gi 608515 (U16306) chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide	3.7
600	AB005287	Bos taurus mRNA for thrombospondin 1, complete cds	0.18	2146000	u0002b protein - Mycobacterium tuberculosis tuberculosis] >gi 1694863 gnl PID e283373 (Z83018) hypothetical protein Rv2968c [Mycobacterium tuberculosis]	2.9
601	AL021108	Drosophila melanogaster cosmid clone 137E7	0.18	3483032	(AL031371) hypothetical protein SC4G2.06 [Streptomyces coelicolor]	2.9
602	U57975	Danio rerio Notch homologue 3 mRNA, complete cds	0.18	85719	collagen alpha 1'(II) chain precursor - African clawed frog (AL021387) similar to Zinc finger, C4 type (two domains); cDNA EST yk452f4.5 comes from this gene; cDNA EST EMBL:T00774 comes from this gene receptor NHR-3 [Caenorhabditis elegans]	1.7
603	M30124	P.aeruginosa autonomously replicating sequence.	0.18	3878017	STEM CELL PROTEIN chicken >gi 62845 (X63371) transforming capacity [Gallus gallus]	1.3
604	X54965	G.sp alpha 5HR DNA	0.18	134304	(X98893) hTAFII68 [Homo sapiens] splicing [Homo sapiens]	1.3
605	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.18	1628403	92 KD TYPE IV COLLAGENASE PRECURSOR IV, 92K, precursor - rat >gi 1022784 (U36476) 92-kDa type IV collagenase [Rattus norvegicus]	1.2
606	U20793	Oryctolagus cuniculus renal sodium-dependent phosphate transporter type II mRNA, complete cds.	0.18	1705984		

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
607	U23427	Human cholecystokinin type A receptor (CCK-A) gene, exons 1 and 2.	0.18	3261734	(Z94752) hypothetical protein Rv1004c	0.97
608	U49953	Rattus norvegicus protein kinase MUK2 mRNA, complete cds	0.18	551238	(X81847) pectate lyase I [Erwinia carotovora]	0.43
609	J00182	Human alpha globin gene cluster on chromosome 16: zeta gene.	0.18	1585259	traJ gene [Amycolatopsis methanolica]	0.41
610	X62513	M.gallopavo gene for metallothionein	0.18	2494740	HYPOTHETICAL 28.3 KD PROTEIN IN GBD 5'REGION (ORF4) >gi 2120954 pir I39562 ORF4 - Alcaligenes eutrophus >gi 695274 (L36817) ORF4	0.31
611	X04862	Goat embryonic alpha globin gene zeta exons 2-3	0.18	86837	androgen receptor B - human	0.082
612	M12450	Rat vitamin D binding protein (DBP) mRNA, complete cds.	0.18	4210432	(AJ130783) APC2 protein [Mus musculus]	0.038
613	AF038539	Mus musculus muscle NSP-like 1 (Nsp1) mRNA, complete cds	0.18	3297877	(AJ224868) GNAS1 [Homo sapiens]	0.029
614	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13	0.18	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	0.009
615	D38754	Pig mRNA for inter-alpha-trypsin inhibitor heavy-chain H1, complete cds	0.18	1397275	(U61947) C06G3.8 gene product [Caenorhabditis elegans]	7e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
616	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.18	630864	LRR47 protein - fruit fly (Drosophila melanogaster) >gi 415947 (X75760) LRR47 [Drosophila melanogaster]	6e-07
617	X54850	S.kluyveri linear plasmid pSKL DNA for open reading frames 1-10	0.18	3183405	HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I >gi 2370504 gnl PID e339194 pombe] >gi 3451305 gnl PID e1316730 (AL031324) very hypothetical protein [Schizosaccharomyces pombe]	2e-08
618	L21954	Human peripheral benzodiazepine receptor gene, exon 4.	0.18	3925211	(AL032626) cDNA EST EMBL:D70654 comes from this gene; cDNA EST EMBL:Z14359 comes from this gene; cDNA EST EMBL:D33409 comes from this gene; cDNA EST EMBL:D36239 comes from this gene; cDNA EST EMBL:Z14766 comes from this gene...	4e-09
619	U09355	Oryctolagus cuniculus protein phosphatase 2A1 B gamma subunit (skeletal muscle isolate) mRNA, complete cds.	0.18	3947877	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]	8e-11
620	X58715	T.cruzi hsp70 mRNA for 70 kDa heat shock protein, partial cds	0.18	3024081	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) (CONTAINS: TELOKIN)	9e-12
621	AF060195	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds	0.18	861276	(U28739) similar to TPR domains in e.g. yeast STI1 protein [Caenorhabditis elegans]	1e-14
622	L27235	Methylobacterium extorquens serine cycle proteins	0.18	2688949	(AF027208) AC133 antigen [Homo sapiens]	1e-14

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
623	AF006573	Drosophila virilis maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.18	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi 3876420 gnl PID e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-23
624	AF001782	Staphylococcus aureus strain SA502A AgrB	0.17	<NONE>	<NONE>	<NONE>
625	AJ223364	Homo sapiens germ-line DNA upstream of Jkappa locus	0.17	<NONE>	<NONE>	<NONE>
626	J03059	Human glucocerebrosidase (GCB) gene, complete cds	0.17	<NONE>	<NONE>	<NONE>
627	AB008860	Fugu rubripes Ca12 gene for pheromone receptor, complete cds	0.17	2198849	(AF004900) E3KARP [Homo sapiens] >gi 2665826 (AF035771) Na ⁺ /H ⁺ exchanger regulatory factor 2 [Homo sapiens] factor 2 [Homo sapiens] >gi 3618353 gnl PID d1034182 exchanger isoform A3 [Homo sapiens]	7.8
628	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.17	539355	SCD25 protein (version 1) - yeast	7.5
629	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17	482118	hypothetical protein C15H7.1 - Caenorhabditis elegans	4.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
630	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17	465932	HYPOTHETICAL 83.2 KD PROTEIN F58A4.11 IN CHROMOSOME III >gi 3874287 gnl PID e1344088 EST EMBL:C12577 comes from this gene; cDNA EST yk227e7.5 comes from this gene; cDNA EST yk303d1.5 comes from this gene; cDNA EST yk314c12.5 comes from this gene; cDNA ... EMBL:C11886 comes from this gene; cDNA EST EMBL:C12577 comes from this gene; cDNA EST yk227e7.5 comes from this gene; cDNA EST yk303d1.5 comes from this gene; cDNA EST yk314c12.5 comes from this gene; cDNA ...	4.4
631	X55065	Chinese hamster metallothionein II gene	0.17	3687237	(AC005169) putative Cys3His zinc-finger protein	1.5
632	U15280	Rattus norvegicus oxytocin receptor (OTR) gene, exon 3 and complete cds	0.17	542565	cyclin E type II - fruit fly (Drosophila melanogaster) >gi 429168 (X75027) Drosophila cyclin E type II [Drosophila melanogaster]	0.45
633	X04862	Goat embryonic alpha globin gene zeta exons 2-3	0.17	86837	androgen receptor B - human	0.080
634	AL010222	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence	0.17	1177322	(X95466) CPG2 protein [Rattus norvegicus] >gi 1588593 prf 2208498A plasticity-related gene [Rattus norvegicus]	7e-07
635	X60111	H.sapiens mRNA for MRP-1	0.17	3237306	(U92715) breast cancer antiestrogen resistance 3 protein	3e-09
636	U49979	Orf virus E10R homolog gene, partial cds, and DNA polymerase gene, complete cds	0.17	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	7e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
637	AF006573	Drosophila virilis maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.17	2500558	PUTATIVE RIBONUCLEASE III (RNAse III) >gi 3876420 gnl PID e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-29
638	AE001141	Borrelia burgdorferi (section 27 of 70) of the complete genome	0.16	1850327	(U52370) fertilin beta [Homo sapiens]	2.3
639	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.12	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	2e-56
640	AF023532	Simulium vittatum ATPase 6 gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.11	<NONE>	<NONE>	<NONE>
641	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.10	3482965	(AL031369) putative protein	0.49
642	AJ001596	Danio rerio mRNA for opioid receptor homologue	0.099	1706694	LANOSTEROL SYNTHASE 5.4.99.7) - fission yeast (Schizosaccharomyces pombe)	2.3
643	U26341	Oryctolagus cuniculus Na and Cl dependent betaine transporter mRNA, complete cds.	0.099	2645804	(AF033381) betaine homocysteine methyl transferase [Mus musculus]	0.59
644	M11633	Bacteriophage Cp-5 (S.pneumoniae) 3' inverted terminal repeat.	0.082	2314695	(AE000649) type IIS restriction enzyme R and M protein	4.3
645	X74103	Streptomyces sp. gene for alkaline serine protease I	0.073	1314734	(U54641) 220 kDa silk protein [Chironomus thummi]	6.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis elegans cosmid F32G8, complete sequence [Caenorhabditis elegans]	0.072	<NONE>	<NONE>	<NONE>
646	Z72509					
647	X70282	X.laevis xanf-1 gene	0.070	3851202	(AC005954) ZO-3 [Homo sapiens] [Homo sapiens]	0.40
		Human DNA sequence from cosmid E141E2, on chromosome 22, complete sequence [Homo sapiens]	0.069	<NONE>	<NONE>	<NONE>
648	Z69906					
649	AF056940	Drosophila virilis retrotransposon Tv1, complete sequence	0.069	2246532	(U93872) ORF 73, contains large complex repeat CR 73	5e-12
650	AJ001151	Homo sapiens genomic sequence	0.068	<NONE>	<NONE>	<NONE>
651	X54455	Bacteriophage BF23 gene 17 and gene 18	0.067	<NONE>	<NONE>	<NONE>
		P.pinea internal transcribed spacers 1 & 2 of ribosomal DNA	0.067	2459733	(U95374) aldehyde dehydrogenase [Haloferax volcanii]	4.3
652	X87936					
653	AF019236	Dictyostelium discoideum TipD (tipD) gene, complete cds	0.067	3882275	(AB018320) KIAA0777 protein [Homo sapiens]	1.1
654	X90592	O.cuniculus mRNA for p53 protein	0.067	1703275	METHIONINE AMINOPEPTIDASE 2 (METAP 2) GLYCOPROTEIN (P67)	0.29
655	U41805	Mus musculus putative T1/ST2 receptor binding protein precursor mRNA, partial cds	0.067	642518	(U17326) neuronal nitric oxide synthase [Homo sapiens]	0.29
656	AB007881	Homo sapiens KIAA0421 mRNA, partial cds	0.066	<NONE>	<NONE>	<NONE>
		Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-109, complete sequence	0.066	<NONE>	<NONE>	<NONE>
657	AL010213					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
658	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.066	1082461	homeotic protein HB9 - human	0.38
659	AF104156	Rattus exulans isolate huahine30 mitochondrial D-loop, partial sequence	0.066	1002380	(U24189) RRM-type RNA binding protein [Caenorhabditis elegans]	0.29
660	X97581	M.musculus mRNA for spalt transcription factor	0.066	4107313	(AL035075) putative myosin heavy chain	0.28
661	D85378	Human clone H20 N-acetylglucosaminyltransferase III DNA, exon 2	0.066	2114473	(U96963) p140mDia [Mus musculus]	0.22
662	M97561	Human (clone LA179) chromosome 21 sequence.	0.065	<NONE>	<NONE>	<NONE>
663	AE001373	Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence	0.065	<NONE>	<NONE>	<NONE>
664	S75479	growth hormone receptor, growth hormone binding protein {GHR/BP gene} [mice, C57 black/6, Genomic, 179 nt, segment 8 of 10]	0.065	<NONE>	<NONE>	<NONE>
665	AF032922	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds	0.065	3061308	(AB006074) topoisomerase III [Mus musculus]	0.82
666	S80986	svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3876 nt]	0.065	1326288	(U58734) weak similarity to ankyrin G [Caenorhabditis elegans]	0.12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
667	X59552	G.domesticus mRNA for ventricular myosin heavy chain	0.065	2497098	HYPOTHETICAL 74.2 KD PROTEIN IN AMD1-RAD52 INTERGENIC REGION >gi 1077180 pir S49745 probable membrane protein YML034w - yeast (Saccharomyces cerevisiae) >gi 575685 (Z46659) unknown orf, len: 656, CAI: 0.13 [Saccharomyces cerevisiae]	0.014
668	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.065	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	5e-33
669	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.064	<NONE>	<NONE>	<NONE>
670	M30039	Sheeppox virus strain KS-1 ORF HM1 gene, partial cds; ORF HM2 and ORF HM3 genes, complete cds; and ORF HM4 gene, partial cds	0.064	<NONE>	<NONE>	<NONE>
671	Z68013	Caenorhabditis elegans cosmid W02H3, complete sequence [Caenorhabditis elegans]	0.064	<NONE>	<NONE>	<NONE>
672	AF041332	Bodo saltans unknown mRNA, kinetoplast gene encoding kinetoplast protein, complete cds	0.064	<NONE>	<NONE>	<NONE>
673	J00451	Mouse germline IgG-3 chain gene, D-J-C region, and switch region.	0.064	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
674	U41289	Dictyostelium discoideum K7 kinesin-like protein mRNA, complete cds	0.064	3482972	(AL031369) putative protein	9.3
675	M37395	L.lactis (strain SK11) proteinase plasmid pSK111 DNA, complete cds.	0.064	993019	(X87246) alternative start codon [Pseudorabies virus]	9.2
676	Z15030	H.sapiens gene for ventricular myosin light chain 2 > :: gb L01652 HUMVM LC Human ventricular myosin light chain 2 gene, seven exons.	0.064	730343	PROLACTIN RECEPTOR PRECURSOR (PRL-R) mouse >gi 220576 gnl PID d1001535 (D10214) prolactin receptor precursor [Mus musculus] >gi 293770 (L14811) prolactin receptor [Mus musculus] >gi 347842 (L13593) prolactin receptor [Mus musculus] receptor:ISOTYPE=long form [Mus musculus]	9.1
677	Z12021	G.max gene for catalase	0.064	2498711	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi 1185461 (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe]	5.3
678	L05668	Entamoeba histolytica protein serine/threonine kinase (pstk1) gene, complete cds.	0.064	733140	(U22453) carboxypeptidase [Simulium vittatum]	5.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
679	U50715	Mus musculus alpha-galactosidase A gene, complete cds	0.064	125398	HYGROMYCIN-B KINASE (HYGROMYCIN B PHOSPHOTRANSFERASE) (APH(7")) >gi 66885 pir WGSMHH hygromycin B phosphotransferase (EC 2.7.1.-) Streptomyces hygroscopicus >gi 581682 (X03615) pot. hyg protein [Streptomyces hygroscopicus] phosphotransferase [synthetic construct] >gi 2739064 cloning vector] >gi 2739068 (AF025747) hygromycin B phosphotransferase [unidentified cloning vector]	2.3
680	Z28182	S.cerevisiae chromosome XI reading frame ORF YKL182w	0.064	1079035	Om(2D) protein - fruit fly (Drosophila ananassae) >gi 443770 gnl PID d1006095 (D26553) ORF	1.8
681	M29917	Human ornithine aminotransferase gene, exon 1.	0.064	2317934	(U97553) unknown [murine herpesvirus 68]	1.4
682	AB020709	Homo sapiens mRNA for KIAA0902 protein, complete cds	0.064	861404	(U29154) T07F12.3 gene product [Caenorhabditis elegans]	0.47
683	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.064	1708118	HOMEBOX PROTEIN HB9 >gi 507425	0.35
684	AB010427	Homo sapiens mRNA for NORI-1, complete cds	0.064	2388676	(AF015539) precollagen P [Mytilus edulis]	0.018
685	U34774	Orf virus ankyrin-like repeat protein, F11L homolog, and F12L homolog genes, complete cds.	0.064	731668	SSF1 PROTEIN >gi 626624 pir S46700 SSF1 protein - yeast (Saccharomyces cerevisiae)	1e-05
686	AF022861	Mus musculus neuropilin-2(a5) mRNA, alternatively spliced, complete cds	0.064	4091978	(AF073359) benzaldehyde dehydrogenase [Pseudomonas sp. DJ77]	1e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
687	U14331	Sus scrofa myogenin gene, complete cds	0.064	2781386	(AC004010) similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	3e-33
688	AF074870	Chironomus pallidivittatus clone 1219 non-telomeric Ssp repeat sequence	0.063	<NONE>	<NONE>	<NONE>
689	Z25523	H.sapiens repeat region DNA.	0.063	<NONE>	<NONE>	<NONE>
690	AE001378	Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence	0.063	<NONE>	<NONE>	<NONE>
691	Z72947	S.cerevisiae chromosome VII reading frame ORF YGR162w	0.063	<NONE>	<NONE>	<NONE>
692	Y14723	Choanomphalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.063	<NONE>	<NONE>	<NONE>
693	X74103	Streptomyces sp. gene for alkaline serine protease I	0.063	1730713	HYPOTHETICAL 108.5 KD PROTEIN IN UME3-PUB1 INTERGENIC REGION >gi 2131866 pir S62935 hypothetical protein YNL023c - yeast (Saccharomyces cerevisiae) >gi 1301855 gnl PID e239870 (Z71299) ORF YNL023c [Saccharomyces cerevisiae]	6.7
694	AF039843	Homo sapiens Sprouty 2 (SPRY2) mRNA, complete cds	0.063	232217	GLUTATHIONE S-TRANSFERASE GST-6.0 (GST B1-1) >gi 421198 pir S29772 glutathione transferase (EC 2.5.1.18) - Proteus mirabilis >gi 2126142 pir S71882 glutathione transferase (EC 2.5.1.18) B - Proteus mirabilis >gi 1053076 (U38482)	5.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
695	M63650	Mouse M-twist gene mRNA, complete cds.	0.063	1730141	FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 2 >gi 2135129 pir S60173 fragile X mental retardation syndrome related protein - human >gi 1098637 (U31501) fragile X mental retardation syndrome related protein [Homo sapiens]	1.8
696	Y13298	Homo sapiens GDP dissociation inhibitor beta pseudogene	0.063	1085930	hypothetical protein 4 - fowl adenovirus 1	1.3
697	X56600	Rat SOD-2 gene for manganese-containing superoxide dismutase	0.063	3882143	(AB018254) KIAA0711 protein [Homo sapiens]	0.60
698	Z23107	M.musculus mRNA for 5HTx serotonin receptor	0.063	1708162	HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN HOMOLOG) (HD PROTEIN)	0.45
699	M20670	Plasmodium vivax circumsporozoite protein gene, 3' end.	0.063	4033395	DNA GYRASE SUBUNIT B subunit [Mycococcus xanthus]	0.35
700	Z62997	H.sapiens CpG DNA, clone 76g11, reverse read cpg76g11.rtl.a.	0.063	1350911	RETINOIC ACID RECEPTOR RXR-BETA sapiens] >gi 3172498 (AF065396) retinoic X receptor B dJ1033B10.11 (Retinoid X receptor beta (RXRB)) [Homo sapiens] >gi 4249766 (AF120161) retinoic X receptor beta	0.16
701	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.063	2981200	(AF048732) cyclin T2b [Homo sapiens]	0.090
702	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.063	3877951	(Z81555) predicted using Genefinder	6e-07
703	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.063	3393018	(AL031174) hypothetical protein	2e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		E.coli genomic DNA.				
704	D90872	Kohara clone #419(54.7-55.1 min.)	0.063	2498198	CYTOCHROME B561 (CYTOCHROME B-561)	3e-19
705	M25528	M.crystallinum ferredoxin-NADP+ reductase (fnrA) mRNA, complete cds.	0.062	<NONE>	<NONE>	<NONE>
706	U45256	Strongyloides ratti microsatellite B DNA	0.062	<NONE>	<NONE>	<NONE>
707	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.062	<NONE>	<NONE>	<NONE>
708	AF044317	Homo sapiens TEL/AML1 fusion gene, partial sequence	0.062	<NONE>	<NONE>	<NONE>
709	Z73975	Caenorhabditis elegans cosmid T06E8, complete sequence [Caenorhabditis elegans]	0.062	3108187	(AC004663) Notch 3 [Homo sapiens]	2.9
710	X54232	Human mRNA for heparan sulfate proteoglycan	0.062	1076741	chitinase (EC 3.2.1.14) precursor - rice precursor - rice >gi 807955 (X87109) chitinase [Oryza sativa]	0.59
711	X03073	Bovine retinal mRNA for transducin beta-subunit	0.062	477578	sialidase - Actinomyces viscosus >gi 141852	0.087
712	Y12573	D.melanogaster Jun and 14-3-3 zeta gene	0.062	3879551	(Z70756) similar to collagen	0.073
713	L26573	Bombus terrestris mitochondrial cytochrome oxidase I, partial cds.	0.062	1684959	(U20600) NADH dehydrogenase subunit [Vanda lamellata]	0.039

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
714	U58994	Human ladinin (LAD) gene, complete cds	0.062	2811078	AMINOPEPTIDASE B (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B) >gi 2039143 (U61696) aminopeptidase B [Rattus norvegicus]	9e-06
715	AB014553	Homo sapiens mRNA for KIAA0653 protein, partial cds	0.062	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	5e-10
716	L16898	Mus musculus collagen alpha 1 type XVIII mRNA, 5'end.	0.062	1723657	HYPOTHETICAL 38.5 KD PROTEIN IN ERV1-GLS2 INTERGENIC REGION >gi 2132587 pir S64322 probable membrane protein YGR031w - yeast (Saccharomyces cerevisiae) >gi 1323010 gnl PID e243277 (Z72816) ORF YGR031w [Saccharomyces cerevisiae]	1e-14
717	X99343	M.tuberculosis guaA/B & choD genes	0.062	3873807	(Z49907) B0491.1 [Caenorhabditis elegans]	2e-19
718	AF010193	Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds	0.061	<NONE>	<NONE>	<NONE>
719	L10182	Myrmeleon sp. 18S ribosomal RNA.	0.061	<NONE>	<NONE>	<NONE>
720	Y14723	Choanomphalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.061	<NONE>	<NONE>	<NONE>
721	L27840	Bovine respiratory syncytial virus nucleoprotein mRNA, complete cds.	0.061	542955	nucleoporin p62 - human	8.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
722	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.061	494454	Sus scrofa >gi 494455 pdb IPOS B Sus scrofa Sus scrofa >gi 1421210 pdb 1PCP Porcine Spasmolytic Protein (Psp) (Nmr, 19 Structures) Spasmolytic Polypeptide >gi 1633061 pdb 2PSP B Chain B, Porcine Pancreatic Spasmolytic Polypeptide	2.9
723	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.061	3845272	(AE001417) hypothetical protein [Plasmodium falciparum]	1.3
724	U26463	Sporidiobolus salmonicolor NADPH-dependent aldehyde reductase gene, complete cds	0.061	1710288	(U79302) unknown [Homo sapiens]	0.44
725	AF035443	Xenopus laevis wee1 homolog mRNA, complete cds	0.061	3979720	EMBL:D33048 comes from this gene; cDNA EST EMBL:D35780 comes from this gene; cDNA EST yk442c6.3 comes from this gene; cDNA EST yk442c6.5 comes from this gene; cDNA EST yk398f6.3 comes from this gene; cDNA E... >gi 3979816 gnl PID e1358315 EST EMBL:D35780 comes from this gene; cDNA EST yk442c6.3 comes from this gene; cDNA EST yk442c6.5 comes from this gene; cDNA EST yk398f6.3 comes from this gene; cDNA E...	2e-04
726	Z48584	Caenorhabditis elegans cosmid ZK1321, complete sequence [Caenorhabditis elegans]	0.061	3183491	HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III >gi 1065510 (U40419) C27F2.7 gene product [Caenorhabditis elegans]	3e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 32.0 KD	
727	X61489	Zea mays pep gene for (C3 type) phosphoenolpyruvate carboxylase	0.061	2496887	PROTEIN C09F5.2 IN CHROMOSOME III >gi 732538 (U22832) C09F5.2 gene product [Caenorhabditis elegans]	1e-15
728	AF025408	Drosophila melanogaster Windbeutel (wind) gene, complete cds	0.061	3702295	(AC005783) R33083_1 [Homo sapiens]	2e-60
729	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.060	<NONE>	<NONE>	<NONE>
730	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.060	<NONE>	<NONE>	<NONE>
731	Y08682	H.sapiens mRNA for carnitine palmitoyltransferase I type I	0.060	3319446	(AF077541) contains similarity to class-I aminoacyl-tRNA synthetases [Caenorhabditis elegans]	8.1
732	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.060	1041119	(D78016) TRAE [Enterococcus faecalis]	8.1
733	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.060	632209	regulatory protein Rex - primate T-lymphotropic virus PTLV-L (fragment)	3.7
734	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.060	3098348	(AF037401) neuropeptide Y/peptide YY receptor Yc [Danio rerio]	2.1
735	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.060	125978	LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) >gi 70146 pir TDHULK leukocyte antigen-related protein precursor - human >gi 34267 sapiens]	1.2
736	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.060	2055394	(U87306) transmembrane receptor UNC5H2 [Rattus norvegicus]	0.32
737	U69668	Human nuclear pore complex-associated protein TPR	0.060	4127854	(Y14063) ChT1 thymocyte antigen [Gallus gallus]	9e-04

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
738	AB014553	Homo sapiens, mRNA for KIAA0653 protein, partial cds	0.060	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	1e-09
739	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.060	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	5e-10
740	Z96260	H. sapiens telomeric DNA sequence, clone 12QTEL101, read 12QTELOO101.seq	0.059	<NONE>	<NONE>	<NONE>
741	M93128	Mouse homeobox protein (EVX2) mRNA, complete cds.	0.059	<NONE>	<NONE>	<NONE>
742	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.059	1652318	(D90904) lysostaphin [Synechocystis sp.]	4.7
743	AB007920	Homo sapiens mRNA for KIAA0451 protein, complete cds	0.059	479491	transcription factor brn-3b - human	0.71
744	M60445	Human histidine decarboxylase (HDC) mRNA, complete cds	0.058	<NONE>	<NONE>	<NONE>
745	U01836	Ustilago maydis exodeoxyribonuclease (REC1) gene, complete cds.	0.058	1171908	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC >gi 1075086 pir D64184 oligopeptide transport system permease protein (oppC)C homolog - Haemophilus influenzae (strain Rd KW20) permease protein (oppC) [Haemophilus influenzae Rd]	1.5
746	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.058	3193265	(AF069131) chitinase [Bacillus subtilis]	0.002
747	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.057	433385	(U03978) dynein heavy chain isotype 7A [Tripneustes gratilla]	3.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Arabidopsis thaliana				
748	AJ005813	mRNA for neoxanthin cleavage enzyme	0.056	<NONE>	<NONE>	<NONE>
749	Y16828	Lagopus lagopus genomic microsatellite sequence, LLST4	0.056	3328678	(AE001299) hypothetical protein [Chlamydia trachomatis]	4.3
750	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.055	<NONE>	<NONE>	<NONE>
751	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.055	137339	69 KD PROTEIN >gi 94375 pir S19150 hypothetical protein, 69K - turnip yellow mosaic virus	0.69
752	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.035	<NONE>	<NONE>	<NONE>
753	M92069	Human retrovirus-like sequence-isoleucine c	0.034	<NONE>	<NONE>	<NONE>
754	S78516	GIL=ankyrin-like repeat [orf virus OV. NZ2. Genomic. 1608 nt]	0.033	2804465	(AF043700) contains similarity to human RNA-binding protein FUS/TLS (SW:Q28009) [Caenorhabditis elegans]	0.15
755	M15646	Chicken myosin alkali light chain mRNA, complete cds, clone pF1.	0.027	3334221	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]	6e-17
756	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.025	3877815	(Z96048) predicted using Genefinder	5.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
757	AJ002291	Streptococcus pneumoniae pbp1b gene, complete	0.025	3880487	(Z68014) similar to ribose-phosphate pyrophosphokinase; cDNA EST EMBL:D73173 comes from this gene; cDNA EST EMBL:D70909 comes from this gene; cDNA EST EMBL:D73449 comes from this gene; cDNA EST EMBL:D76167 comes from this ge...	1.7
758	X79104	C.botulinum (NCTC 7272 type A) HA-33 and P-21 genes.	0.024	2648615	(AE000970) tungsten formylmethanofuran dehydrogenase, subunit B (fwdB 2) [Archaeoglobus fulgidus]	6.1
759	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.024	1663698	(D83785) expressed ubiquitously; product similar to D.melanogaster mam protein. [Homo sapiens]	4.7
760	U36197	Chlamydomonas reinhardtii cobalamin-independent methionine synthase mRNA, complete cds	0.024	585723	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPAR-GAMMA) >gi 283818 pir C42214 peroxisome proliferator-activated receptor gamma chain - African clawed frog >gi 214668 (M84163) peroxisome proliferator activated receptor gamma [Xenopus laevis]	0.42
761	L38865	Macaca mulatta (clone MMVA63) T-cell receptor alpha (TCR A) mRNA, partial cds.	0.023	<NONE>	<NONE>	<NONE>
762	AF035948	Mus musculus insulin receptor substrate-3	0.023	2500587	SPLICEOSOME ASSOCIATED PROTEIN 49 spliceosome-associated protein SAP-49 - human >gi 536217	0.40
763	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.023	110072	proline-rich protein MP4 - mouse >gi 53182	0.18

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
764	X91212	L.esculentum mRNA for HD-ZIP protein	0.022	<NONE>	<NONE>	<NONE>
765	AC004498	Homo sapiens chromosome 5, P1 clone 1209C1 (LBNL H104), complete sequence [Homo sapiens]	0.022	<NONE>	<NONE>	<NONE>
766	U07083	Human prostatic acid phosphatase (ACPP) gene, exon 1	0.022	<NONE>	<NONE>	<NONE>
767	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.022	<NONE>	<NONE>	<NONE>
768	X56488	L.esculentum LAT59 gene 5'flanking region, expressed during pollen maturation	0.022	<NONE>	<NONE>	<NONE>
769	M34651	Pseudorabies virus with upstream and downstream sequences.	0.022	<NONE>	<NONE>	<NONE>
770	X66727	P.taeda gene for protochlorophyllide reductase	0.022	3878517	(Z92806) K10G4.4 [Caenorhabditis elegans]	4.3
771	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.022	1854452	(D89501) similar to salivary proline-rich protein P-B [Homo sapiens]	4.3
772	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.022	3021699	(AB005298) BAI 2 [Homo sapiens]	0.64
773	X71932	H.sapiens XB gene for tenascin-X, intron 14	0.022	627059	liver stage antigen LSA-1 - Plasmodium falciparum >gi 9916 (X56203) liver stage antigen	0.058
774	X87369	C.perfringens nanH gene & ORF1.2.3 & 4	0.022	2062407	(U78975) poly(ADP-ribose) glycohydrolase [Bos taurus]	0.056

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
775	Y14971	Gallus gallus mRNA for K60 protein	0.022	134091	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) >gi 85864 pir S02016 U1 snRNP 70K protein - African clawed frog >gi 65179 (X12430) U1 70K [Xenopus laevis]	0.032
776	AF003133	Caenorhabditis elegans cosmid T21E3	0.022	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-08
777	AF003133	Caenorhabditis elegans cosmid T21E3	0.022	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-08
778	U57645	Human helix-loop-helix proteins Id-1 (ID-1) and Id-1' (ID-1) genes, complete cds	0.021	<NONE>	<NONE>	<NONE>
779	U67570	Methanococcus jannaschii section 112 of 150 of the complete genome	0.021	<NONE>	<NONE>	<NONE>
780	L01584	Trypanosoma cruzi calcium-binding protein (CUB2.8) gene, complete cds.	0.021	<NONE>	<NONE>	<NONE>
781	L04787	Borrelia hermsii outer membrane lipoprotein	0.021	<NONE>	<NONE>	<NONE>
782	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
783	L36890	Saccharomyces cerevisiae mitochondrion transfer RNA-Thr1 (tRNA-Thr) gene; transfer RNA-Val (tRNA-Val) gene; oxi2 gene, complete cds; ORF2 and origin of replication (ori5).	0.021	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
784	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	0.021	<NONE>	<NONE>	<NONE>
785	M87504	Tetrahymena thermophila histone H3 (HHT2) gene, complete cds	0.021	<NONE>	<NONE>	<NONE>
786	U94346	Human calpain-like protease (htra-3) mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
787	L01584	Trypanosoma cruzi calcium-binding protein (CUB2.8) gene, complete cds.	0.021	<NONE>	<NONE>	<NONE>
788	U36530	Pongo pygmaeus CT microsatellite, clone #1, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus)	0.021	<NONE>	<NONE>	<NONE>
789	X03833	Human gene for interleukin 1 alpha (IL-1 alpha)	0.021	416974	EARLY TRANSCRIPTION FACTOR 70 KD SUBUNIT	8.9
790	U20806	Dictyostelium discoideum guanine nucleotide-binding protein alpha subunit 5 (G alpha 5) gene, complete cds.	0.021	1401211	(U58510) RNA helicase homolog [Chlorarachnion CCMP621]	8.8
791	Z59258	H.sapiens CpG DNA, clone 13d2, reverse read cpg13d2.rtlc.	0.021	3121732	ACONITATE HYDRATASE (CITRATE HYDRO-LYASE) (ACONITASE) >gi 2183256 (AF002133) aconitase [Mycobacterium avium]	7.0
792	AF030692	Plasmodium falciparum strain 7G8 chloroquine resistance candidate protein (cg2) gene, complete cds	0.021	3024190	NINE PROTEIN >gi 2120251 pir S66581 hypothetical protein 56 - phage S2 >gi 1051114 (X92588) orf56; related to nin60 (ninE) of bacteriophage lambda	5.8
793	U67570	Methanococcus jannaschii section 112 of 150 of the complete genome	0.021	2341037	(AC000104) F19P19.17 [Arabidopsis thaliana]	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
794	D86566	Human DNA for NOTCH4, partial cds	0.021	1708619	NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT-10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT]	3.1
795	L11648	Streptomyces coelicolor sigma factor (rpoX) gene, complete cds.	0.021	79833	hypothetical 119.5K protein (uvrA region) - Micrococcus luteus	1.8
796	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.021	128000	NEUROENDOCRINE CONVERTASE 1 PRECURSOR (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) propeptide processing protease [Mus cookii]	1.0
797	U30938	Rattus norvegicus microtubule-associated protein 2	0.021	468600	(X74416) beta-3 integrin [Takifugu rubripes]	1.0
798	D82364	Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52	0.021	693723	27 kda amelogenin {alternatively spliced}	0.61
799	U40041	Gallus gallus eHAND mRNA, complete cds	0.021	3449308	(AB011541) MEGF8 [Homo sapiens]	0.21
800	X71932	H.sapiens XB gene for tenascin-X, intron 14	0.021	627059	liver stage antigen LSA-1 - Plasmodium falciparum >gi 9916 (X56203) liver stage antigen	0.054
801	AF042333	Oryza sativa 24-methylene lophenol C24(1)methyltransferase mRNA, complete cds	0.021	854065	(X83413) U88 [Human herpesvirus 6]	0.014
802	L37380	Rat apical endosomal glycoprotein mRNA, complete cds.	0.021	3334377	TRANSMEMBRANE PROTEASE, SERINE 2	1e-05
803	AF003133	Caenorhabditis elegans cosmid T21E3	0.021	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	3e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rabbit mRNA for				
804	X57689	calcium channel BI-2 (lambda CBP109 and CB101)	0.021	2959370	(AL022117) hypothetical protein	1e-10
805	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.021	1109830	(U41534) coded for by C. elegans cDNA CEES142F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	5e-11
806	X77753	H.sapiens TROP-2 gene	0.021	1723657	HYPOTHETICAL 38.5 KD PROTEIN IN ERV1-GLS2 INTERGENIC REGION >gi 2132587 pir S64322 probable membrane protein YGR031w - yeast (Saccharomyces cerevisiae) >gi 1323010 gnl PID e243277 (Z72816) ORF YGR031w [Saccharomyces cerevisiae]	5e-11
807	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.021	2137872	zinc finger protein PZF - mouse >gi 453376	2e-19
808	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
809	AJ224935	Homo sapiens Promotor Region and PCK2 gene	0.020	<NONE>	<NONE>	<NONE>
810	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
811	X99941	A.thaliana GBF1 gene	0.020	<NONE>	<NONE>	<NONE>
812	X65138	M.musculus mRNA for tyrosine kinase > :: gb S57168 S57168 Sek=Eph-related receptor protein tyrosine kinase [mice. mRNA, 4242 nt]	0.020	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
813	L04787	Borrelia hermsii outer membrane lipoprotein	0.020	<NONE>	<NONE>	<NONE>
814	AJ223633	Enterococcus faecium genes encoding enterocin L50A and enterocin L50B plus 5' and 3' flanking regions	0.020	<NONE>	<NONE>	<NONE>
815	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.020	<NONE>	<NONE>	<NONE>
816	AE001539	Helicobacter pylori, strain J99 section 100 of 132 of the complete genome	0.020	172292	(L11895) transmembrane protein [Saccharomyces cerevisiae]	8.4
817	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	94173	pol polypeptide - Chinese hamster intracisternal A-particle CHIAP34	8.0
818	M55264	Herpesvirus saimiri dihydrofolate reductase (DHFR) and snRNA (HSUR) genes, complete cds.	0.020	2924250	(Z98745) dJ29K1.2 [Homo sapiens]	6.5
819	AF052163	Homo sapiens clone 24456 mRNA sequence	0.020	1706288	D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR) >gi 2119482 pir I49246 D4 dopamine receptor - mouse >gi 758427 (U19880) D4 dopamine receptor [Mus musculus] >gi 1095539 prf 2109259A dopamine D4 receptor [Mus musculus]	4.9
820	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	2113798	(Z83259) AmphiBrf38 [Branchiostoma floridae]	4.7
821	AF052163	Homo sapiens clone 24456 mRNA sequence	0.020	3874733	(Z67754) cDNA EST EMBL:T02354 comes from this gene; cDNA EST EMBL:D32698 comes from this gene; cDNA EST EMBL:D35411 comes from this gene	4.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
822	L11002	Rat ankyrin binding glycoprotein-1 related mRNA sequence.	0.020	552132	(K01664) Bkm-like protein [Drosophila melanogaster]	3.8
823	AE001539	Helicobacter pylori, strain J99 section 100 of 132 of the complete genome	0.020	172292	(L11895) transmembrane protein [Saccharomyces cerevisiae]	3.8
824	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.020	3879798	(Z01120) similar to TFR Domain (2 domains); cDNA EST yk390b10.3 comes from this gene; cDNA EST EMBL:D71652 comes from this gene; cDNA EST yk275f8.3 comes from this gene; cDNA EST yk393b9.3 comes from this gene; cDNA EST yk37... >gi 3880220 gnl PID e 1349842 yk390b10.3 comes from this gene; cDNA EST EMBL:D71652 comes from this gene; cDNA EST yk275f8.3 comes from this gene; cDNA EST yk393b9.3 comes from this gene; cDNA EST yk37...	1.3
825	U97519	Homo sapiens podocalyxin-like protein mRNA, complete cds	0.020	1345633	C1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE C1-tetrahydrofolate synthase [Rattus norvegicus]	0.066
826	AF003133	Caenorhabditis elegans cosmid T21E3	0.020	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-07
827	U32857	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence	0.019	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					NEUROGENIC LOCUS	
828	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.019	2506381	NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) mammary gene mRNA, complete cds.], gene product [Mus musculus]	3.3
829	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.019	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T008...	6e-15
830	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.018	<NONE>	<NONE>	<NONE>
831	U24578	Human RP1 and complement C4B precursor (C4B) genes, partial cds.	0.013	478673	proline-rich protein precursor - kidney bean vulgaris]	3.1
832	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.011	<NONE>	<NONE>	<NONE>
833	U57649	Dibenzofuran-degrading bacterium DPO360 2,3-dihydroxybiphenyl 1,2-dioxygenase (bphC) gene, complete cds and 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid hydrolase	0.011	<NONE>	<NONE>	<NONE>
834	X15642	Z.mays gene for phosphoenolpyruvate carboxylase	0.011	<NONE>	<NONE>	<NONE>
835	X51623	C.elegans collagen gene col-13	0.010	1695686	(D83706) pyruvate carboxylase [Bacillus stearothermophilus]	3.1
836	U83656	Rattus norvegicus NF-KB gene, promotor region	0.008	4240195	(AB020660) KIAA0853 protein [Homo sapiens]	10.0

232

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
837	AJ222657	Homo sapiens gene encoding retina-specific guanylyl cyclase	0.008	417704	POL POLYPROTEIN (ORF1A/1B) [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; HELICASE; PROTEASE]	7.4
838	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.008	544024	CHLORIDE CHANNEL PROTEIN, SKELETAL MUSCLE (CHLORIDE CHANNEL PROTEIN 1) (CLC-1) human >gi 397143 (Z25587) human CIC-1 muscle chloride channel [Homo sapiens] >gi 398161 (Z25884) human CIC-1 muscle chloride channel [Homo sapiens]	4.6
839	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.008	532468	(U13643) similar to reverse transcriptase; possible pseudogene [Caenorhabditis elegans]	3.8
840	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.008	4101160	(AF002589) cytochrome oxidase I [Austrofundulus limnaeus]	2.7
841	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.008	1711520	SRB-8/9 PROTEIN >gi 1334996	1.6
842	U48734	Human non-muscle alpha-actinin mRNA, complete cds	0.008	2829922	(AC002291) extensin [Arabidopsis thaliana]	0.11
843	U66669	Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
844	D16492	Mouse mRNA for P100 serine protease of Ra-reactive factor (RaRF), complete cds	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human				
845	D90923	immunodeficiency virus type 1 proviral DNA for envelope glycoprotein, partial cds. isolate 03S	0.007	<NONE>	<NONE>	<NONE>
846	AB011087	Homo sapiens mRNA for KIAA0515 protein, partial cds	0.007	<NONE>	<NONE>	<NONE>
847	AE000688	Aquifex aeolicus section 20 of 109 of the complete genome	0.007	<NONE>	<NONE>	<NONE>
848	X63723	B.bovis WC1.1 mRNA	0.007	<NONE>	<NONE>	<NONE>
849	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
850	J00097	Human beta globin region Alu repetitive sequence type T.	0.007	<NONE>	<NONE>	<NONE>
851	D90923	Human immunodeficiency virus type 1 proviral DNA for envelope glycoprotein, partial cds. isolate 03S	0.007	<NONE>	<NONE>	<NONE>
852	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
853	X91618	T.castaneum hunchback gene	0.007	<NONE>	<NONE>	<NONE>
854	X03838	Rat nontranscribed spacer (NTS) downstream of 28S rRNA gene	0.007	<NONE>	<NONE>	<NONE>
855	M55049	Rattus norvegicus interleukin-2 receptor alpha chain (CD25) mRNA, complete cds.	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
856	Z64318	H.sapiens CpG DNA, clone 9e2, reverse read cpg9e2.r1a	0.007	<NONE>	<NONE>	<NONE>
857	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
858	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
859	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
860	X95276	P.falciparum complete gene map of plastid-like DNA	0.007	<NONE>	<NONE>	<NONE>
861	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
862	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
863	AB000383	Leucania seperata nuclear polyhedrosis virus DNA for p13, xe, envelope protein, complete cds	0.007	<NONE>	<NONE>	<NONE>
864	D86566	Human DNA for NOTCH4, partial cds	0.007	<NONE>	<NONE>	<NONE>
865	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
866	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	3047072	(AF058825) No definition line found [Arabidopsis thaliana]	8.9
867	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.007	975754	(U29359) SpaO [Salmonella enterica]	8.6
868	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	1213557	(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c...	8.4
869	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	2499568	PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL/D-ASPARTYL METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] >gi 1171337 melanogaster]	8.3
870	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.007	4092077	(AF095353) toll-like receptor 4 mutant [Mus musculus]	6.2
871	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	151377	(M80653) tetraheme [Pseudomonas stutzeri]	6.2
872	L42319	Bos taurus (clone Sal3.8) tristetrapiroline	0.007	2507337	TRANSCRIPTION TERMINATION FACTOR RHO	5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
873	M59815	Human complement component C4A gene, exons 10 through 41.	0.007	3876769	(Z69637) Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HUMAN); cDNA EST yk219g12.5 comes from this gene; cDNA EST yk319d8.5 comes from this gene; cDNA EST yk339d11.5 comes from this gene; cDNA EST yk371c9.3...	5.3
874	X63723	B.bovis WC1.1 mRNA	0.007	2969893	(AJ001858) human SIM2 [Homo sapiens]	5.3
875	AB009864	Expression vector pME18S-FL3, complete sequence	0.007	2137618	p45 NF-E2 related factor 2 - mouse musculus]	5.1
876	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	2804497	(AF043705) contains similarity to C2H2-type zinc fingers	5.0
877	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.007	440298	(L27469) product of alternative splicing [Drosophila melanogaster]	4.7
878	X58869	Chicken mRNA for aldehyde dehydrogenase	0.007	1185062	(L75945) flagellar export protein [Borrelia burgdorferi]	4.1
879	AF027735	Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds	0.007	2394390	(AF017434) pmi-like gene product [Methylobacterium extorquens]	4.0
880	AF105228	Bos taurus tuftelin mRNA, complete cds	0.007	3036802	(AL022373) putative protein HYPOTHETICAL 60.2 KD PROTEIN T27F2.1 IN CHROMOSOME V >gi 3880311 gn PID e1349855 BX42 (SW:BX42_DROME); cDNA EST EMBL:C07233 comes from this gene; cDNA EST EMBL:C08532 comes from this gene; cDNA EST yk501h10.3 comes from this gene; cDNA EST yk501f1.3...	3.9
881	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.007	2500814		3.8

237

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
882	X93567	L.major mRNA for beta-tubulin (1404bp)	0.007	2317862	(U78289) ty lactone synthase modules 4 & 5 [Streptomyces fradiae]	3.0
883	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	3881103	(AL032646) predicted using Genefinder; cDNA EST EMBL:D76407 comes from this gene; cDNA EST EMBL:C08999 comes from this gene; cDNA EST yk199b12.5 comes from this gene; cDNA EST yk282a4.5 comes from this gene; cDNA EST EMBL:C0...	2.7
884	AF041056	Homo sapiens WSCR4 gene, exons 3 and 4	0.007	135817	THROMBIN RECEPTOR PRECURSOR human >gi 339677 (M62424) thrombin receptor [Homo sapiens]	2.2
885	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.007	1723518	HYPOTHETICAL 32.2 KD PROTEIN C22E12.04 IN CHROMOSOME I >gi 1220279 (Z70043) unknown	2.1
886	M74798	Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene, 3' end.	0.007	1001282	(D64003) polyA polymerase HYPOTHETICAL 111.9 KD PROTEIN C34E10.8 IN CHROMOSOME III >gi 500731 (U10402) weakly similar to protein C kinase substrate [Caenorhabditis]	1.9
887	Z62997	H.sapiens CpG DNA, clone 76g11, reverse read cpg76g11.rtl.a.	0.007	1176532	DVA-I POLYPROTEIN PRECURSOR nematode polyprotein antigen precursor [Dictyocaulus viviparus] >gi 1585421 prf 2124414A polyprotein antigen/allergen [Dictyocaulus viviparus]	1.8
888	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	2498317	(AB018320) KIAA0777 protein [Homo sapiens]	1.2
889	L29426	Synechocystis species (strain PCC 6803) drg-A gene, complete cds.	0.007	3882275		1.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
890	D83329	Mus musculus DNA for prostaglandin D2 synthase, complete cds	0.007	1001741	(D64004) hypothetical protein	0.97
891	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	1723928	HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR YGL149w - yeast (Saccharomyces	0.94
892	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	121452	GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR >gi 82606 pir A24266 glutenin high molecular weight chain 12 precursor - wheat >gi 21779	0.79
893	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	927287	(U30294) ORF2 [Prevotella ruminicola]	0.35
894	Y11918	H.sapiens IMAGE cDNA clone 26881	0.007	1055188	(U40061) contains similarity to transmembrane domains like those found in sugar transporter proteins	0.26
895	L36827	Mus Musculus alphaA-crystallin-binding protein I	0.007	4063019	(AF083061) ABC transporter TliF [Pseudomonas fluorescens]	0.21
896	L36827	Mus Musculus alphaA-crystallin-binding protein I	0.007	4063019	(AF083061) ABC transporter TliF [Pseudomonas fluorescens]	0.20
897	Z65719	H.sapiens CpG DNA, clone 54c10, reverse read cpg54c10.rt1a.	0.007	1097307	HIC-1 gene [Homo sapiens]	0.20
898	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.007	1174915	UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) >gi 284488 pir S28381 utrophin protein) [Homo sapiens]	0.002
899	AF051730	Mus musculus cathepsin S (CatS) gene, exon 6	0.007	1707017	(U78721) RNA helicase isolog [Arabidopsis thaliana]	0.001

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Oryctolagus				
900	U62398	cuniculus gp42/basigin/OX-47/HT7 mRNA, complete cds.	0.007	2370494	(Z98944) hypothetical protein	2e-04
901	X76341	M.musculus glutathione reductase mRNA.	0.007	3513303	(AC005594) R26984_1 [Homo sapiens]	8e-07
902	M26215	Rat (lambda 20B0.5) M-type 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase	0.007	3036809	(AL022373) putative protein (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]	6e-15
903	AB007902	Homo sapiens KIAA0442 mRNA, partial cds	0.007	2662165		2e-17
904	U93364	Lactococcus lactis cremoris plasmid pNZ4000 insertion sequence IS982 putative transposase gene and eps gene cluster (epsRXABCDEFGH IJKL), complete cds	0.007	2731377	(U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]	1e-31
905	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
906	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
907	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
908	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
909	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
910	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
911	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
912	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
913	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	<NONE>	<NONE>	<NONE>
914	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
915	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
916	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	4049856	(AF063866) ORF MSV064 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	9.6
917	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	3880536	(Z82070) predicted using Genefinder; similar to Lectin C-type domain short and long forms (2 domains); cDNA EST EMBL:C10633 comes from this gene; cDNA EST EMBL:C12424 comes from this gene; cDNA EST yk191e7.3 comes from this ...	7.9
918	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	3877761	(Z81552) F56G4.1 [Caenorhabditis elegans] >gi 3878615 gnl PID e1348240 (Z83118) F56G4.1	7.5
919	X80289	H.sapiens PTPL1 mRNA for protein tyrosine phosphatase	0.006	1168791	CATHEPSIN E PRECURSOR precursor - rabbit >gi 402729 (L08418) procathepsin E	7.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
920	AF074386	<i>Sambucus nigra</i> hevein-like protein mRNA, complete cds	0.006	1346371	DIACYLGLYCEROL KINASE, BETA DIACYLGLYCEROL KINASE) >gi 477059 pir A47744 diacylglycerol kinase (EC 2.7.1.107) beta - rat 90kDa-diacylglycerol kinase [Rattus	5.5
921	U72396	<i>Lycopersicon esculentum</i> class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.006	2196567	(D88588) lipoprotein [Escherichia coli]	4.3
922	AF074387	<i>Sambucus nigra</i> hevein-like protein mRNA, complete cds	0.006	2113798	(Z83259) AmphiBrf38 [Branchiostoma floridae]	4.3
923	AB012106	<i>Brassica rapa</i> mRNA for SRK45, complete cds	0.006	1388166	(U58282) Bowel [Drosophila melanogaster]	4.3
924	AF074386	<i>Sambucus nigra</i> hevein-like protein mRNA, complete cds	0.006	2496785	HYPOTHETICAL 20.1 KD PROTEIN Y4YS	4.2
925	AF012899	<i>Sambucus nigra</i> ribosome inactivating protein precursor mRNA, complete cds	0.006	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi 101170 pir A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	2.7
926	AF064029	<i>Helianthus tuberosus</i> lectin 1 mRNA, complete cds	0.006	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi 101170 pir A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	2.5
927	AJ005813	<i>Arabidopsis thaliana</i> mRNA for neoxanthin cleavage enzyme	0.006	3258584	(U41263) The 3' UTR of this gene overlaps the 3' UTR of T19D12.6(confirmed by EST hits) [Caenorhabditis elegans]	2.0
928	U33949	Human Down Syndrome region of chromosome 21, genomic sequence, clone A12H1-1A6.	0.006	3850997	(AF067150) beta-hydroxyacyl-ACP dehydratase precursor	1.9

242

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1175	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1176	Y09232	H.sapiens fertilin alpha pseudogene	2e-04	<NONE>	<NONE>	<NONE>
1177	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<NONE>	<NONE>	<NONE>
1178	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1179	AF072847	Homo sapiens putative swelling-activated chloride channel (CLNS1A) gene, intron 6	2e-04	<NONE>	<NONE>	<NONE>
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1181	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1182	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	1213557	(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c...	8.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1183	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	729008	EPITHELIAL DISCOIDIN DOMAIN RECEPTOR I PRECURSOR (TYROSINE- PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (TRK E) (PROTEIN-TYROSINE KINASE RTK 6) sapiens]	8.3
1184	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA. complete cds	2e-04	2507582	HYPOTHETICAL 138.1 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION >gi 1788436 (AE000300) putative regulator [Escherichia coli]	7.8
1185	AF074386	Sambucus nigra hevein-like protein mRNA. complete cds	2e-04	1085500	collagen alpha 1(IX) chain - mouse musculus] >gi 744962 prf 2015346A collagen:SUBUNIT=alpha1:ISO TYPE=IX [Mus musculus]	7.8
1186	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath- A) mRNA, complete cds	2e-04	2623967	(Y13942) GTN Reductase [Agrobacterium radiobacter]	7.4
1187	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	2497316	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS) products receptor precursor - bovine >gi 163651 (M91212) receptor for advanced glycosylation end products [Bos taurus]	5.3
1188	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath- B) mRNA, complete cds	2e-04	1001710	(D64004) hypothetical protein	3.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1189	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	3258584	(U41263) The 3' UTR of this gene overlaps the 3' UTR of T19D12.6(confirmed by EST hits) [Caenorhabditis elegans]	2.1
1190	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	2736338	(AF038623) contains similarity to RNA recognition motifs	0.89
1191	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	2e-04	2196567	(D88588) lipoprotein [Escherichia coli]	0.69
1192	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	3319874	(AJ006096) F-spondin [Branchiostoma floridae]	5e-04
1193	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha (ODA11) gene, exons 2-15, and partial cds.	2e-04	3876775	(Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531)	2e-09
1194	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1195	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1196	L34219	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds.	1e-04	<NONE>	<NONE>	<NONE>
1197	X51890	Rhesus monkey interleukin-3 gene	1e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
1198	AE001421	falciparum chromosome 2, section 58 of 73 of the complete sequence	1e-04	<NONE>	<NONE>	<NONE>
1199	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1200	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1e-04	2576287	(Y15086) HepC protein [Cylindrotheca fusiformis]	4.7
1201	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	1e-04	3395673	(AB016623) RWC-3 [Oryza sativa]	0.14
1202	AF038035	Homo sapiens BRCA1-associated RING domain protein (BARD1) gene, exons 2 and 3	9e-05	<NONE>	<NONE>	<NONE>
1203	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	9e-05	<NONE>	<NONE>	<NONE>
1204	AB012106	Brassica rapa mRNA for SRK45, complete cds	9e-05	<NONE>	<NONE>	<NONE>
1205	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	9e-05	<NONE>	<NONE>	<NONE>
1206	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	9e-05	1351553	HYPOTHETICAL LIPOPROTEIN MG348 PRECURSOR >gi 1361668 pir E64238 hypothetical protein MG348 - Mycoplasma genitalium (SGC3) >gi 3844931	8.8

246

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1207	D50006	Human DNA for alpha-platelet-derived growth factor receptor, exon 6-10	9e-05	3063639	(AF056494) NADH dehydrogenase subunit 5 [Panorpa japonica]	5.1
1208	U50423	Human Down Syndrome region of chromosome 21, clone A41B8-1B7.	9e-05	124273	INHIBIN ALPHA CHAIN PRECURSOR bovine >gi163195 (M13273) inhibin A subunit [Bos taurus]	3.0
1209	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	9e-05	4007782	(X72850) 2,4-dihydroxybenzoate monooxygenase [Sphingomonas sp.]	2.3
1210	AC005276	Homo sapiens clone fragment UWGC:gap3 from 7q31.3, complete sequence [Homo sapiens]	9e-05	1492075	(U60315) MC132L [Molluscum contagiosum virus subtype 1]	1.0
1211	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-05	2887423	(AB007884) KIAA0424 [Homo sapiens]	2e-10
1212	X77772	C.fuscus gamma-M2-1 crystallin mRNA.	9e-05	2072425	(U83115) non-lens beta gamma-crystallin like protein [Homo sapiens]	7e-25
1213	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1214	L06178	Apis mellifera ligustica complete mitochondrial genome	8e-05	<NONE>	<NONE>	<NONE>
1215	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1216	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1217	L06178	Apis mellifera ligustica complete mitochondrial genome	8e-05	<NONE>	<NONE>	<NONE>
1218	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1219	AF100694	Pontin52 mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1220	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1221	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	1722841	WNT-11 PROTEIN PRECURSOR (XWNT-11) clawed frog >gi 439108 (L23542) maternal protein	9.9
1222	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	1205991	(U35637) nebulin [Homo sapiens]	9.6
1223	AF024605	Homo sapiens serine protease-like protease Sequence 2 from patent US 5736377	8e-05	3242783	(AF055354) respiratory burst oxidase protein B	8.6
1224	Y13148	Rattus norvegicus mRNA for PAG608 gene	8e-05	2314243	(AE000616) alpha-ketoglutarate permease (kgtP)	8.1
1225	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	8e-05	1170586	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195) (K1AA0051) >gi 627594 pir A54854 Ras GTPase activating-related protein - human sapiens] >gi 536844 (L33075) ras GTPase-activating-like protein [Homo sapiens]	7.8
1226	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	464239	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 1085185 pir S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SGC4) >gi 552446 (L06178) NADH dehydrogenase subunit 4 [Apis mellifera ligustica]	3.5
1227	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	544353	F-SPONDIN PRECURSOR	3.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1228	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-05	483243	apolipoprotein B-100 - chicken (fragment)	3.4
1229	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-05	91207	proline-rich protein - mouse (fragment) musculus]	2.2
1230	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	2499181	ZONADHESIN PRECURSOR >gi 1066466	2.2
1231	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	2499181	ZONADHESIN PRECURSOR >gi 1066466	1.9
1232	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	2833647	(AF027972) flagelliform silk protein [Nephila clavipes]	1.6
1233	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-05	1163063	(Z49821) MYO2 [Saccharomyces cerevisiae]	0.90
1234	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	1653488	(D90914) hypothetical protein	0.30
1235	M26510	Chicken nonmuscle myosin heavy chain (MHC) gene, complete cds.	8e-05	112159	plectin - rat	0.003
1236	U56402	Human chromatin structural protein homolog	8e-05	2088823	(AF003384) weak similarity to the peptidase family A2	1e-13
1237	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	437181	(U02289) GTPase-activating protein [Caenorhabditis elegans]	2e-17
1238	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	465983	HYPOTHETICAL 80.8 KD PROTEIN ZC21.4 IN CHROMOSOME III	8e-27

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1239	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	7e-05	<NONE>	<NONE>	<NONE>
1240	U83656	Rattus norvegicus NF-KB gene, promotor region	7e-05	3880858	(AL031633) predicted using Genefinder; cDNA EST yk304f12.5 comes from this gene [Caenorhabditis elegans]	9.3
1241	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-05	3080538	(AL022600) hypothetical protein	9.2
1242	X89398	H.sapiens ung gene for uracil DNA-glycosylase	7e-05	549700	HYPOTHETICAL 23.7 KD PROTEIN IN MDH1-VMA5 INTERGENIC REGION >gi 539182 pir S37908 hypothetical protein YKL083w - yeast (Saccharomyces cerevisiae) >gi 486120 (Z28082) ORF YKL083w	1.8
1243	M83753	Bovine follicle stimulating hormone-beta subunit gene, complete cds.	7e-05	2398621	(AJ000342) DMBT1 protein, 5.8 kb transcript [Homo sapiens]	1.8
1244	M80829	Rat troponin T cardiac isoform gene, complete cds	5e-05	854065	(X83+13) U88 [Human herpesvirus 6]	2e-08
1245	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	4e-05	120240	FLAGELLIN B2 PRECURSOR Methanococcus voltae >gi 150063 (M72148) flagellin	5.2
1246	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1247	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1248	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rattus norvegicus				
1249	AF093268	homer-1c mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1250	AB012106	Brassica rapa mRNA for SRK45, complete cds	3e-05	2773226	(AF039716) Similar to protein kinase [Caenorhabditis elegans]	6.7
1251	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2072961	(U93568) putative p150 [Homo sapiens]	5.6
1252	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-05	121855	EXOGLUCANASE II PRECURSOR cellulose 1,4-beta cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus cellobiohydrolase II [Trichoderma reesei]	4.6
1253	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	3880516	(AL021572) similar to CTP SYNTHASE (EC 6.3.4.2) (UTP-AMMONIA LIGASE) (CTP SYNTHETASE)	3.3
1254	M88299	Mouse brain-1 POU-domain protein, complete cds	3e-05	1947048	(U66102) intimin [Escherichia coli]	3.0
1255	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	3e-05	3122872	CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA (S/G2 NUCLEAR ANTIGEN) >gi 1082650 pir JC2522 nuclear autoantigen - human >gi 805095 (U17989) GS2NA	2.8
1256	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	1352145	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - Thermus aquaticus >gi 155083 (M84341) cytochrome c oxidase subunits precursor [Thermus thermophilus]	2.6
1257	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-05	2811015	SEGMENTATION POLARITY PROTEIN ENGRAILED >gi 2076747 (U42429) engrailed [Anopheles gambiae] >gi 2148918 (U42214) engrailed [Anopheles gambiae]	2.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1258	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	3e-05	1657752	(U62325) FE65-like protein [Homo sapiens]	1.7
1259	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2072961	(U93568) putative p150 [Homo sapiens]	1.5
1260	U76523	Sambucus nigra lectin precursor mRNA, complete cds	3e-05	1352145	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - Thermus aquaticus >gi 155083 (M84341) cytochrome c oxidase subunits precursor [Thermus thermophilus]	1.1
1261	X91890	H.sapiens regulatory region of HOXA7 gene	3e-05	111013	Sxr (Bkm-homolog) sex-determining region protein - mouse	1.0
1262	L36936	Homo sapiens metase gene, partial cds.	3e-05	1944352	(D84239) IgG Fc binding protein [Homo sapiens]	0.99
1263	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-05	417782	SMP2 PROTEIN >gi 320853 pir S30911 SMP2 protein - yeast (Saccharomyces cerevisiae) gene [Saccharomyces cerevisiae]	0.89
1264	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	1708501	INTEGRIN ALPHA CHAIN-LIKE PROTEIN alpha Int1p [Candida albicans]	0.39
1265	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-05	1587031	cis-Golgi matrix protein GM130 [Rattus norvegicus]	0.20
1266	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-05	2072964	(U93569) putative p150 [Homo sapiens]	0.049

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					glycosylated and myristilated	
1267	Z96668	H.sapiens telomeric DNA sequence, clone 7PTELO01, read 7PTELOO001.seq	3e-05	542429	smaller surface antigen - Plasmodium falciparum >gi 836640 (X76298) glycosylated and myristilated smaller surface antigen gallus] >gi 1092178 prf 2023165B surface antigen	0.029
1268	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-05	3879121	(Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES...	2e-13
1269	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	3e-05	2497677	ZYXIN (ZYXIN 2) sapiens] >gi 1545954 gn PID e223417 (X95735) zyxin	2e-23
1270	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1e-05	<NONE>	<NONE>	<NONE>
1271	X16318	Canine mRNA for signal recognition particle 54k protein	1e-05	3122612	PITUITARY HOMEBOX 3 (HOMEBOX PROTEIN PITX3) >gi 2645427 (AF005772) homeobox protein Pitx3 [Mus musculus]	4.4
1272	AB012105	Brassica rapa mRNA for SLG45, complete cds	1e-05	1652458	(D90905) DNA mismatch repair protein MutL [Synechocystis sp.]	0.62

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1273	U57843	Human phosphatidylinositol 3-kinase delta catalytic subunit mRNA, complete cds	1e-05	475909	(X67098) ORF1A [Homo sapiens]	0.22
1274	Z96569	H.sapiens telomeric DNA sequence, clone 2QTELO54, read 2QTELOO054.seq	1e-05	2137043	unknown protein - rabbit (fragment) cuniculus]	0.005
1275	AE000810	Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome	1e-05	3877579	(Z62271) Summary to Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes... Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes...	6e-27
1276	AB012113	Homo sapiens gene for CC chemokine PARC precursor, complete cds	9e-06	<NONE>	<NONE>	<NONE>
1277	AC005830	Homo sapiens Xp22-154-155 BAC GSHB-52411 (Genome Systems Human BAC Library), complete sequence [Homo sapiens]	9e-06	<NONE>	<NONE>	<NONE>
1278	D86245	Human MHC (HLA) DRB intron 1 DNA, partial sequence	9e-06	1051253	(U37531) mucin apoprotein [Mus musculus]	1.3
1279	D79998	Human mRNA for KIAA0176 gene, partial cds	9e-06	2833253	HYPOTHETICAL PROTEIN KIAA0176 sapiens]	4e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(Z69635) Similarity to Yeast	
1280	U10246	Toxoplasma gondii RH uracil phosphoribosyl transferase gene, complete cds.	9e-06	3876090	uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-33
1281	U10246	Toxoplasma gondii RH uracil phosphoribosyl transferase gene, complete cds.	9e-06	3876090	(Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-34
1282	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-06	<NONE>	<NONE>	<NONE>
1283	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-06	<NONE>	<NONE>	<NONE>
1284	U66340	Human Rh blood group C antigen (RHCE) gene, exon 2, partial cds	8e-06	1707155	(U80837) F07E5.6 gene product [Caenorhabditis elegans]	9.6
1285	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-06	<NONE>	<NONE>	<NONE>
1286	M29930	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17.	4e-06	<NONE>	<NONE>	<NONE>
1287	L42103	Homo sapiens (subclone 5_d3 from P1 H25) DNA sequence.	3e-06	<NONE>	<NONE>	<NONE>

255

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1288	AF012244	cerberus-like (Cer-1) gene, complete cds	3e-06	<NONE>	<NONE>	<NONE>
1289	Z69366	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST.	3e-06	<NONE>	<NONE>	<NONE>
1290	Z69366	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST.	3e-06	<NONE>	<NONE>	<NONE>
1291	X85232	H.sapiens chromosome 3 sequences	3e-06	<NONE>	<NONE>	<NONE>
1292	M32674	Human platelet glycoprotein IIIa, exons 7, 8 and 9.	3e-06	<NONE>	<NONE>	<NONE>
1293	D16879	Human HepG2 3' region cDNA, clone hmd2a01	3e-06	998296	(U33484) ependymin [Hemiodus sp.]	5.6
1294	U18614	Lagothrix lagotricha interphotoreceptor retinoid-binding protein (IRBP) gene, intron 1, complete sequence	3e-06	1613846	(U71440) polyprotein [Rice tungro spherical virus]	5.0
1295	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-06	1477646	(U53204) plectin [Homo sapiens] >gi 1477651 (U63610) plectin [Homo sapiens]	4.0
1296	AF016898	Homo sapiens B-ATF gene, complete cds	3e-06	1085177	reverse transcriptase - fruit fly reverse transcriptase [Drosophila yakuba]	3.0
1297	AB018490	Homo sapiens DNA, trinucleotide repeats region	3e-06	3876572	(Z81522) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain) [Caenorhabditis elegans]	3.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1298	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	3e-06	4240137	(AB020631) KIAA0824 protein [Homo sapiens]	2.7
1299	M37929	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 11-12.	3e-06	1653775	(D90916) thiol:disulfide interchange protein DsbD [Synechocystis sp.]	1.7
1300	M37929	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 11-12.	3e-06	1653775	(D90916) thiol:disulfide interchange protein DsbD [Synechocystis sp.]	1.7
1301	U60496	Glycine max actin (Soy86) gene, partial cds	3e-06	1730738	ACTIN-LIKE PROTEIN ARP5 Ynl2430p [Saccharomyces cerevisiae]	2e-05
1302	X14363	Yersinia pseudotuberculosis rplC, rplD, rplW, rplB and rpsS genes for ribosomal proteins L3, L4, L23, L2 and S19	3e-06	585879	50S RIBOSOMAL PROTEIN L2 maritima >gi 437926 (Z21677) ribosomal protein L2	2e-12
1303	Z34969	H.sapiens DNA for microsatellite polymorphism	2e-06	<NONE>	<NONE>	<NONE>
1304	X64707	H.sapiens BBC1 mRNA	1e-06	<NONE>	<NONE>	<NONE>
1305	AC005830	Homo sapiens Xp22-154-155 BAC GSHB-524I1 (Genome Systems Human BAC Library), complete sequence [Homo sapiens]	1e-06	<NONE>	<NONE>	<NONE>
1306	J04058	Human electron transfer flavoprotein alpha-subunit mRNA, complete cds.	1e-06	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1307	L25647	Homo sapiens fibroblast growth factor receptor gene (located in the central MHC) signal peptide and consecutive exon	1e-06	1586734	mxcQ gene [Methylobacterium organophilum]	5.4
1308	L26261	Human MHC class III HLA-RP1 gene.	1e-06	1684985	(U20633) NADH dehydrogenase subunit [Neuwiedia veratrifolia]	1.8
1309	AF002283	Mus musculus alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds	1e-06	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-17
1310	M10935	Human haptoglobin gene (alpha-2 allele), complete cds and haptoglobin-related gene, exon 1 and three Alu repeats.	6e-07	<NONE>	<NONE>	<NONE>
1311	AC002251	Homo sapiens (subclone 1_g6 from BAC H76) DNA sequence	4e-07	2144491	coagulation factor Xa (EC 3.4.21.6) precursor norvegicus]	4.2
1312	AF047717	Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds	4e-07	699196	(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]	1e-06
1313	U14417	Human Ral guanine nucleotide dissociation stimulator mRNA, partial cds.	4e-07	544402	GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) >gi 321257 pir S28415 guanine nucleotide dissociation stimulator ralGDS - mouse >gi 193573 (L07924) guanine nucleotide dissociation stimulator [Mus musculus]	8e-08
1314	Z79027	H.sapiens flow-sorted chromosome 6 HindIII fragment. SC6pA20G8	3e-07	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1315	U67167	intestinal mucin (MUC2) gene, promoter region and partial cds	3e-07	<NONE>	<NONE>	<NONE>
1316	AF086256	Homo sapiens full length insert cDNA clone ZD41C11	3e-07	<NONE>	<NONE>	<NONE>
1317	U67228	Human clone HS4.61 Alu-Ya5 sequence	3e-07	1938437	(U97003) contains similarity to C4-type zinc fingers and a ligand-binding domain of nuclear hormone receptors	2.3
1318	U94346	Human calpain-like protease (htra-3) mRNA, complete cds	3e-07	2911858	(AF047659) No definition line found [Caenorhabditis elegans]	0.39
1319	Y15724	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	1e-07	<NONE>	<NONE>	<NONE>
1320	X13596	Bean DNA for glycine-rich cell wall protein GRP 1.8	1e-07	<NONE>	<NONE>	<NONE>
1321	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end.	1e-07	1326385	(U58751) C07G1.7 gene product [Caenorhabditis elegans]	8.0
1322	Z55905	H.sapiens CpG DNA, clone 71f4, forward read cpg71f4.ft1a	1e-07	1076802	extensin-like protein - maize >gi 600118 mays]	0.61
1323	X03541	Human mRNA of trk oncogene > :: gb I96186 I96186 Sequence 23 from patent US 5734039	1e-07	325465	(M74509) [Human endogenous retrovirus type C oncovirus sequence.], gene product [Homo sapiens]	3e-04
1324	AF027766	Canis familiaris Y-linked zinc finger protein	1e-07	220643	(D10628) zinc finger protein [Mus musculus]	7e-08
1325	D13613	Bovine mRNA for rabphilin-3A, complete cds > :: dbj E07809 E07809 cDNA encoding rabphilin-3A	1e-07	2822161	(AC004082) rab3 effector-like; 35% Similarity to AF007836 (PID:g2317778) [Homo sapiens]	6e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for c-			(J04169) gag-onc fusion protein	
1326	X57110	cbl proto-oncogene	1e-07	323270	[Cas NSI retrovirus]	3e-14
		Human mRNA for c-			PROTO-ONCOGENE C-CBL	
1327	X57110	cbl proto-oncogene	1e-07	115855	human >gi 29731 (X57110) c-	4e-19
		cbl protein [Homo sapiens]				
		Homo sapiens				
1328	AC001178	(subclone 2_g12 from BAC H94) DNA sequence	4e-08	<NONE>	<NONE>	<NONE>
		Human interleukin-8				
1329	U11866	receptor type B (IL8RB) gene, promoter and exons 1-6	4e-08	<NONE>	<NONE>	<NONE>
		Homo sapiens				
1330	AC001225	(subclone 2_e6 from BAC H94) DNA sequence	4e-08	478184	histone H1 II-1 (clone L95) - midge	6.5
		Human modulator				
1331	M73837	recognition factor 2 (MRF-2) mRNA, complete cds.	4e-08	141448	HYPOTHETICAL 32.6 KD PROTEIN IN TRANSPOSON TN4556 >gi 80758 pir JQ0428 hypothetical 32.6K protein - Streptomyces fradiae transposon Tn4556	4.7
		Homo sapiens clone				
1332	AC006164	UWGC:y28gap from 6p21, complete sequence [Homo sapiens]	4e-08	2580578	(AF000996) ubiquitous TPR motif, Y isoform [Homo sapiens]	1.2
		Human mRNA for				
1333	X01060	transferrin receptor	4e-08	135514	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA 11) - rabbit	0.61
		H.sapiens INE2				
1334	Y10697	mRNA	4e-08	124909	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR) >gi 186555 sapiens]	0.14
		Rattus norvegicus				
1335	U60416	myr 6 myosin heavy chain mRNA, complete cds	4e-08	102189	myosin I, high molecular weight - Acanthamoeba sp	3e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 55.2 KD	
1336	U23804	Drosophila melanogaster putative GTP-binding regulatory protein beta chain (GPB) mRNA, partial cds.	4e-08	2494916	TRP-ASP REPEATS CONTAINING PROTEIN T10F2.4 IN CHROMOSOME III protein; similar to G-Beta repeat region (Trp-Asp domains) of guanine nucleotide binding protein	1e-28
1337	AE000213	Escherichia coli K-12 MG1655 section 103 of 400 of the complete genome	4e-08	3294172	(AL022325) tF27C3.1.1 (protein similar to C. elegans protein B0035.16) (isoform 1) [Homo sapiens]	2e-67
1338	D89821	Mus musculus mRNA for RhoM, complete cds	2e-08	3024539	RHO-RELATED GTP-BINDING PROTEIN RHOD (RHO-RELATED PROTEIN HP1) (RHOHP1) sapiens]	1e-04
1339	U74382	Human telomeric repeat DNA-binding protein (PIN2) mRNA, complete cds	1e-08	<NONE>	<NONE>	<NONE>
1340	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	1e-08	<NONE>	<NONE>	<NONE>
1341	L21936	Human succinate dehydrogenase flavoprotein subunit	1e-08	3201678	(AF060886) adenine phosphoribosyltransferase [Leishmania tarentolae]	4.0
1342	AB009777	Homo sapiens gene for osteonidogen, promoter region	1e-08	479388	tritin - wheat >gi 391929 gnl PID d1003454	2.2
1343	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	1e-08	1730173	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 2 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) isomerase [Clarkia concinna]	1.9
1344	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	1e-08	1730173	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 2 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) isomerase [Clarkia concinna]	1.7
1345	AC000980	Homo sapiens (subclone 1_g2 from P1 H31) DNA sequence	1e-08	439877	(L27428) reverse transcriptase [Homo sapiens]	1.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1346	U48734	Human non-muscle alpha-actinin mRNA, complete cds	1e-08	168237	(M76546) hydroxyproline-rich protein [<i>Helianthus annuus</i>]	0.19
1347	M76724	Human leukocyte adhesion receptor alpha subunit	1e-08	1177607	(X92485) pva1 [<i>Plasmodium vivax</i>]	0.19
1348	AF067959	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds	1e-08	3165574	(AF067942) No definition line found [<i>Caenorhabditis elegans</i>]	0.15
1349	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	1e-08	2072964	(U93569) putative p150 [<i>Homo sapiens</i>]	0.001
1350	X57103	Human h-lys gene for lysozyme (upstream region)	7e-09	<NONE>	<NONE>	<NONE>
1351	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-09	231629	BILE-SALT-ACTIVATED LIPASE PRECURSOR ESTER LIPASE) (STEROL ESTERASE) (CHOLESTEROL ESTERASE) salt-activated lipase [<i>Homo sapiens</i>] sapiens]	0.22
1352	L34741	Aplysia californica prohormone convertase (PC2) mRNA, complete cds.	5e-09	322054	cytochrome-c oxidase (EC 1.9.3.1) chain II precursor - <i>Synechocystis</i> sp. (PCC 6803) >gi 581739 sp.]	5.0
1353	AF052959	Homo sapiens type XV collagen (COL15A1) gene, exon 6	4e-09	131269	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 72708 pir QJLV6A photosystem II chlorophyll a-binding protein psbB - liverwort (<i>Marchantia polymorpha</i>) chloroplast >gi 11700	1.8

262

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1354	L15470	Streptomyces clavuligerus (NRRL 3585) clavulanic acid biosynthesis protein (cla) gene, complete cds and clavamate synthase 2 (cs2) gene, partial cds.	4e-09	586028	POSSIBLE ACAMINASE (ACAMINASE UREOHYDROLASE) (AUH) (PROCLAVAMINIC ACID AMIDINO HYDROLASE) >gi 1361423 pir S57669 Proclavaminic acid amidino hydrolase - Streptomyces clavuligerus >gi 295171 Proclavaminic acid amidino hydrolase [Streptomyces clavuligerus] >gi 1586122 prf 2203286B proclavaminic acid amidino hydrolase [Streptomyces clavuligerus]	4e-13
1355	AB002302	Human mRNA for KIAA0304 gene, complete cds	2e-09	131600	GENERAL SECRETION PATHWAY PROTEIN L product [Klebsiella pneumoniae] >gi 149311 (M32613) pulL	2.5
1356	L34219	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds.	1e-09	<NONE>	<NONE>	<NONE>
1357	AB002302	Human mRNA for KIAA0304 gene, complete cds	1e-09	2224549	(AB002302) KIAA0304 [Homo sapiens]	5.0
1358	D85731	Homo sapiens HSPA1L gene for Heat shock protein 70 testis variant, 5'UTR, partial sequence	1e-09	1389766	(U58658) unknown [Homo sapiens]	1.3
1359	AF064483	Homo sapiens natural resistance-associated macrophage protein 2 (NRAMP2) gene, exon 17, alternatively spliced non-IRE form, complete cds	8e-10	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.72

263

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1360	AF002283	Mus musculus alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds	6e-10	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-21
1361	M26220	African green monkey origin of replication	5e-10	2143455	gene DMR-N9 protein - mouse (fragment)	8.8
1362	Z78006	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA7F10	4e-10	2072977	(U93574) putative p150 [Homo sapiens]	0.005
1363	U82303	Homo sapiens unknown protein mRNA, partial cds	2e-10	1825711	(U88183) similar to the immunoglobulin superfamily, most similar to neural cell adhesion proteins [Caenorhabditis elegans]	0.031
1364	AF079764	Drosophila melanogaster enhancer of polycomb	2e-10	3757890	(AF079764) enhancer of polycomb [Drosophila melanogaster]	1e-10
1365	L24123	Homo sapiens NRF1 protein (NRF1) mRNA.	2e-10	3004573	(AC004520) similar to NFE2-related transcription factors; similar to I48694 (PID:g2137676) [Homo sapiens]	4e-53
1366	M91454	Orangutan alpha-globin gene duplicate region.	1e-10	464239	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 1085185 pir S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SGC4) >gi 552446 (L06178) NADH dehydrogenase subunit 4 [Apis mellifera ligustica]	6.0
1367	D87117	House mouse; Musculus domesticus brain mRNA for SAP102, complete cds	6e-11	473912	(L31961) phosphoprotein [Mus cookii]	2.2
1368	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>

264

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1369	AC001002	(subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1370	AB007874	Homo sapiens KIAA0414 mRNA, partial cds	5e-11	<NONE>	<NONE>	<NONE>
1371	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1372	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1373	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1374	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1375	Z21852	H.sapiens mRNA for HERV-K long terminal repeat	5e-11	419481	gag polyprotein - human endogenous virus S71	4.6
1376	AB007928	Homo sapiens mRNA for KIAA0459 protein, partial cds	5e-11	2947238	(AF051782) diaphanous 1 [Homo sapiens]	2.8
1377	D87117	House mouse; Musculus domesticus brain mRNA for SAP102, complete cds	5e-11	473912	(L31961) phosphoprotein [Mus cookii]	1.8
1378	AJ131501	Homo Sapiens DNA sequence between two AML1 gene promoters, 6423 BP	5e-11	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.20
1379	M27826	Human endogenous retroviral protease mRNA, complete cds.	5e-11	88558	retroviral proteinase-like protein - human	0.002

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 55.2 KD	
1380	U23804	Drosophila melanogaster putative GTP-binding regulatory protein beta chain (GPB) mRNA, partial cds.	5e-11	2494916	TRP-ASP REPEATS CONTAINING PROTEIN T10F2.4 IN CHROMOSOME III protein; similar to G-Beta repeat region (Trp-Asp domains) of guanine nucleotide binding protein	1e-30
1381	Z22784	M.musculus troponin I gene.	3e-11	3892202	(AF072889) transcription repressor brain factor 2	0.053
1382	AB007880	Homo sapiens KIAA0420 mRNA, complete cds	2e-11	<NONE>	<NONE>	<NONE>
1383	AF020361	9 Homo sapiens BAX gene, exon 6, partial sequence	2e-11	<NONE>	<NONE>	<NONE>
1384	L35600	Homo sapiens DNA sequence.	2e-11	1174952	GLYCOPROTEIN D PRECURSOR gD [Bovine herpesvirus 1]	0.25
1385	U21943	Human organic anion transporting polypeptide	2e-11	2738223	(U95011) brain-specific organic anion transporter	9e-19
1386	U90878	Homo sapiens carboxyl terminal LIM domain protein	2e-11	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-23
1387	U31929	Human orphan nuclear receptor (DAX1) gene, complete cds	6e-12	<NONE>	<NONE>	<NONE>
1388	M25828	Human von Willebrand factor gene, exon 1, 2, and 3, and three Alu repetitive elements.	6e-12	<NONE>	<NONE>	<NONE>
1389	AB020648	Homo sapiens mRNA for KIAA0841 protein, partial cds	3e-12	<NONE>	<NONE>	<NONE>
1390	Z15026	H.sapiens genes for tumor necrosis factor (Tnfa) and lymphotoxine (Tnfb)	2e-12	<NONE>	<NONE>	<NONE>
1391	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	2e-12	<NONE>	<NONE>	<NONE>
1392	Z47046	Human cosmid QLL2C9 from Xq28	2e-12	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20E2	2e-12	106322	hypothetical protein (L1H 3' region) - human	1.5
1393	Z79007					
1394	U34377	Human tyrosine kinase TXK (txk) gene, exon 13.	1e-12	151484	(M55524) ORF 4; putative [Pseudomonas aeruginosa]	4.3
1395	D70845	Mus musculus apg-1 gene for novel member of heat shock protein 110, promoter region	1e-12	113658	ALKALINE PROTEINASE PRECURSOR (ALP) precursor - fungus (Acremonium chrysogenum)	3.5
1396	M63978	Human vascular endothelial growth factor gene, exon 8.	1e-12	3982737	(AF069731) calmodulin-dependent protein kinase II beta M isoform [Rattus norvegicus]	0.083
1397	U60266	Homo sapiens lysosomal alpha-mannosidase (manB) mRNA, complete cds	8e-13	<NONE>	<NONE>	<NONE>
1398	Z68297	Caenorhabditis elegans cosmid F11A10, complete sequence [Caenorhabditis elegans]	7e-13	2393734	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	5e-34
1399	Z68297	Caenorhabditis elegans cosmid F11A10, complete sequence [Caenorhabditis elegans]	7e-13	2393734	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	3e-38
1400	Z68885	Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.	6e-13	<NONE>	<NONE>	<NONE>
1401	X76104	H.sapiens DAP-kinase mRNA	6e-13	2911154	(AB007143) ZIP-kinase [Mus musculus]	0.007
1402	Z78668	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA13G4	5e-13	106322	hypothetical protein (L1H 3' region) - human	2e-06
1403	L35600	Homo sapiens DNA sequence.	3e-13	3184290	(AC004136) hypothetical protein [Arabidopsis thaliana]	1.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cloning vector				
1404	AF090452	pKODT complete sequence	2e-13	3876730	(Z49966) F35C11.4 [Caenorhabditis elegans]	7.8
1405	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	2e-13	419481	gag polyprotein - human endogenous virus S71	3.4
1406	AF005219	Homo sapiens transcription factor HOXD13	2e-13	2822166	(AC004080) transcription factor HOXA13 [Homo sapiens]	5e-09
1407	AB018301	Homo sapiens mRNA for KIAA0758 protein, partial cds	2e-13	3882237	(AB018301) KIAA0758 protein [Homo sapiens]	1e-23
1408	D70845	Mus musculus apg-1 gene for novel member of heat shock protein 110, promoter region	1e-13	113658	ALKALINE PROTEINASE PRECURSOR (ALP) precursor - fungus (Acremonium chrysogenum)	3.1
1409	AG000691	Homo sapiens genomic DNA, 21q region, clone: T171BG33	8e-14	930045	(X15332) alpha-1 (III) collagen [Homo sapiens]	3e-04
1410	D30785	Mouse mRNA for neuropsin, complete cds	8e-14	3559978	(AJ005641) serine protease [Rattus rattus]	2e-12
1411	U32710	Haemophilus influenzae Rd section 25 of 163 of the complete genome	8e-14	4106673	(AL035064) queuine trna-ribosyltransferase [Schizosaccharomyces pombe]	2e-38
1412	AG000836	Homo sapiens genomic DNA, 21q region, clone: 64E11X19	7e-14	1363925	hypothetical protein 2 - North American opossum (fragment) >gi 897721 (Z48955) ORF-2, putative RT [Didelphis virginiana]	1.1
1413	Z62664	H.sapiens CpG DNA, clone 71d11, forward read cpg71d11.ft1a	7e-14	3953461	(AC002328) F20N2.6 [Arabidopsis thaliana]	0.085
1414	AB014532	Homo sapiens mRNA for KIAA0632 protein, partial cds	7e-14	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.040

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1415	Z96478	H.sapiens telomeric DNA sequence, clone 20PTEL004, read 20PTELOO004.seq	7e-14	2981631	(AB012223) ORF2 [Canis familiaris]	2e-04
1416	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-14	<NONE>	<NONE>	<NONE>
1417	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	4e-14	<NONE>	<NONE>	<NONE>
1418	AF033349	Homo sapiens MLL gene breakpoint cluster region, intron 1, partial sequence	3e-14	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	9.3
1419	AC001526	Homo sapiens (subclone 4_f6 from P1 H54) DNA sequence	3e-14	99861	extensin - almond >gi 20420 (X65718) extensin	9.2
1420	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-14	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	0.15
1421	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-14	3913573	EPHRIN-A2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 6) (LERK-6) sapiens] >gi 2924761 (AC004258) EPL6_HUMAN [Homo sapiens]	8.7
1422	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-15	119040	E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K) >gi 74142 pir Q1AD25 early E1B 21K protein II - human adenovirus 5 >gi 58489 (X02996) mRNA 5 first reading frame [Human adenovirus type 5] adenovirus type 5] >gi 209797 (J01969) 21 kD protein	1.5

769

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					transcription factor GATA-4,	
1423	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-15	477102	retinoic acid-inducible - mouse >gi 293345 (M98339) GATA-binding transcription factor [Mus musculus]	0.57
1424	AB012223	Canis familiaris LINE 1 element ORF2 mRNA, complete cds	8e-15	92385	hypothetical protein - rat (fragment)	0.003
1425	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<NONE>	<NONE>	<NONE>
1426	X12433	Human pHS1-2 mRNA with ORF homologous to membrane receptor proteins	3e-15	422532	collagen alpha 3(IV) chain - sea urchin	8.9
1427	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	1353143	PROBABLE NUCLEAR HORMONE RECEPTOR E02H1.7 >gi 3875431 gnl PID e1344980 (Z47075) similar to Zinc finger, C4 type (two domains) [Caenorhabditis elegans]	5.0
1428	Z69651	Human DNA sequence from cosmid L75B9. Huntington's Disease Region, chromosome 4p16.3	3e-15	403460	(L24521) transformation-related protein [Homo sapiens]	0.60
1429	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-15	108750	Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine >gi 440 (X62916) anti-testosterone antibody [Bos taurus]	1.1
1430	X83299	H.sapiens SMA3 mRNA	2e-15	671530	(X83299) SMA3 gene product [Homo sapiens]	0.32
1431	U01877	Human p300 protein mRNA, complete cds. > :: gb I62297 I62297 Sequence 1 from patent US 5658784	2e-15	3024341	E1A-ASSOCIATED PROTEIN P300	0.019

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1432	X16516	Mouse MHC (Qa) Q2k gene for class I antigen. exons 4-8	1e-15	2496897	HYPOTHETICAL 45.1 KD PROTEIN CT6C10.6 IN CHROMOSOME III >gi 3874384 gnl PID e1344078 EST EMBL:C08256 comes from this gene; cDNA EST EMBL:C09941 comes from this gene; cDNA EST yk340a10.3 comes from this gene; cDNA EST yk340a10.5 comes from this gene [Ca...	7e-08
1433	M74165	Chicken tensin mRNA, complete cds.	1e-15	283920	tensin - chicken >gi 212752 (M74165) tensin	2e-19
1434	X71893	H.sapiens gene for immunoglobulin kappa light chain variable region O4 and O5	9e-16	<NONE>	<NONE>	<NONE>
1435	U05227	Human Rar protein mRNA, complete cds.	9e-16	3036779	(Z84479) match: multiple proteins; match: O00407 Q12829 P22127 P36861 Q40219; match: P70550 Q41022 P22125 Q08155 P35286; match: P51148 P51147 P35293 P36861 P35289; match: P35284 Q40217 P51152 P51157 P51158; match: Q41022	3e-06
1436	M23404	Chicken erythrocyte anion transport protein (band3) mRNA, complete cds.	9e-16	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	1e-28
1437	X16145	Rat mRNA for liver alpha-L-Fucosidase (EC 3.2.1.51)	9e-16	67502	alpha-L-fucosidase (EC 3.2.1.51) 1 precursor, tissue - human >gi 178409 (M29877) alpha-L-fucosidase precursor (EC 3.2.1.5) [Homo sapiens]	2e-29
1438	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-16	<NONE>	<NONE>	<NONE>
1439	AF076981	Mus musculus brain mitochondrial carrier protein BMCPI (Bmcp1) mRNA, complete cds	8e-16	3851540	(AF078544) brain mitochondrial carrier protein-1 [Homo sapiens]	2e-13

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens MN/CA9			!!!! ALU SUBFAMILY J	
1440	Z54349	GENE	5e-16	728831	WARNING ENTRY	0.002
1441	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	3e-16	309123	(M35526) complement component C5D [Mus musculus]	3.1
1442	X64587	M.musculus mRNA for splicing factor U2AF (65 kD)	3e-16	2143767	glycoprotein - rat >gi 986943 (L08134) glycoprotein [Rattus norvegicus] norvegicus]	0.003
1443	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	3e-16	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-20
1444	Z73987	Human DNA sequence from cosmid N120B6 on chromosome 22. Contains ESTs. complete sequence [Homo sapiens]	1e-16	<NONE>	<NONE>	<NONE>
1445	M58318	Homo sapiens ala gene.	1e-16	<NONE>	<NONE>	<NONE>
1446	U44103	Human small GTP binding protein Rab9 mRNA, complete cds	1e-16	1552584	(Z80233) hypothetical protein Rv0029	1.3
1447	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	9e-17	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	2e-20
1448	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-17	<NONE>	<NONE>	<NONE>
1449	M76762	Mus musculus ribosomal protein (Ke3) gene, exons 1 to 5. and complete cds.	1e-17	1073048	pupR protein - Pseudomonas putida >gi 525260	0.36
1450	D50561	Human DNA, replication enhancing element (REE1)	4e-18	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.78
1451	D16431	Human mRNA for hepatoma-derived growth factor, complete cds	4e-18	3242079	(AJ006984) proline-rich protein	0.018

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1452	AF088983	Mus musculus heat shock protein hsp40-3 mRNA, complete cds	4e-18	3873707	(Z73102) Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene [Caenorhabditis elegans]	9e-25
1453	U60205	Human methyl sterol oxidase (ERG25) mRNA, complete cds	3e-18	<NONE>	<NONE>	<NONE>
1454	AF038177	Homo sapiens clone 23899 mRNA sequence	1e-18	1360775	G protein-coupled receptor 74 - equine herpesvirus 2 >gi 695246 (U20824) G protein-coupled receptor [Equine herpesvirus 2]	5.1
1455	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	1e-18	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-21
1456	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	1e-18	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-22
1457	U34374	Human tyrosine kinase TXK (txk) gene, exons 9 and 10.	1e-19	<NONE>	<NONE>	<NONE>
1458	AB006969	Homo sapiens hGAA1 mRNA, complete cds	1e-19	4151809	(AF102855) synaptic SAPAP-interacting protein Synamon	0.19
1459	AB002293	Human mRNA for KIAA0295 gene, partial cds	1e-19	2224531	(AB002293) KIAA0295 [Homo sapiens]	6e-17
1460	Z59664	H.sapiens CpG DNA, clone 168f9, reverse read cpg168f9.rt1a.	5e-20	3880251	(Z82055) predicted using Genefinder	6.5
1461	M73837	Human modulator recognition factor 2 (MRF-2) mRNA, complete cds.	5e-20	284313	modulator recognition factor 2 - human factor 2 [Homo sapiens]	0.019

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1462	U24267	Human pyrroline-5-carboxylate dehydrogenase	5e-20	2506350	DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE PRECURSOR (P5C DEHYDROGENASE) >gi 1353248 sapiens] >gi 1353250 (U24267) pyrroline 5-carboxylate dehydrogenase [Homo sapiens] >gi 1589585 prf 2211355A Delta1-pyrroline-5-carboxylate dehydrogenase [Homo sapiens]	5e-04
1463	U13262	Mus musculus myelin gene expression factor	4e-20	536926	(U13262) myelin gene expression factor [Mus musculus]	3e-07
1464	U13262	Mus musculus myelin gene expression factor	4e-20	3126878	(AF061832) M4 protein deletion mutant [Homo sapiens]	1e-08
1465	Z61239	H.sapiens CpG DNA, clone 48f10, forward read cpg48f10.ft1a	4e-20	1669601	(D88747) AR401 [Arabidopsis thaliana]	8e-19
1466	U89915	Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds	1e-20	3462455	(U89915) junctional adhesion molecule [Mus musculus]	7e-11
1467	AF029071	Gallus gallus p52 pro-apototic protein mRNA, complete cds	7e-22	2599492	(AF029071) p52 pro-apototic protein [Gallus gallus]	1e-15
1468	M25636	Figure 4. Nucleotide sequence of the pKS36 1.797 kb insert.	6e-22	1196398	(M21305) unknown protein [Homo sapiens]	0.65
1469	AB020655	Homo sapiens mRNA for KIAA0848 protein, complete cds	6e-22	4240325	(AB020725) KIAA0918 protein [Homo sapiens]	1e-19

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1470	S80935	chorionic gonadotropin beta 1 (CG beta 1) subunit	5e-22	115310	PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR >gi 84917 pir A31893 collagen alpha 1(IV) chain precursor - fruit fly (Drosophila melanogaster) melanogaster] >gi 157078 (M96575) type IV collagen pro-collagen [Drosophila melanogaster]	0.027
1471	AF053066	Homo sapiens microsatellite D5S2926 sequence	2e-22	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-04
1472	U55177	Danio rerio carbonic anhydrase homolog CAH-Z mRNA, complete cds	2e-22	3123190	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi 2576335 (U55177) CAH-Z [Danio rerio]	5e-14
1473	AF064250	Gallus gallus ubiquitin specific protease 66	2e-22	2736064	(AF016107) ubiquitin specific protease 41 [Gallus gallus]	7e-37
1474	AF030880	Homo sapiens pendrin (PDS) mRNA, complete cds	2e-22	729367	DRA PROTEIN (DOWN-REGULATED IN ADENOMA) >gi 2135020 pir A47456 down-regulated in adenoma (DRA) - human >gi 291964 (L02785) Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transer. activ. domain 620-640.; homeobox motif 653-676 [Homo sapiens]	4e-53
1475	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-23	<NONE>	<NONE>	<NONE>
1476	X57398	Human mRNA for pM5 protein	3e-23	107350	Pm5 protein - human >gi 1335273 gnl PID e36241	1e-04
1477	AB010998	Rattus norvegicus PAD-R11 mRNA for Peptidylarginine deiminase type I, complete cds	2e-23	<NONE>	<NONE>	<NONE>
1478	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	2e-23	171200	(J04734) CDC6 protein [Saccharomyces cerevisiae]	9.8
1479	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	2e-23	171200	(J04734) CDC6 protein [Saccharomyces cerevisiae]	8.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens MLL-				
1480	AF024541	AF4 fusion protein mRNA, partial cds	2e-23	2136142	serine/proline-rich FEL protein, splice form 1 - human	1e-20
1481	L13773	Human AF-4 mRNA, complete cds.	2e-23	3063962	(AF031404) MLL-AF4 fusion protein [Homo sapiens]	1e-20
1482	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-24	<NONE>	<NONE>	<NONE>
1483	U75467	Drosophila melanogaster Rga and Atu genes, complete cds	8e-24	1658503	(U75467) Atu [Drosophila melanogaster]	2e-37
1484	D17076	Human HepG2 partial cDNA, clone hmd5a09m5	7e-24	<NONE>	<NONE>	<NONE>
1485	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-24	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gij416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	7e-10
1486	M11167	Human 28S ribosomal RNA gene.	2e-24	3875481	(Z81054) predicted using Genefinder; Similarity to UDP-glucuronosyltransferases	5.1
1487	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-24	549173	USP1 PROTEIN PRECURSOR >gij169623	1.2
1488	AB003468	Cloning vector pAP3neo DNA, complete sequence	2e-24	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.058
1489	X03541	Human mRNA of trk oncogene >:: gb I96186 I96186 Sequence 23 from patent US 5734039	2e-24	325465	(M74509) [Human endogenous retrovirus type C oncovirus sequence.], gene product [Homo sapiens]	3e-04
1490	L81652	Homo sapiens (subclone 2_g11 from P1 H43) DNA sequence	2e-24	225047	reverse transcriptase related protein [Homo sapiens]	4e-12
1491	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	2e-24	2078282	(U95760) Sno [Drosophila melanogaster]	2e-41
1492	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-25	2623773	(AF004835) tyrocidine synthetase 3 [Brevibacillus brevis]	8.6

276

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1493	AB002405	Homo sapiens mRNA for LAK-4p, complete cds	8e-25	2496822	HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X >gi 746502 (U23516) B0416.1 gene product [Caenorhabditis elegans]	9e-11
1494	K03002	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A.	8e-25	1514614	(X92842) nuclear protein [Mus musculus]	1e-13
1495	U61232	Human tubulin-folding cofactor E mRNA, complete cds	7e-25	1465772	(U61232) cofactor E [Homo sapiens]	2e-05
1496	U10245	Arabidopsis thaliana Col-O putative RNA helicase A mRNA, complete cds.	5e-25	1353239	(U10245) putative RNA helicase A [Arabidopsis thaliana]	1e-37
1497	X89211	H.sapiens DNA for endogenous retroviral like element	3e-25	2065210	(Y12713) Pro-Pol-dUTPase polyprotein	5e-06
1498	L81652	Homo sapiens (subclone 2_g11 from P1 H43) DNA sequence	3e-25	2072961	(U93568) putative p150 [Homo sapiens]	5e-16
1499	X82895	H.sapiens mRNA for DLG2	2e-25	2497511	MAGUK P55 SUBFAMILY MEMBER 2 (MPP2 PROTEIN) (DISCS, LARGE HOMOLOG 2)	1e-34
1500	M36654	Mouse homeo box 2.6 (Hox-2.6) mRNA, complete cds.	9e-26	3323169	(AE001255) T. pallidum predicted coding region TP0854	1.9
1501	L36315	Mus musculus (clone pMLZ-1) zinc finger protein	9e-26	1806134	(Z67747) zinc finger protein [Mus musculus]	4e-05
1502	AB018281	Homo sapiens mRNA for KIAA0738 protein, complete cds	9e-26	728831	!!! ALU SUBFAMILY J WARNING ENTRY	1e-07
1503	AF017433	Homo sapiens putative transcription factor CR53	9e-26	3219985	ZINC FINGER PROTEIN ZFP-29	1e-17

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1504	AC001225	(subclone 2_e6 from BAC H94) DNA sequence	8e-26	2653713	(U91823) small S protein [Hepatitis B virus]	4.3
1505	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-26	283446	cyteine-rich surface antigen 72, CRP72 - Giardia lamblia (fragment)	3.4
1506	X94912	H.sapiens Pr22 gene	3e-26	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	4e-09
1507	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-26	<NONE>	<NONE>	<NONE>
1508	U44103	Human small GTP binding protein Rab9 mRNA, complete cds	1e-26	3327038	(AB014512) KIAA0612 protein [Homo sapiens]	8.7
1509	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-27	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.14
1510	AG001212	Homo sapiens genomic DNA, 21q region, clone: 9H11N46	9e-27	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.012
1511	AF027131	Mus musculus mucin glycoprotein MUC3 mRNA, partial cds	9e-27	2589172	(U76551) mucin Muc3 [Rattus norvegicus]	2e-14
1512	U49057	Rattus norvegicus CTD-binding SR-like protein rA9 mRNA, complete cds	5e-27	1438534	(U49057) rA9 [Rattus norvegicus]	1e-04
1513	J03764	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9.	3e-27	<NONE>	<NONE>	<NONE>
1514	Z78160	M.musculus partial cochlear mRNA (clone 28D2)	3e-27	1490362	(Z78160) unknown [Mus musculus]	2e-05
1515	Z64210	H.sapiens CpG DNA, clone 99b4, reverse read cpg99b4.rt1a	3e-27	2257538	(AB004538) LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN) [Schizosaccharomyces pombe]	1e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1516	L35659	(subclone H8 6_h6 from P1 35 H5 C8) DNA sequence.	1e-27	<NONE>	<NONE>	<NONE>
1517	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	1644471	(U72686) odorant receptor 4 [Danio rerio]	7.5
1518	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2738388	(AF003534) hypothetical protein 004L [Chilo iridescent virus]	6.7
1519	AB009271	Homo sapiens gene for BCNT, partial cds	1e-27	3880909	(AL032636) Y40B1B.3 [Caenorhabditis elegans]	4.6
1520	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.85
1521	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	121805	ENDOGLUCANASE A PRECURSOR	0.58
1522	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3722000	(AF035323) survival motor neuron protein [Bos taurus]	0.10
1523	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3328188	(AF074902) laminin alpha chain [Caenorhabditis elegans]	0.083
1524	AF074382	Homo sapiens Ikb kinase gamma subunit	1e-27	3641280	(AF074382) Ikb kinase gamma subunit [Homo sapiens]	0.041
1525	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1526	L78778	Homo sapiens (subclone 2_e10 from P1 H49) DNA sequence	1e-27	225047	reverse transcriptase related protein [Homo sapiens]	2e-09
1527	L03427	Human zinc finger protein basoenuclin mRNA, complete cds.	1e-27	1488275	(U59694) zinc finger protein basoenuclin [Homo sapiens]	9e-22
1528	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	4e-28	2257538	(AB004538) LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN) [Schizosaccharomyces pombe]	2e-04

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1529	Z64210	H.sapiens CpG DNA, clone 99b4, reverse read cpg99b4.rt1a .	4e-28	3878570	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3...	7e-11
1530	U55177	Danio rerio carbonic anhydrase homolog CAH-Z mRNA, complete cds	4e-28	3123190	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi 2576335 (U55177) CAH-Z [Danio rerio]	5e-21
1531	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds	4e-28	1351839	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) >gi 930358 taurus]	3e-27
1532	AF016591	Homo sapiens survival motor neuron pseudogene, complete sequence	3e-28	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-08
1533	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	2.5
1534	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.004
1535	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	6e-04
1536	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1537	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1538	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-09
1539	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-09
1540	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-10
1541	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-11
1542	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	8e-12
1543	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1544	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1545	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1546	AF100694	Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1547	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1548	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1549	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1550	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1551	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1552	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1553	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1554	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1555	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1556	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1557	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1558	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1559	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1560	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1561	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1562	AF100694	Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1563	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1564	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1565	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1566	M87708	Human simple repeat polymorphism.	1e-28	<NONE>	<NONE>	<NONE>
1567	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1568	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3924779	(AF100694) similar to human B; cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from... >gi 3924881 gnl PID e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	3.0
1569	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	0.66

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1570	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3924779	(AF100694) similar to laminin B, cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi 3924881 gnl PID e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	0.65
1571	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.49
1572	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.49
1573	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	283446	cyteine-rich surface antigen 72, CRP72 - Giardia lamblia (fragment)	0.45
1574	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2498937	SPERMATOPHORIN SP23 PRECURSOR mealworm >gi 161725 (M92928) structural protein	0.33
1575	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1492050	(U60315) MC107L [Molluscum contagiosum virus subtype 1]	0.18
1576	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.088
1577	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.018
1578	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.016

284

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1579	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.012
1580	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.010
1581	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.002
1582	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	0.002
1583	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1584	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.002
1585	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1586	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.001

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1587	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.001
1588	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1589	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-04
1590	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-04
1591	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	2e-04
1592	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-04
1593	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1594	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-05
1595	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05
1596	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05
1597	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-06
1598	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-06
1599	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-06
1600	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	544357	RNA-BINDING PROTEIN FUS/TLS protein [human. Peptide, 526 aa] [Homo sapiens]	4e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1601	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1602	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1603	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-07
1604	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	8e-07
1605	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	7e-07
1606	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-07
1607	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-07

284

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1608	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-07
1609	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-07
1610	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-07
1611	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	7e-08
1612	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-08
1613	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-09

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1614	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-09
1615	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-09
1616	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	7e-10
1617	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-10
1618	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-10
1619	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1620	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-10
1621	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-11
1622	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-12
1623	AF032896	Petromyzon marinus polyadenylate binding protein	1e-28	1082703	polyadenylate binding protein II human	2e-27
1624	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.013
1625	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	2133579	spermatophorin Sp23 - yellow mealworm molitor]	6e-04
1626	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	3876465	(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E cDNA EST yk375g.7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gen...	9e-06
1627	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-29	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ADP-RIBOSYLATION	
1628	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	728883	FACTOR 3 fruit fly (Drosophila melanogaster) >gi 507234 (L25063) ADP ribosylation factor 3 [Drosophila melanogaster]	0.016
1629	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	544357	RNA-BINDING PROTEIN FUS/TLS protein [human, Peptide, 526 aa] [Homo sapiens] (AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-07
1630	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	4056454	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) dehydrogenase precursor - rat Acyl-CoA dehydrogenase [Rattus norvegicus]	1e-08
1631	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds	4e-29	1168287	(Z95556) accD1 [Mycobacterium tuberculosis]	6e-37
1632	Y07660	M.tuberculosis accBC gene	4e-29	2113935		3e-47
1633	X55367	Human alpha-satellite DNA from clone pTRA-2.	1e-29	<NONE>	<NONE>	<NONE>
1634	L81866	Homo sapiens (subclone 1_f1 from P1 H54) DNA sequence	1e-29	<NONE>	<NONE>	<NONE>
1635	S75940	{Alu repeats, clone 52H10} [human, colonic mucosa, Genomic, 943 nt]	1e-29	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-07
1636	AB001907	Homo sapiens PACE4 gene, exon 13	1e-29	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	2e-09
1637	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	5e-30	<NONE>	<NONE>	<NONE>

292

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	
1638	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-30	4056454		3e-10
1639	M27072	Xenopus laevis poly(A)-binding protein (ABP-EF) mRNA, complete cds.	4e-30	1352709	POLYADENYLATE-BINDING PROTEIN polyadenylate-binding protein - African clawed frog laevis]	5e-21
1640	X58386	B.taurus mRNA for bovine vacuolar ATPase subunit A	2e-30	2773154	(AF039573) abscisic acid- and stress-inducible protein	4.3
1641	Y07660	M.tuberculosis accBC gene	1e-30	2113935	(Z95556) accD1 [Mycobacterium tuberculosis]	4e-47
1642	AJ236940	Sus scrofa mRNA for hypothetical protein (5' clone 7C4)	4e-31	4102021	(AF007561) delta 6-desaturase [Borago officinalis]	7.4
1643	AF039400	Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) mRNA, complete cds	2e-31	3721912	(AB017156) gob-5 [Mus musculus]	7e-08
1644	L77036	Homo sapiens (subclone 5_d9 from P1 H19) DNA sequence.	1e-31	461663	BOMBYXIN B-2 HOMOLOG PRECURSOR silkmoth >gi 217385 gnl PID d1003528 (D13924) Samia bombyxin homolog B-2 [Samia cynthia]	1.1
1645	X61971	H.sapiens mRNA for macropain subunit delta	1e-31	296734	(X61971) macropain subunit delta [Homo sapiens]	3e-06
1646	L00016	human mitochondrial trnas and partial proteins 4 & 5; histidyl-, seryl-, leucyl-trna genes: urf4 and urf5 (partial).	5e-32	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1647	M17887	Human acidic ribosomal phosphoprotein P2 mRNA, complete cds.	5e-32	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1659	U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds.	6e-34	3395443	(AC004683) putative ammonium transporter, 3' partial	4.7
1660	AF013988	Homo sapiens serine protease mRNA, complete cds	4e-34	2507226	PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (R-PTP-EPSILON) >gi 1439605 (U62387) protein tyrosine phosphatase-e [Mus musculus]	3.2
1661	U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds.	2e-34	104757	LEP100 protein precursor - chicken >gi 212254 gallus]	1.6
1662	AJ233632	Homo sapiens endogenous retroviral sequence ERV-L pol gene, clone ERV-L Human6	2e-34	3860513	(AJ233597) reverse transcriptase [Mus famulus]	4e-10
1663	AF086310	Homo sapiens full length insert cDNA clone ZD51F08	8e-35	2947070	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]	2.3
1664	X17206	Human mRNA for LLRep3	3e-35	730652	40S RIBOSOMAL PROTEIN S2 (STRINGS OF PEARLS PROTEIN) >gi 1085158 pir S50325 ribosomal protein S2 - fruit fly (Drosophila melanogaster) melanogaster] >gi 515972 (U01335) ribosomal protein S2	2e-10
1665	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	3e-35	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	2e-16
1666	U62801	Human protease M mRNA, complete cds	2e-35	3929231	(AF091247) potassium channel [Rattus norvegicus]	1.0
1667	AF020760	Homo sapiens serine protease (Omi) mRNA, complete cds	1e-35	2738915	(AF020760) serine protease [Homo sapiens]	9e-14

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1668	Z93943	sequence from cosmid U235H3 on chromosome X	8e-36	1196432	(M22333) unknown protein [Homo sapiens]	3e-10
1669	X06778	Rabbit 18S rRNA	7e-36	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.011
1670	AB007962	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0493	3e-36	3329243	(AE001350) hypothetical protein [Chlamydia trachomatis]	3.1
1671	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-36	141103	HYPOTHETICAL PROTEIN ORF-1137 mouse	0.038
1672	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-36	198651	(M29325) ORF1 [Mus musculus]	0.006
1673	U49082	Human transporter protein (g17) mRNA, complete cds	3e-36	1840045	(U49082) transporter protein [Homo sapiens]	2e-15
1674	J03133	Human transcription factor SP1 mRNA, 3' end.	3e-36	477133	HF-1 regulatory element binding protein - rat	2e-31
1675	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds	1e-36	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	4e-37
1676	M34857	Mouse Hox-2.5 mRNA.	9e-37	106296	homeotic protein Hox B9 - human (fragment)	0.15
1677	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	9e-37	2072960	(U93568) p40 [Homo sapiens]	3e-05
1678	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	8e-37	4185944	(Y17833) env protein [Human endogenous retrovirus K]	1e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1679	Z93943	sequence from cosmid U235H3 on chromosome X	9e-38	106322	hypothetical protein (L1H 3' region) - human	4e-13
1680	X97303	H.sapiens mRNA for Ptg-12 protein	4e-38	466044	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi 630780 pir S44909 ZK686.4 protein - Caenorhabditis elegans >gi 304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]	3e-37
1681	Y08999	H.sapiens mRNA for Sop2p-like protein	3e-38	3334339	SOP2-LIKE PROTEIN	5e-06
1682	Z62887	H.sapiens CpG DNA, clone 74g6, forward read cpg74g6.ft1a	2e-38	1245686	(U53181) F36D4.2 gene product [Caenorhabditis elegans]	0.19
1683	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase region mRNA, partial cds	1e-38	59977	(Z14310) tripartite fusion transcript PLA2L [Human endogenous retrovirus]	1e-06
1684	D86974	Human mRNA for KIAA0220 gene, partial cds	1e-38	3337386	(AC002544) Unknown gene product splice form-2 [Homo sapiens]	8e-11
1685	M31013	Human nonmuscle myosin heavy chain (NMHC) mRNA, 3' end.	1e-38	4115748	(AB022023) nonmuscle myosin heavy chain B	2e-11
1686	AF006087	Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds	4e-39	<NONE>	<NONE>	<NONE>
1687	X58374	D.melanogaster crn mRNA	4e-39	2655888	(AL009171) 62D9.a [Drosophila melanogaster]	4e-42
1688	D85815	Human DNA for rhoHP1, complete cds	1e-39	134080	GTP-BINDING PROTEIN TC10 ras-like protein [Homo sapiens]	3e-26

206

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1689	U49057	Rattus norvegicus CTD-binding SR-like protein rA9 mRNA, complete cds	4e-40	1438534	(U49057) rA9 [Rattus norvegicus]	5e-05
1690	Y08999	H.sapiens mRNA for Sop2p-like protein	4e-40	3334339	SOP2-LIKE PROTEIN	9e-08
1691	AB002293	Human mRNA for KIAA0295 gene, partial cds	4e-40	2224531	(AB002293) KIAA0295 [Homo sapiens]	1e-30
1692	AF086222	Homo sapiens full length insert cDNA clone ZC66E08	1e-40	2829669	DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) >gi 1707502 gnl PID e254627 (X99227) double-stranded RNA-specific editase [Homo sapiens] editase 1 hRED1-L [Homo sapiens] >gi 2039300 (U76421) dsRNA adenosine deaminase DRADA2b [Homo sapiens]	0.61
1693	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase (SCAD-SRL) mRNA, complete cds	1e-40	4105190	(AF044127) peroxisomal short-chain alcohol dehydrogenase	2e-06
1694	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	6e-23
1695	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	6e-23
1696	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	5e-23
1697	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	5e-23
1698	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	1e-40	3882205	(AB018285) KIAA0742 protein [Homo sapiens]	6e-31

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ATP-BINDING CASSETTE	
1699	X75927	M.musculus abc2 mRNA	1e-40	728773	TRANSPORTER 1 ABC1 - human >gi 495257 (X75926) abc1 [Mus musculus]	3e-37
1700	AF038200	Homo sapiens clone 23954 mRNA sequence	5e-41	3211975	(AF068195) putative glialblastoma cell differentiation-related protein [Homo sapiens]	5e-14
1701	U20521	Human estrogen sulfotransferase (STE) gene, exon 8 and complete cds	4e-41	<NONE>	<NONE>	<NONE>
1702	AF026548	Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds	2e-41	3182923	[3-METHYL-2-OXOBUTANOATE DEHYDROGENASE (LIPOAMIDE)] KINASE PRECURSOR alpha-ketoacid dehydrogenase kinase precursor [Homo sapiens]	2e-09
1703	Y07660	M.tuberculosis accBC gene	2e-41	465847	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi 280542 pir S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder: similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST ...	3e-38
1704	AG001237	Homo sapiens genomic DNA, 21q region, clone: 9H11N46	1e-41	106322	hypothetical protein (L1H 3' region) - human	5e-09
1705	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds	1e-41	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	3e-12
1706	AF055029	Homo sapiens clone 24711 mRNA sequence	5e-42	3250681	(AL024486) putative protein	2.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					1-	
1707	Z49747	O.cuniculus mRNA for phospholipase C	5e-42	130227	PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) >gi 163538 (M20638) phospholipase C-III [Bos taurus]	5e-36
1708	M93651	Human set gene, complete cds.	2e-42	<NONE>	<NONE>	<NONE>
1709	AJ236940	Sus scrofa mRNA for hypothetical protein (5' clone 7C4)	2e-42	2062403	(U79010) delta 6 desaturase [Borago officinalis]	8.5
1710	J03634	Human erythroid differentiation protein mRNA	2e-42	1708436	INHIBIN BETA A CHAIN PRECURSOR	2e-10
1711	AJ223777	Mus musculus mRNA for striatin	6e-43	2494917	STRIATIN >gi 1495773 gnl PID e254158	2e-32
1712	AF016411	Homo sapiens potassium channel subunit KCNA3.1B	2e-43	2708514	(AF016411) KCNA3.1B [Homo sapiens]	3e-13
1713	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	1e-43	111814	hypothetical protein 3 - rat >gi 56589	2e-06
1714	X82895	H.sapiens mRNA for DLG2	6e-44	2497511	MAGUK P55 SUBFAMILY MEMBER 2 (MPP2 PROTEIN) (DISCS. LARGE HOMOLOG 2)	6e-52
1715	U17077	Human BENE mRNA, partial cds.	3e-44	53912	(X57960) ribosomal protein L7 [Mus musculus] >gi 55489	8e-30
1716	AJ222700	Homo sapiens mRNA for TSC-22 protein	2e-44	<NONE>	<NONE>	<NONE>
1717	J03634	Human erythroid differentiation protein mRNA	2e-44	124279	INHIBIN BETA A CHAIN PRECURSOR PROTEIN) (EDF) >gi 87936 pir B24248 inhibin beta-A chain precursor - human >gi 181947 (J03634) erythroid differentiation protein precursor [Homo sapiens] sapiens] >gi 226850 prf 1608260B inhibin beta.A [Homo sapiens]	0.73

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1718	AB014518	Homo sapiens mRNA for KIAA0618 protein, complete cds	7e-45	1911548	(S80864) cytochrome c-like polypeptide sapiens]	1.6
1719	X76808	H.sapiens genomic DNA clone d2	7e-45	868201	(U29380) similar to adenylate cyclase [Caenorhabditis elegans]	2e-09
1720	AB021288	Homo sapiens mRNA for beta 2-microglobulin, complete cds	2e-45	2465521	(U95995) RNA-dependent RNA polymerase [Cryptosporidium parvum]	0.15
1721	X63468	H.sapiens mRNA for transcription factor TFIIE alpha	8e-46	<NONE>	<NONE>	<NONE>
1722	AF019226	Homo sapiens D2-2 mRNA, 3'UTR	7e-46	<NONE>	<NONE>	<NONE>
1723	D31764	Human mRNA for KIAA0064 gene, complete cds	2e-46	3123050	HYPOTHETICAL PROTEIN KIAA0064	1e-15
1724	K02774	Human MHC class II HLA-DR-beta-psi (DW4/DR4) pseudogene, exons 3,4, 5,6, clones cosII-3301 and cosII-801.	1e-46	4185946	(Y17834) gag protein [Human endogenous retrovirus K]	2e-14
1725	X92109	H.sapiens hcgIX gene	9e-47	2498185	BRIDE OF SEVENLESS PROTEIN PRECURSOR >gi 1079166 pir A47550 bride of sevenless precursor - fruit fly (Drosophila virilis) >gi 290216 virilis]	1.4
1726	X93334	H.sapiens mitochondrial DNA, complete genome	8e-47	128753	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 86696 pir A00435 NADH dehydrogenase (ubiquinone)	4e-15
1727	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-47	<NONE>	<NONE>	<NONE>
1728	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	3e-47	4185944	(Y17833) env protein [Human endogenous retrovirus K]	7e-18
1729	Z63594	H.sapiens CpG DNA, clone 87t9, forward read cpg87t9.ft1a.	1e-47	3322743	(AE001222) T. pallidum predicted coding region TP0454	2.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		R.rattus mRNA for				
1730	X62295	vascular type-1 angiotensin II receptor	4e-48	1209756	(U43629) integral membrane protein [Beta vulgaris]	1e-07
1731	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-48	<NONE>	<NONE>	<NONE>
1732	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	4e-49	4240299	(AB020712) KIAA0905 protein [Homo sapiens]	2e-20
1733	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	3e-49	4240299	(AB020712) KIAA0905 protein [Homo sapiens]	2e-20
1734	X62295	R.rattus mRNA for vascular type-1 angiotensin II receptor	1e-49	1209756	(U43629) integral membrane protein [Beta vulgaris]	7e-12
1735	AJ007509	Homo sapiens mRNA for E1B-55kDa- associated protein	1e-49	3319956	(AJ007509) E1B-55kDa- associated protein	4e-24
1736	X97303	H.sapiens mRNA for Ptg-12 protein	1e-49	466044	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi 630780 pir S44909 ZK686.4 protein - Caenorhabditis elegans >gi 304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]	8e-31
1737	AF038404	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds	4e-50	<NONE>	<NONE>	<NON
1738	L43618	Homo sapiens polycystic kidney disease (PKD1) gene, exons 35-42	4e-50	903758	(L43619) polycystic kidney disease 1 protein [Homo sapiens]	3e-1
1739	AF009424	Homo sapiens clone 22 mRNA, alternative splice variant alpha-1, complete cds	4e-50	2271473	(AF009426) clone 22 [Homo sapiens]	5e

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					monosaccharid transport protein	
1740	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA sequence.	2e-50	99758	STP4 - Arabidopsis thaliana >gi 16524 (X66857) sugar transport protein [Arabidopsis thaliana]	6.4
1741	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	2e-50	2072960	(U93568) p40 [Homo sapiens]	2e-05
1742	U80745	Homo sapiens CTG7a mRNA, partial cds	1e-50	<NONE>	<NONE>	<NONE>
1743	D84514	Bovine mRNA for p97, partial cds	1e-50	3978527	(AF103728) structural polyprotein [Sindbis virus]	9.9
1744	M22960	Human protective protein mRNA, complete cds.	1e-50	131081	LYSOSOMAL PROTECTIVE PROTEIN PRECURSOR (CATHEPSIN A) (CARBOXYPEPTIDASE C) human >gi 190283 (M22960) protective protein precursor	1e-12
1745	X86018	H.sapiens mRNA for MUF1 protein	1e-50	1082610	muf1 protein - human >gi 762953 (X86018) muf1 [Homo sapiens]	1e-21
1746	U03495	Human transcription factor LSF-ID mRNA, complete cds.	7e-51	2136296	transcription factor LSF - human >gi 476099	1e-21
1747	AB015344	Homo sapiens HRIHFB2157 mRNA, partial cds	5e-51	3970874	(AB015344) HRIHFB2157 [Homo sapiens]	2e-35
1748	M93339	Human zinc finger protein mRNA.	4e-51	3024110	MYC-ASSOCIATED ZINC FINGER PROTEIN sapiens]	2e-06
1749	U71363	Human zinc finger protein zfp6 (ZF6) mRNA, partial cds	4e-51	2689441	(AC003682) F1S547_1 [Homo sapiens]	2e-11
1750	X56932	H.sapiens mRNA for 23 kD highly basic protein	4e-51	730451	60S RIBOSOMAL PROTEIN L13A (23 KD HIGHLY BASIC PROTEIN) >gi 345897 pir S29539 basic protein, 23K - human >gi 23691 (X56932) 23 kD highly basic protein [Homo sapiens]	1e-11
1751	Z79054	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA.21E11	2e-51	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1752	AF068245	BAF60b gene, partial sequence	5e-52	<NONE>	<NONE>	<NONE>
1753	AJ236932	Sus scrofa mRNA for hypothetical protein (5' clone 4B8)	5e-52	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1754	AF003693	Mus musculus scaffold protein Pbp1 homolog mRNA, complete cds	6e-53	2197106	(AF003693) scaffold protein Pbp1 homolog [Mus musculus]	2e-54
1755	M27319	Human calmodulin mRNA, complete cds.	5e-53	115528	CALMODULIN >gi 102408 pir JC1309 calmodulin - Stylonychia lemnae (SGC5) >gi 161195	0.002
1756	M74555	Mouse house-keeping protein mRNA, complete cds.	5e-53	284775	house-keeping protein - mouse >gi 193871	5e-30
1757	X92720	H.sapiens mRNA for phosphoenolpyruvate carboxykinase	6e-54	2135915	phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32) precursor, mitochondrial - human carboxykinase (GTP) [Homo sapiens]	6e-21
1758	AF007872	Homo sapiens torsinB (DQ1) mRNA, partial cds	2e-54	2760121	(AB002405) LAK-4p [Homo sapiens]	0.27
1759	U49507	Mus musculus B6CBA Lisch7 mRNA, partial cds.	2e-54	1236083	(U49507) Lisch7 [Mus musculus]	3e-27
1760	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13.	1e-55	2370371	(Y14657) hydrophobin [Pleurotus ostreatus] >gi 2982620 gnl PID e1283986 (AJ225061) POH2 hydrophobin [Pleurotus ostreatus]	2.0
1761	U83702	Human cytochrome c oxidase subunit VIa gene, exon 3 and complete cds	8e-56	2982994	(AE000682) hypothetical protein [Aquifex aeolicus]	7.0
1762	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	7e-56	3021409	(Y12781) transducin (beta) like 1 protein [Homo sapiens]	7e-39

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1763	AB020673	Homo sapiens mRNA for KIAA0866 protein, complete cds	8e-57	2104553	(AF001548) Myosin heavy chain (MHY11) (5'partial) [Homo sapiens]	4e-04
1764	AJ236932	Sus scrofa mRNA for hypothetical protein (5': clone 4B8)	3e-57	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1765	L06900	Human dystrophin gene, intron 1 containing pseudo exon.	1e-58	4185129	(AC005724) unknown protein [Arabidopsis thaliana] thaliana]	7.0
1766	X93334	H.sapiens mitochondrial DNA, complete genome	9e-59	1492050	(U60315) MC107L [Mollusum contagiosum virus subtype 1]	0.17
1767	AF064856	Rattus sp. 7acomp protein mRNA, complete cds	3e-59	3169626	(AF064856) 7acomp protein [Rattus sp.]	2e-31
1768	AF081484	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds	2e-59	32015	(X06956) alpha-tubulin [Homo sapiens]	4e-22
1769	X71427	Homo sapiens mRNA for FUS-CHOP protein fusion	1e-60	746557	(U23523) histidine-rich [Caenorhabditis elegans]	0.45
1770	AF013988	Homo sapiens serine protease mRNA, complete cds	1e-60	2564316	(AB006622) No similarities to any reported proteins [Homo sapiens]	0.26
1771	U25691	Mus musculus lymphocyte specific helicase mRNA, complete cds	7e-61	2137490	lymphocyte specific helicase - mouse musculus]	3e-25
1772	X93334	H.sapiens mitochondrial DNA, complete genome	4e-61	70656	ubiquitin / ribosomal protein S27a - human extension protein, HUBCEP80 [human, Peptide, 156 aa] ubiquitin extention protein [Cavia porcellus]	9e-08
1773	D38255	Homo sapiens mRNA for CAB1, complete cds	4e-61	2135214	gene MLN 6+ protein - human	4e-23
1774	U25691	Mus musculus lymphocyte specific helicase mRNA, complete cds	8e-62	2137490	lymphocyte specific helicase - mouse musculus]	8e-26

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1775	M21731	Human lipocortin-V mRNA, complete cds.	6e-62	3212603	Human Annexin V With Proline Substitution By Thioproline	2e-20
1776	AF021936	Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta (MRCK-beta) mRNA, complete cds	2e-62	2736153	(AF021936) myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta [Rattus norvegicus]	3e-27
1777	Y12059	H.sapiens HUNKI mRNA	1e-62	3184498	(AC004798) R31546_1 [Homo sapiens]	3e-09
1778	L37368	Human (clone E5.1) RNA-binding protein mRNA, complete cds.	6e-63	477578	sialidase - Actinomyces viscosus >gi 141852	7.8
1779	M27877	Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.	5e-63	1731443	ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) >gi 106023 pir A32891 finger protein 1, placental - human	3e-33
1780	AF095448	Homo sapiens putative G protein-coupled receptor	2e-63	3116131	(AL023288) hypothetical protein	4.6
1781	L19437	Human transaldolase mRNA containing transposable element, complete cds	2e-63	1553119	(U63159) transaldolase [Mus musculus]	4e-18
1782	L41351	Homo sapiens prostasin mRNA, complete cds	1e-63	2833277	PROSTASIN PRECURSOR precursor - human >gi 862305 (L41351) prostasin [Homo sapiens] >gi 1143194 (U33446) prostasin [Homo sapiens]	6e-14
1783	AF053470	Homo sapiens 10kD protein (BC10) mRNA, complete cds	6e-64	482237	hypothetical protein K03H1.9 - Caenorhabditis elegans	0.029

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1784	D37791	Mouse mRNA for beta-1,4-galactosyltransferase	6e-64	3880102	(Z93390) similar to FYVE zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans] zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans]	3e-16
1785	AF015770	Mus musculus radical fringe (radical-fringe) mRNA, complete cds	6e-64	2204355	(U94350) radical fringe precursor [Mus musculus]	1e-36
1786	Z79054	H.sapiens flow-sorted chromosome 6 HindIII fragment. SC6pA21E11	2e-64	<NONE>	<NONE>	<NONE>
1787	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end.	1e-64	2447063	(U42580) A565R [Paramecium bursaria Chlorella virus 1]	8.8
1788	Y10211	H.sapiens LAG-3 gene, promoter region	7e-65	1944540	(X14112) tegument protein [human herpesvirus 1]	2.3
1789	M19045	Human lysozyme mRNA, complete cds.	2e-65	<NONE>	<NONE>	<NONE>
1790	U01882	Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds	2e-65	585401	LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN) >gi 480045 pir S36249 lipB protein - Pseudomonas glumae >gi 49207 (X70354) helper protein	4.2
1791	AF069517	Homo sapiens RNA binding protein DEF-3 mRNA, complete cds	2e-65	3212101	(AF069517) RNA binding protein DEF-3 [Homo sapiens]	1e-25

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens jerky gene product homolog mRNA, complete cds				
1792	AF004715		2e-65	2314829	(AF004715) jerky gene product homolog [Homo sapiens]	2e-45
1793	X59652	C. longicaudatus hprt mRNA for hypoxanthine	3e-66	631625	hypoxanthine (guanine) phosphoribosyltransferase - long tailed hamster phosphoribosyltransferase [Cricetulus longicaudatus]	6e-54
1794	U94350	Mus musculus radical fringe precursor mRNA, complete cds	3e-67	2204355	(U94350) radical fringe precursor [Mus musculus]	2e-33
1795	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds	3e-68	2317725	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]	7e-51
1796	J03137	Cow phosphoinositide-specific phospholipase C	3e-69	226908	phospholipase C 154 [Bos taurus]	3e-25
1797	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	1e-69	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	2e-33
1798	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds	4e-70	2317725	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]	3e-19
1799	X65157	M.musculus mRNA for desmoyokin, partial	5e-74	109781	desmoyokin - mouse (fragment) >gi 50675	9e-37
1800	Z97207	Mus musculus mRNA for B-IND1 protein	2e-74	2231019	(Z97207) B-IND1 protein [Mus musculus]	6e-21
1801	U27196	Gallus gallus zinc finger protein (Fzf-1) mRNA, complete cds	6e-75	984814	(U27196) zinc finger protein [Gallus gallus] gallus]	2e-44

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1802	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial	3e-77	3123027	70 KD WD-REPEAT TUMOR-SPECIFIC ANTIGEN >gi 2505957 gn PID e353992 (Y15054) 70 kD tumor-specific antigen [Rattus norvegicus]	4e-42
1803	X65157	M.musculus mRNA for desmoyokin, partial	3e-79	109781	desmoyokin - mouse (fragment) >gi 50675	9e-33
1804	U50736	Rattus norvegicus cardiac adriamycin responsive protein mRNA, complete cds	2e-84	1362781	cytokine inducible nuclear protein C193 - human >gi 793841 (X83703) nuclear protein [Homo sapiens]	7e-30
1805	AF072865	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	2e-84	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	6e-43
1806	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	6e-85	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	1e-41
1807	U19181	Rattus norvegicus Rabin3 mRNA, complete cds.	2e-87	624225	(U19181) Rabin3 [Rattus norvegicus]	2e-41
1808	U40342	Mus musculus ninein mRNA, complete cds.	1e-91	1113865	(U40342) ninein [Mus musculus]	2e-36
1809	X67877	R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein	4e-92	136077	TROPOMYOSIN BETA 3, FIBROBLAST chicken >gi 515694 (M23082) tropomyosin [Gallus gallus]	0.56
1810	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	5e-93	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	1e-50
1811	AF035527	Mus musculus EHF (Ehf) mRNA, complete cds	2e-95	3138930	(AF035527) EHF [Mus musculus]	2e-47

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1812	AB016930	Cricetus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	6e-96	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetus griseus]	7e-41
1813	AB005549	Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds	7e-97	3868778	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	3e-41
1814	X90849	G.gallus PB1 gene	2e-97	2134381	polybromo 1 protein - chicken chicken >gi 951231 (X90849) polybromo 1 protein [Gallus gallus]	1e-34
1815	S79873	h-lamp-2=lysosome-associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	3e-98	<NONE>	<NONE>	<NONE>
1816	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	2e-98	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	9e-39
1817	L14684	Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.	e-100	585084	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi 543383 pir S40780 translation elongation factor G, mitochondrial - rat >gi 310102	2e-30
1818	X84692	M.musculus Spnr mRNA for RNA binding protein	e-133	1363238	spermatid perinuclear RNA-binding protein Spnr - mouse >gi 673454 (X84692) spermatid perinuclear RNA binding protein [Mus musculus]	5e-35
1819	U50736	Rattus norvegicus cardiac adriamycin responsive protein mRNA, complete cds	e-113	1362781	cytokine inducible nuclear protein C193 - human >gi 793841 (X83703) nuclear protein [Homo sapiens]	2e-36
1820	S66855	HoxB9=Hox-2.5 [mice, embryos, mRNA Partial, 786 nt]	e-107	1708355	HOMEODOMAIN PROTEIN HOX-B9 (HOX-2.5)	8e-37

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HoxB9=Hox-2.5				
1821	S66855	[mice, embryos, mRNA Partial, 786 nt]	e-108	1708355	HOMEODOMAIN PROTEIN HOXB9 (HOX-2.5)	4e-37
1822	U92072	Rattus norvegicus m-tomosyn mRNA, complete cds	e-102	3790389	(U92072) m-tomosyn [Rattus norvegicus]	2e-38
1823	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-129	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi 407339 gnl PID d1005029 (D17577) Kif1b [Mus musculus]	2e-39
1824	AF062484	Mus musculus SDP8 mRNA, complete cds	e-122	3126981	(AF062484) SDP8 [Mus musculus]	5e-40
1825	X73683	R.norvegicus mRNA for histone H3.3	e-109	122075	(H3.3Q) histone H3.3 - fruit fly (Drosophila melanogaster) histone H3.3B - chicken >gi 2119023 pir S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136 [Oryctolagus cuniculus] >gi 8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi 51198 gallus] >gi 161190 (M17876) histone H3 [Spisula solidissima] >gi 211853 (M11393) histone 3.3 [Gallus gallus] >gi 306848 (M11354) H3.3 histone [Homo sapiens] melanogaster:] >gi 963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus]	2e-40
1826	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	e-102	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	2e-40
1827	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-131	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi 407339 gnl PID d1005029 (D17577) Kif1b [Mus musculus]	7e-42

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1828	AB016930	<i>Cricetulus griseus</i> mRNA for Phosphatidylglycerophosphate synthase, complete cds	e-131	4159682	(AB016930) Phosphatidylglycerophosphate synthase [<i>Cricetulus griseus</i>]	3e-43
1829	U09874	<i>Mus musculus</i> SKD3 mRNA, complete cds.	e-122	2493735	SKD3 PROTEIN SKD3 [<i>Mus musculus</i>]	7e-48
1830	X99145	<i>C.familiaris</i> mRNA for C3VS protein	e-110	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [<i>Canis familiaris</i>]	2e-49
1831	X99836	<i>P.walti</i> mRNA for rnp associated protein 55	e-106	4200286	(X99836) rap55 [<i>Pleurodeles waltl</i>]	2e-50
1832	AF077003	<i>Mus musculus</i> SH3 domain-containing adapter protein mRNA, complete cds	e-121	3550240	(AF077003) SH3 domain-containing adapter protein; CD2AP	3e-51
1833	AF060246	<i>Mus musculus</i> strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	e-118	3372657	(AF060246) zinc finger protein 106 [<i>Mus musculus</i>]	1e-52
1834	Z14030	<i>R.norvegicus</i> mRNA for TRAP-complex gamma subunit.	e-120	1174453	TRANSLOCON-ASSOCIATED PROTEIN, GAMMA SUBUNIT (TRAP-GAMMA) (SIGNAL SEQUENCE RECEPTOR GAMMA SUBUNIT) (SSR-GAMMA) >gi 423185 pir S33294 translocon-associated protein gamma chain - rat norvegicus]	7e-54
1835	AF077003	<i>Mus musculus</i> SH3 domain-containing adapter protein mRNA, complete cds	e-132	3550240	(AF077003) SH3 domain-containing adapter protein; CD2AP	5e-54
1836	L20427	<i>Rattus norvegicus</i> dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	e-116	457372	(L20427) dihydroxypolyprenylbenzoate methyltransferase dihydroxypolyprenylbenzoate methyltransferase [<i>Rattus norvegicus</i>]	4e-56

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1837	X80169	M.musculus mRNA for 200 kD protein	e-122	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	2e-56
1838	AF080568	Rattus norvegicus CTP:phosphoethanolamine cytidyltransferase mRNA, complete cds	e-119	3396102	(AF080568) CTP:phosphoethanolamine cytidyltransferase	6e-58
1839	X99145	C.familiaris mRNA for C3VS protein	e-121	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [Canis familiaris]	2e-53
1840	AF019075	Pan troglodytes breast and ovarian cancer susceptibility (BRCA1) gene, partial cds	e-145	2218154	(AF005068) breast and ovarian cancer susceptibility protein splice variant [Homo sapiens]	1e-58
1841	U55042	Bos taurus myosin X, complete cds	e-122	1755049	(U55042) myosin X [Bos taurus]	1e-61
1842	AJ007780	Mus musculus mRNA for poly(ADP-ribose) polymerase-2	e-119	3283975	(AF072521) poly-(ADPribosyl)-transferase homolog PARP	4e-62
1843	AF072865	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	e-105	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	3e-62
1844	U55042	Bos taurus myosin X, complete cds	e-121	1755049	(U55042) myosin X [Bos taurus]	1e-62
1845	X61506	Mouse E46 mRNA for E46 protein	e-139	114909	BRAIN PROTEIN E46	9e-67
1846	D90335	Bovine mRNA for GTP-binding protein alpha-subunit	e-148	585174	GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-14 SUBUNIT (GL1) >gi 108711 pir A40891 GTP-binding protein GL1 alpha chain - bovine protein, alpha-subunit [Bos taurus]	2e-69
1847	U49507	Mus musculus B6CBA Lisch7 mRNA, partial cds.	e-140	2121326	(AC002128) Lisch7 [Homo sapiens]	2e-74

Table 4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
5	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
6	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
7	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
8	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
9	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
10	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
11	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
12	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
13	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
14	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
15	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
16	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
17	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
18	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
19	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
20	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
21	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
22	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
23	<NONE>	<NONE>	<NONE>	1079469	tMDC I protein - crab-eating macaque	9.3
24	<NONE>	<NONE>	<NONE>	3043656	(AB011138) KIAA0566 protein [Homo sapiens]	9.3
25	<NONE>	<NONE>	<NONE>	112175	potassium channel protein RK5 - rat protein [Rattus norvegicus]	8.6
26	<NONE>	<NONE>	<NONE>	3769624	(AF091565) olfactory receptor [Rattus norvegicus]	7.2
27	<NONE>	<NONE>	<NONE>	3876443	(Z81517) F28B1.6 [Caenorhabditis elegans]	7.1
28	<NONE>	<NONE>	<NONE>	2224464	(AB001684) ORF249 [Chlorella vulgaris]	6.9
29	<NONE>	<NONE>	<NONE>	1519707	(U67940) ORFveg106; random cDNA sequence [Dictyostelium discoideum]	6.7
30	<NONE>	<NONE>	<NONE>	227491	protein kinase C II [Xenopus laevis]	6.7
31	<NONE>	<NONE>	<NONE>	630575	C50C3.4 protein - Caenorhabditis elegans	6.0
32	<NONE>	<NONE>	<NONE>	137290	35 KD PROTEIN IN RNA2 clover necrotic mosaic virus >gi 61466 (X08021) ORF for 35 kDa polypeptide (AA 1-317) [Red clover necrotic mosaic virus]	6.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
33	<NONE>	<NONE>	<NONE>	30041	(X16711) pid:g30041 [Homo sapiens]	5.9
34	<NONE>	<NONE>	<NONE>	2493585	CELL DIVISION PROTEIN FTSW	5.7
35	<NONE>	<NONE>	<NONE>	1001450	(D63999) hypothetical protein	5.7
36	<NONE>	<NONE>	<NONE>	3182918	NITROGEN REGULATORY PROTEIN AREA	5.2
37	<NONE>	<NONE>	<NONE>	140011	MITOCHONDRIAL RIBOSOMAL PROTEIN S5 Emericella nidulans mitochondrion (SGC3) >gi 12709 nidulans] >gi 472822 (J01390) unknown protein	4.3
38	<NONE>	<NONE>	<NONE>	3979943	(AL034393) predicted using Genefinder; similar to WD domain, G-beta repeat; cDNA EST yk362f7.5 comes from this gene; cDNA EST yk362f7.3 comes from this gene [Caenorhabditis elegans]	4.0
39	<NONE>	<NONE>	<NONE>	950203	(U31329) polyketide synthase [Aspergillus terreus]	3.3
40	<NONE>	<NONE>	<NONE>	3560232	(AL031530) hypothetical zinc finger protein [Schizosaccharomyces pombe]	3.0
41	<NONE>	<NONE>	<NONE>	730071	AXONEME-ASSOCIATED PROTEIN MST101(1) product [Drosophila hydei]	2.6
42	<NONE>	<NONE>	<NONE>	2506641	HYPOTHETICAL 21.7 KD PROTEIN IN INTE-PIN INTERGENIC REGION >gi 1787402 (AE000214) orf, hypothetical protein [Escherichia coli]	2.5
43	<NONE>	<NONE>	<NONE>	3511232	(AF071556) anthranilate dioxygenase large subunit	2.4
44	<NONE>	<NONE>	<NONE>	1150900	(U43139) envelope glycoprotein gp120 [Human immunodeficiency virus type 1] (Z75536) similar to dynein heavy chain; cDNA EST EMBL:D27549 comes from this gene; cDNA EST EMBL:D34859 comes from this gene [Caenorhabditis elegans]	1.9
45	<NONE>	<NONE>	<NONE>	3876099		1.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
46	<NONE>	<NONE>	<NONE>	3881150	(AL032647) predicted using Genefinder	1.4
47	<NONE>	<NONE>	<NONE>	132200	COLANIC ACID CAPSULAR BIOSYNTHESIS ACTIVATION PROTEIN A >gi 95605 pir S17701 rcsA protein	1.1
48	<NONE>	<NONE>	<NONE>	2204286	(U61380) germination protein [Bacillus megaterium]	1.0
49	<NONE>	<NONE>	<NONE>	1723955	HYPOTHETICAL 11.4 KD PROTEIN IN FOX1-KEX1 INTERGENIC REGION >gi 2132566 pir S64222 probable membrane protein YGL204c - yeast (Saccharomyces cerevisiae) >gi 1322838 gnl PID e243803 (Z72726) ORF YGL204c [Saccharomyces cerevisiae]	0.84
50	<NONE>	<NONE>	<NONE>	3201564	(AJ006514) prolipoprotein diacylglycerol transferase [Vibrio cholerae]	0.31
51	<NONE>	<NONE>	<NONE>	2808721	(AL021428) hypothetical protein Rv0064	0.27
52	<NONE>	<NONE>	<NONE>	602434	(U17986) GABA/noradrenaline transporter [Homo sapiens]	0.13
53	<NONE>	<NONE>	<NONE>	3347955	(AF076184) cytosolic sorting protein PACS-1b [Rattus norvegicus]	0.12
54	<NONE>	<NONE>	<NONE>	1255887	(U55344) coded for by C. elegans cDNA yk92b4.5; coded for by C. elegans cDNA yk73a1.5; coded for by C. elegans cDNA yk102e9.5; coded for by C. elegans cDNA yk71c8.5; coded for by C. elegans cDNA yk66d11.5; coded for by C. elegans cDNA yk66c3...	0.074
55	<NONE>	<NONE>	<NONE>	103076	Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster)	0.003
56	<NONE>	<NONE>	<NONE>	107560	Ras inhibitor (clone JC265) - human sapiens]	0.002

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
57	<NONE>	<NONE>	<NONE>	103076	Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (<i>Drosophila melanogaster</i>)	2e-04
58	<NONE>	<NONE>	<NONE>	2702370	(AF038604) contains similarity to <i>Drosophila</i> ovarian tumor locus protein (GB:X13693) [<i>Caenorhabditis elegans</i>]	6e-05
59	<NONE>	<NONE>	<NONE>	3859713	(AL033501) phox domain protein [<i>Candida albicans</i>]	3e-05
60	<NONE>	<NONE>	<NONE>	2088839	(AF003386) F59E12.5 gene product [<i>Caenorhabditis elegans</i>]	2e-08
61	<NONE>	<NONE>	<NONE>	121059	GC-RICH SEQUENCE DNA-BINDING FACTOR GCF - human >gi 179412 (M29204) DNA-binding factor [<i>Homo sapiens</i>]	4e-09
62	<NONE>	<NONE>	<NONE>	3875246	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...	9e-24
63	<NONE>	<NONE>	<NONE>	1465834	(U64857) No definition line found [<i>Caenorhabditis elegans</i>]	9e-28
64	<NONE>	<NONE>	<NONE>	3327136	(AB014561) KIAA0661 protein [<i>Homo sapiens</i>]	1e-29
65	<NONE>	<NONE>	<NONE>	3880433	(Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [<i>Caenorhabditis elegans</i>]	8e-31
66	D42133	Rat annexin V gene, exon7 and exon8	5.0	<NONE>	<NONE>	<NONE>
67	L35679	<i>Homo sapiens</i> (subclone H8 2_d11 from P1 35 H5 C8) DNA sequence.	5.0	1086902	(U41278) coded for by <i>C. elegans</i> cDNA yk79g8.5; coded for by <i>C. elegans</i> cDNA cm10c8; coded for by <i>C. elegans</i> cDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [<i>Caenorhabditis elegans</i>]	6.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HIV-1 strain BX220				
68	U90184	from USA, envelope glycoprotein C2V3 region (env) gene, partial cds	5.0	1297070	(Z71986) convicilin precursor [Vicia narbonensis]	6.6
69	U61465	Human myosin VIIa (MYO7A) gene, 5' exon 37	5.0	2313225	(AE000535) L-lactate permease (lctP) [Helicobacter pylori 26695]	5.0
70	AF013717	Homo sapiens periplakin (PPL) mRNA, partial cds	5.0	3719238	(AF064869) brain-enriched guanylate kinase-associated protein 2; BEGA2 [Rattus norvegicus]	3.8
71	X58245	Soybean mRNA for HMG-1 like protein	5.0	2995363	(AL022245) biotin synthase	0.99
72	AF102425	Fraseria paniculata tRNA-Leu (trnL) gene, intron, chloroplast sequence	4.9	3522958	(AC004411) putative pectinesterase [Arabidopsis thaliana]	6.4
73	X82817	H.sapiens PTP1C/HCP-variant gene	4.9	3875514	(Z81494) cDNA EST EMBL:D27474 comes from this gene; cDNA EST EMBL:D27473 comes from this gene; cDNA EST EMBL:T00471 comes from this gene; cDNA EST EMBL:D34192 comes from this gene; cDNA EST EMBL:D37241 comes from this gene; ...	2.8
74	U04827	Mus musculus brain fatty acid-binding protein	4.9	3676132	(AL031765) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=31.96; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SPTREMBL:Q93319; 2-match_description=HYPOTHETICAL PROTEIN C33A11.2;....	2e-09
75	AF038859	Neospora hughesi strain NE1 internal transcribed spacer 1, complete sequence	4.8	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		M.musculus MFH-1				
76	Y08222	gene	4.8	<NONE>	<NONE>	<NONE>
77	AJ224475	Borrelia burgdorferi left chromosomal subtelomeric region (pfpB gene)	4.8	4218141	(AJ236702) HMR1 protein [Antirrhinum majus]	8.3
78	U02486	Mus musculus LAF putative membrane protein (KRAG) gene, exon 3 and complete cds	4.8	3258103	(AP000006) 367aa long hypothetical protein [Pyrococcus horikoshii]	2.7
79	AB000280	Rat mRNA for peptide/histidine transporter, complete cds	4.8	806317	(M29067) unknown protein [Saccharomyces cerevisiae]	0.001
80	Z49771	A.cepa mitochondrial gene for NADH dehydrogenase subunit 3 and ribosomal protein S12	4.5	<NONE>	<NONE>	<NONE>
81	M63494	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 6 and 7, clones lambda-Fc(3.2.93).	4.3	<NONE>	<NONE>	<NONE>
82	Z14035	S.pombe car1 gene	2.0	3790665	(AF099000) No definition line found [Caenorhabditis elegans]	1.2
83	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes	2.0	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]	2e-26
84	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	2.0	4176500	(AL031177) dJ889M15.3 (novel protein)	9e-59
85	U79292	Human clone 23734 mRNA sequence	1.9	<NONE>	<NONE>	<NONE>
86	V00159	Chloroplast Euglena gracilis gene coding for the 5S and 16S rRNA.	1.9	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.9	<NONE>	<NONE>	<NONE>
87	U95094					
88	X93206	H.salinarium TATA box-binding protein genes and ORFs	1.9	<NONE>	<NONE>	<NONE>
89	U60979	Caenorhabditis elegans programmed cell death specifier (ces-2) gene, complete cds	1.9	<NONE>	<NONE>	<NONE>
90	X56272	C. tentans ORF's (A-E) for hemoglobin	1.9	<NONE>	<NONE>	<NONE>
91	L22383	Homo sapiens DNA sequence, repeat region.	1.9	<NONE>	<NONE>	<NONE>
92	U82814	Hirudo medicinalis neuron-specific protein mRNA, complete cds	1.9	3822533	(AF094531) immunoglobulin heavy chain precursor	2.0
93	U18504	Haplomitrium hookeri 18S rRNA gene, partial sequence.	1.9	1083969	hypothetical protein 6 - fowlpox virus virus]	2.0
94	X53676	Pseudomonas stutzeri nosDFY genes involved in copper processing	1.9	2980781	(AL022198) putative protein	0.70
95	U60086	Dictyostelium discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds.	1.9	3879530	(Z49130) cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene	6e-05
96	U33447	Human putative G-protein-coupled receptor (GPR17) gene, complete cds	1.9	3880034	(Z75550) similar to cell division control protein [Caenorhabditis elegans]	7e-14
97	M81327	Sus scrofa lactoferrin mRNA, complete cds. > :: gb I28421 I28421 Sequence 5 from patent US 5571691	1.8	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>S. iniae</i> lctP & lctO genes and ORF1	1.8	<NONE>	<NONE>	<NONE>
98	Y07622					
99	M60474	Mouse myristoylated alanine-rich C-kinase substrate (MARCKS) mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE>
100	Y13901	Homo sapiens FGFR-4 gene	1.8	<NONE>	<NONE>	<NONE>
101	U44400	Human Down Syndrome region of chromosome 21, clone A31D6-1D6.	1.8	<NONE>	<NONE>	<NONE>
102	U92808	Ruminococcus albus beta-glucosidase (gluA) mRNA, complete cds	1.8	<NONE>	<NONE>	<NONE>
103	L25051	Candida albicans argininosuccinate lyase (ARG4) gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
104	AE000546	Helicobacter pylori 26695 section 24 of 134 of the complete genome	1.8	<NONE>	<NONE>	<NONE>
105	J00978	Xenopus laevis major beta-globin gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
106	U41716	Human immunodeficiency virus type 1 isolate JW95-5, vpr gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
107	X66286	G.gallus mRNA for tensin	1.8	<NONE>	<NONE>	<NONE>
108	U76636	Xenopus calbindin D28k mRNA, complete cds	1.8	<NONE>	<NONE>	<NONE>
109	J00664	rabbit embryonic beta-4-globin gene.	1.8	<NONE>	<NONE>	<NONE>
110	M21535	Human erg protein (ets-related gene) mRNA, complete cds.	1.8	2983160	(AE000693) hypothetical protein [Aquifex aeolicus]	7.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
111	M80829	Rat troponin T cardiac isoform gene, complete cds	1.8	999450	(Z46595) incomplete interleukin- 11 receptor isoform [Homo sapiens]	7.3
112	D37887	Cyprinus carpio c-myc gene for c-Myc, complete cds	1.8	3023408	BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN (BRANCHED-CHAIN AMINO ACID UPTAKE CARRIER) >gi 1075007 pir D64056 membrane-associated component, branched amino acid transport system (brnQ) homolog - Haemophilus influenzae (strain Rd KW20) system II carrier protein (brnQ) [Haemophilus influenzae Rd]	7.2
113	AF019765	Homo sapiens G protein-coupled receptor kinase 1 and G protein-coupled receptor kinase 1b (GRK1) gene, alternatively spliced, alternative exon 6, exon 7, and partial cds	1.8	498643	(U10270) G-box binding factor 1 [Zea mays]	7.2
114	AF025967	Helicobacter pylori J166 virulence regulon transcriptional activator homolog gene, partial cds, strain-specific genomic sequence B2	1.8	3850108	(AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]	5.7
115	U13183	Xenopus laevis (Xwnt-4) mRNA, complete cds.	1.8	2494853	PROBABLE HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II) protein [Escherichia coli] >gi 1786406 (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli]	5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
116	S68944	Na+/Cl(-)-dependent neurotransmitter transporter	1.8	2276316	(Z96810) GLYT-1 LIKE [Homo sapiens]	5.5
117	M92905	Rat calcium channel alpha-1 subunit (rbB-I) mRNA, complete cds.	1.8	3165522	(AF067607) Similar to cuticular collagen; C18H7.3	5.5
118	X12429	Xenopus laevis UI 70K gene exon 10	1.8	2735957	(AF015685) reverse transcriptase domain protein	3.3
119	D83333	Mouse hepatitis virus genomic RNA for spike protein, partial cds	1.8	3876559	(Z91072) similarity to human cyclin A/CDK2-associated protein P19 (RNA polymerase elongation factor) (SW:SKP1_HUMAN); cDNA EST EMBL:T00114 comes from this gene; cDNA EST yk390f11.5 comes from this gene; cDNA EST yk402e11.5 co...	3.3
120	AF016972	Cervus elaphus REDDEER mitochondrial D-loop, complete sequence	1.8	3878057	(Z99942) similar to von Willebrand factor type A domain; cDNA EST yk412d4.5 comes from this gene; cDNA EST yk412d4.3 comes from this gene	3.2
121	AB010741	Oncorhynchus mykiss mRNA for rtSox24, complete cds	1.8	1730805	HYPOTHETICAL 21.0 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION >gi 2132762 pir S63129 probable membrane protein YNL174w - yeast (Saccharomyces cerevisiae) >gi 1302152 gnl PID e239548 (Z71451) ORF YNL174w [Saccharomyces cerevisiae]	2.5
122	U32844	Haemophilus influenzae Rd section 159 of 163 of the complete genome	1.8	728910	A-TYPE INCLUSION PROTEIN (ATI) camelpox virus >gi 62381 (X69774) 84kDa A-type inclusion protein [unidentified]	1.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
123	U18321	Human ionizing radiation resistance conferring protein mRNA, complete cds.	1.8	2133273	ribosomal protein YS7 homolog <i>Emericella nidulans</i>	1.4
124	M28668	Human cystic fibrosis mRNA, encoding a presumed transmembrane conductance regulator (CFTR). > :: gb I11500 I11500 Sequence 1 from Patent US 5407796	1.8	90492	filaggrin precursor - mouse (fragment)	0.87
125	AF064553	Mus musculus NSD1 protein mRNA, complete cds	1.8	2501207	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi 1065461 (U40411) Similar to protein disulfide-isomerase. [<i>Caenorhabditis elegans</i>]	0.87
126	AB002314	Human mRNA for KIAA0316 gene, complete cds	1.8	115131	REGULATORY PROTEIN BRLA (BRISTLE A PROTEIN) >gi 83718 pir A28913 regulatory protein brlA - <i>Emericella nidulans</i> >gi 168029 (M20631) brlA protein	0.84
127	L42096	Homo sapiens (subclone 10_d2 from P1 H21) DNA sequence.	1.8	2135624	metalloproteinase 1 (EC 3.4.24.-) - human	0.65
128	M37278	R.norvegicus renin gene, exons 1-9.	1.8	4050087	(AF109907) S164 [<i>Homo sapiens</i>]	0.58
129	X82879	Artificial sequences DNA for ART 2 consensus	1.8	310929	(L13442) cysteine-rich extensin-like protein-4 [<i>Nicotiana tabacum</i>]	0.52
130	D89729	Homo sapiens mRNA for CRM1 protein, complete cds	1.8	3559944	(AJ010792) Muc5AC protein [<i>Mus musculus</i>]	0.38
131	U78076	Mus musculus sepiapterin reductase gene, exons 1 and 2	1.8	2984225	(AE000766) enolase-phosphatase E-1 [<i>Aquifex aeolicus</i>]	0.095

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
132	X52133	Paramecium 168G gene for 168G surface protein	1.8	115316	COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) >gi 105686 pir S15435 collagen alpha 1(VIII) chain precursor - (U61944) coded for by C. elegans cDNA yk112f3.5; coded for by C. elegans cDNA cm21d2; coded for by C. elegans cDNA CEESR07F; coded for by C. elegans cDNA yk112f3.3; coded for by C. elegans cDNA CEESR29F [Caenorhabditis elegans]	0.073
133	M77830	Human desmoplakin I mRNA, complete cds.	1.8	1397246	(U43192) myosin II heavy chain [Naegleria fowleri]	1e-04
134	AJ224150	Plasmodium berghei EF-1alpha A-gene	1.8	1353761	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	2e-05
135	AJ005518	Mus musculus somatostatin receptor 2 gene, exon1 and 5' flanking region	1.8	1326350	(AL031174) hypothetical protein	2e-08
136	AF002217	Ralstonia eutropha megaplasmid pHG1 nitric oxide reductase (norB) gene, complete cds	1.8	3393018	(AL033388) 3-oxoacyl-[acyl-carrier-protein]-synthase	2e-08
137	AF039035	Caenorhabditis elegans cosmid C53A3	1.8	3850109	(AL022600) putative mannose-1 phosphate guanyl transferase [Schizosaccharomyces pombe]	3e-11
138	M81769	S.domesticus immunoglobulin rearranged gamma chain mRNA, VJC region, complete cds.	1.8	3080527	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I >gi 984224 (Z54096) unknown	3e-14
139	Y11106	P.pastoris PYC1 gene	1.8	1175412	(AL021687) putative protein [Arabidopsis thaliana] >gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]	1e-15
140	U87803	Human putative Ca2+/calmodulin-dependent protein kinase kinase gene, 3' flanking region, partial sequence	1.8	2828280		3e-17

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
		falciparum				
141	AE001430	chromosome 2, section 67 of 73 of the complete sequence	1.8	1931647	(U95973) endomembrane protein EMP70 precursor isolog	2e-20
142	L19708	Rat N-methyl-D-aspartate receptor (NMDAR1) gene, first exon.	1.8	1731181	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi 3874230 gnl PID e1351618 protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans]	3e-21
143	Y10728	P.schwarzi mitochondrial cytb gene, partial	1.8	3878644	(Z81103) predicted using Genefinder; cDNA EST yk303g11.5 comes from this gene; cDNA EST yk303g11.3 comes from this gene [Caenorhabditis elegans]	1e-28
144	AB006631	Homo sapiens mRNA for KIAA0293 gene, partial cds	1.8	4176500	(AL031177) dJ889M15.3 (novel protein)	7e-45
145	AF106967	Mus musculus I3 protein mRNA, complete cds	1.7	<NONE>	<NONE>	<NONE>
146	AE001073	Archaeoglobus fulgidus section 34 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
147	U12977	Pseudomonas lemoignei poly(3-hydroxybutyrate) depolymerase A precursor (phaZ5) gene, complete cds, and glycerol-3-phosphate-dehydrogenase homolog, complete cds.	1.7	<NONE>	<NONE>	<NONE>
148	M27038	Mus musculus (SK/CamRk) germline IgK chain gene, J1-5 region.	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens HBF-1				
149	X74142	mRNA for transcription factor Streptococcus thermophilus DeoD gene, partial cds and EpsA, EpsB, EpsC, EpsD, EpsE, EpsF, EpsG, EpsH, EpsI, EpsJ, EpsK, EpsL, EpsM, Orf14.9 protein genes, complete cds	1.7	<NONE>	<NONE>	<NONE>
150	U40830	Rabbit Ig germline gamma H-chain (allotype d12,e15) C-region gene, 3' end.	1.7	<NONE>	<NONE>	<NONE>
151	L29172	Human lysozyme mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
152	M19045	Borrelia burgdorferi (section 45 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
153	AE001159	Plasmid pFdA (from Fremyella diplosiphon) DNA sequence, including unidentified cds and stem loop.	1.7	<NONE>	<NONE>	<NONE>
154	L17027	Arabidopsis thaliana Columbia GTP binding protein beta subunit (AGB1) mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
155	U12232	Arabidopsis thaliana ATPK6 mRNA for ribosomal-protein S6 kinase homolog, complete cds	1.7	<NONE>	<NONE>	<NONE>
156	D42056	Rhizobium leguminosarum prsD, prsE, ORF3 genes	1.7	<NONE>	<NONE>	<NONE>
157	X98117					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
158	AF039084	Spinacia oleracea heat shock 70 protein protein, complete cds	1.7	<NONE>	<NONE>	<NONE>
159	Z12651	R.norvegicus gene for catechol methyltransferase	1.7	<NONE>	<NONE>	<NONE>
160	AF002968	Fringilla coelebs mitochondrial control region, partial sequence	1.7	<NONE>	<NONE>	<NONE>
161	AE001160	Borrelia burgdorferi (section 46 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
162	U67553	Methanococcus jannaschii section 95 of 150 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
163	M86247	S.ruminantium plasmid pS23 DNA.	1.7	<NONE>	<NONE>	<NONE>
164	S74436	oIL-8=interleukin-8 [sheep, spleen cells, mRNA, 1435 nt]	1.7	<NONE>	<NONE>	<NONE>
165	D12719	Candida maltosa ALK7 (CYP52A10) and ALK8 complete cds	1.7	<NONE>	<NONE>	<NONE>
166	U02625	Geotrichum candidum NRRL Y-553 lipase gene, partial cds.	1.7	321245	230k bullous pemphigoid antigen BPM1 - mouse	9.3
167	Z58881	H.sapiens CpG DNA, clone 114a4, reverse read cpg114a4.rtl.a .	1.7	1854675	(U66298) bone morphogenetic protein-6 [Rattus norvegicus]	9.1
168	U43674	Agrobacterium tumefaciens conjugal transfer region 1 genes	1.7	1352066	LARGE PROLINE-RICH PROTEIN BAT2 MHC class III histocompatibility antigen HLA-B-associated transcript 2 - human >gi 179339 (M33509) HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >gi 179345 (M33518) HLA-B-associated transcript 2 (BAT2) [Homo.sapiens]	9.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
169	AL023827	Caenorhabditis elegans cosmid Y12A6A, complete sequence [Caenorhabditis elegans]	1.7	731440	PROTOPORPHYRINOGEN OXIDASE (PPO) yeast (Saccharomyces cerevisiae) >gi 603606 (U18778) Hem14p: protoporphyrinogen oxidase [Saccharomyces cerevisiae] >gi 1403536 gnl PID e249333 (Z71381) protoporphyrinogen oxidase [Saccharomyces cerevisiae]	8.9
170	X69662	X.laevis mRNA for glutathione synthetase, large subunit	1.7	4038057	(AC005897) hypothetical protein [Arabidopsis thaliana]	8.8
171	Z35824	S.cerevisiae chromosome II reading frame ORF YBL063w	1.7	3021450	(Y15515) prdl-a [Hydra vulgaris]	7.0
172	M65139	Cowpea chlorotic mottle virus (CCMV) 1a protein gene, complete cds.	1.7	2506307	COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR 1(XII) chain - chicken >gi 222811 gnl PID d1001160 gallus] >gi 2326442 gnl PID e39435 (X61024) collagen type XII alpha 1 chain [Gallus gallus]	7.0
173	X15065	Drosophila distal BX-C region (bithorax complex) pH189 5' region;	1.7	1723625	HYPOTHETICAL 10.0 KD PROTEIN IN ALPA-GABD INTERGENIC REGION (F87) >gi 1033124 (U36840) ORF_f87 [Escherichia coli] >gi 1788982 (AE000348) orf, hypothetical protein	6.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
174	Z46255	S.cerevisiae chromosome VI lambda clone.	1.7	3875228	(Z46792) similar to lethal(1) discs large-1 tumor suppressor protein-like repeats; cDNA EST EMBL:D33495 comes from this gene; cDNA EST EMBL:D35117 comes from this gene; cDNA EST EMBL:D36356 comes from this gene; cDNA EST EMB... >gi 3879984 gnl PID e1351767 suppressor protein-like repeats; cDNA EST EMBL:D33495 comes from this gene; cDNA EST EMBL:D35117 comes from this gene; cDNA EST EMBL:D36356 comes from this gene; cDNA EST EMB...	6.7
175	U01066	Human CD4 promoter, partial sequence.	1.7	125448	THYMIDINE KINASE saimiriine herpesvirus 1 (strain 11[Onc]) >gi 60341	6.7
176	U34743	Phalaenopsis sp. 'hybrid SM9108' homeobox protein mRNA, complete cds	1.7	1022918	(U38184) ATPase subunit 6 [Trypanosoma cruzi]	6.7
177	U14662	Baboon herpesvirus HVP2 gB glycoprotein (UL27) gene, complete cds.	1.7	3218378	(AL023862) hypothetical protein SC3F9.07 [Streptomyces coelicolor]	6.7
178	AB017006	Homo sapiens PMS2L15 mRNA, partial cds	1.7	1465855	(U64859) glutamine-rich protein [Caenorhabditis elegans]	6.7
179	U92651	Brassica oleracea var. botrytis tonoplast intrinsic protein bobTIP26-1 mRNA, complete cds	1.7	3023675	DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein heavy chain [Schizosaccharomyces pombe]	6.6
180	AF000634	Lytechinus variegatus notch homolog mRNA, complete cds	1.7	148574	(M58520) endo-1,4-beta-glucanase [Fibrobacter succinogenes]	6.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
181	M92354	Arabidopsis thaliana anthranilate synthase alpha subunit gene, complete cds.	1.7	738308	blue light photoreceptor [Arabidopsis thaliana]	6.5
182	AJ234856	Hordeum vulgare genomic DNA fragment; clone MWG2234.rev	1.7	3142302	(AC002411) Strong similarity to myosin heavy chain gb Z34293 from A. thaliana. [Arabidopsis thaliana]	6.5
183	U76827	Stercorarius parasiticus bird J33 cytochrome b protein, partial cds	1.7	3413810	(Y17034) Bassoon [Mus musculus]	5.4
184	U05211	Saccharomyces cerevisiae Ttp1p (TTP1) gene, complete cds.	1.7	403173	(L24492) lipoprotein [Rhodococcus erythropolis]	4.9
185	AF076974	Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds	1.7	1170140	PUTATIVE ENDOGLUCANASE TYPE K PRECURSOR (ENDO-1,4-BETA-GLUCANASE) (CELLULASE)	4.1
186	AE000753	Aquifex aeolicus section 85 of 109 of the complete genome	1.7	1169357	DNA ADENINE METHYLASE site-specific DNA-methyltransferase (adenine-specific) dam methylase gene product [Vibrio cholerae]	4.0
187	AF005638	Tupaia glis apolipoprotein AI prepropeptide mRNA, complete cds	1.7	3355682	(AL031124) putative secreted lyase	4.0
188	M23090	Human germline IgK chain gene V3-region, clone Humkv328h5	1.7	2257483	(AB004534) pi003 [Schizosaccharomyces pombe]	4.0
189	M24001	Mink enteritis virus antigenic type 2 capsid protein genes VP1 and VP2, complete cds.	1.7	2143504	myotonic dystrophy kinase - mouse (fragment) kinase, DM-kinase {C-terminal, alternatively spliced, clone delta II,III,IV,V} [mice, brain, Peptide Partial, 474 aa] [Mus sp.]	3.9
190	X59964	H.sapiens CST4 gene for Cystatin D	1.7	1766075	(U37273) winged helix protein CWH-2 [Gallus gallus]	3.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 11.7 KD	
191	X95276	<i>P.falciparum</i> complete gene map of plastid-like DNA (IR-B)	1.7	3219951	PROTEIN C6B12.13 IN CHROMOSOME I >gi 2330843 gnl PID e334047 pombe]	3.0
192	D84487	Rat PMSG-induced ovarian mRNA, 3' sequence, N10	1.7	173164	(J02719) valyl-tRNA synthetase [<i>Saccharomyces cerevisiae</i>]	2.3
193	L14851	<i>Rattus norvegicus</i> neurexin III-alpha gene, complete cds.	1.7	3323586	(AF060869) single-strand binding protein [<i>Salmonella typhimurium</i>]	2.3
194	M97002	<i>Xenopus laevis</i> /gilli hybrid pseudo-IgH chain gene, V region, clone LG7G342A.	1.7	2118407	MHC sex-limited protein - mouse (fragment) musculus]	2.3
195	L07025	<i>Bacillus thuringiensis</i> delta-endotoxin (CryA(a)) gene, 5' end. > :: gb I34520 I34520 Sequence 1 from patent US 5596071 > :: gb I39790 I39790 Sequence 1 from patent US 5616495 > :: gb AR008487 AR008487 Sequence 1 from patent US 5753492	1.7	2496940	HYPOTHETICAL 53.4 KD PROTEIN D1054.13 IN CHROMOSOME V >gi 3875316 gnl PID e1344967	1.8
196	S73149	insulin-like growth factor II {intron 7} [human, Genomic, 1702 nt]	1.7	3327038	(AB014512) KIAA0612 protein [Homo sapiens]	1.8
197	D86990	Human (lambda) DNA for immunoglobulin light chain	1.7	494367	Fv Fragment (Murine Se155-4) Complex With The Trisaccharide: Alpha-D-Galactose(1-2)[alpha-D-Abequose(1-3)]alpha-D-Mannose (P1-Ome) (Part Of The Cell-Surface Carbohydrate Of Pathogenic Salmonella)	1.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmid pFdA (from				
198	L17027	Freymyella diplosiphon) DNA sequence, including unidentified cds and stem loop.	1.7	1082702	poliovirus receptor-related protein - human	1.4
199	AL022273	Caenorhabditis elegans cosmid H22D14, complete sequence [Caenorhabditis elegans]	1.7	3924605	(AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]	1.4
200	U89926	Drosophila melanogaster cut gene, partial sequence	1.7	2245100	(Z97343) DNA-binding protein homolog	1.3
201	Z25749	H.sapiens gene for ribosomal protein S7	1.7	2493459	PROTEIN KINASE C SUBSTRATE, 60.1 KD PROTEIN, HEAVY CHAIN (PKCSH) (80K-H PROTEIN) >gi 1215746	1.1
202	U59841	Fundulus heteroclitus lactate dehydrogenase B	1.7	3005587	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]	0.82
203	X55763	Rabbit mRNA for smooth muscle calcium channel blocker (CaCB) receptor	1.7	3883128	(AF082302) arabinogalactan-protein [Arabidopsis thaliana]	0.82
204	Z75528	Caenorhabditis elegans cosmid C18B12A, complete sequence [Caenorhabditis elegans]	1.7	940397	(D10123) core [Hepatitis C virus]	0.80
205	U50912	Human XIST gene, poly purine-pyrimidine repeat region	1.7	2338027	(AF005370) large tegument protein [Alcelaphine herpesvirus 1]	0.59
206	X12817	Ovis aries beta-lactoglobulin gene	1.7	987050	(X65335) lacZ gene product [unidentified cloning vector]	0.45
207	AF004419	Homo sapiens troponin T (TNNT2) gene, exon 13	1.7	2996364	(AF053947) unknown [Yersinia pestis] >gi 3883090	0.22
208	L43643	Gallus domesticus DNA microsatellite marker MCW119	1.7	464896	TRANSDUCIN-LIKE ENHANCER PROTEIN 1 enhancer-of-split homolog TLE-1 - human >gi 307510	0.20

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
209	Z73278	S.cerevisiae chromosome XII reading frame ORF YLR106c	1.7	1351657	HYPOTHETICAL 123.9 KD PROTEIN C30D11.04C IN CHROMOSOME I >gi 2130411 pir S62562 hypothetical protein SPAC30D11.4c - fission yeast nuclear pore complex protein [Schizosaccharomyces pombe]	0.20
210	M22345	Mouse endogenous provirus gag, pol, and env region DNA.	1.7	2444455	(AF020765) hypothetical protein [Myxococcus xanthus]	0.12
211	AE000360	Escherichia coli K-12 MG1655 section 250 of 400 of the complete genome	1.7	2736361	(AF039038) No definition line found [Caenorhabditis elegans]	0.12
212	AB020692	Homo sapiens mRNA for KIAA0885 protein, complete cds	1.7	2605924	(AF029726) histidine kinase C [Dictyostelium discoideum]	0.094
213	S69429	testis-determining gene/SRY homolog [Sminthopsis macroura=striped-faced dunnarts, Genomic, 855 nt]	1.7	2499016	TONB PROTEIN >gi 1666536 (U23764) TonB [Pseudomonas aeruginosa]	0.092
214	S69429	testis-determining gene/SRY homolog [Sminthopsis macroura=striped-faced dunnarts, Genomic, 855 nt]	1.7	2499016	TONB PROTEIN >gi 1666536 (U23764) TonB [Pseudomonas aeruginosa]	0.088
215	U67205	Mus musculus ACF7 neural isoform 3 (mACF7) mRNA, partial cds	1.7	2047349	(AF000198) weak similarity to HSP90 [Caenorhabditis elegans]	0.052
216	X98188	Artificial DNA sequence for mammalian lambda-neo minichromosome, 1400 bp	1.7	2493779	PUTATIVE CUTICLE COLLAGEN C09G5.6 collagen; cDNA EST yk244c3.5 comes from this gene; cDNA EST yk244c3.3 comes from this gene [Caenorhabditis elegans]	0.042
217	U70139	Mus musculus putative CCR4 protein mRNA, partial cds	1.7	2252630	(U95973) hypothetical protein [Arabidopsis thaliana]	0.041

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
218	L38808	Homo sapiens alpha-1 type V collagen (COL5A1) gene, 5' flank and exon 1.	1.7	2895760	(AF045246) universal minicircle sequence binding protein minicircle sequence binding protein [Crithidia fasciculata]	0.039
219	Z72151	B.napus mRNA for AMP-binding protein	1.7	190475	(K02576) salivary proline-rich protein 1 [Homo sapiens]	0.011
220	X94152	R.norvegicus mRNA for cysteine sulfinate decarboxylase	1.7	2136212	synapsin IIb - human >gi 1594277 (U40215) synapsin IIb [Homo sapiens]	0.008
221	L20255	Mouse stathmin gene sequence.	1.7	2317934	(U97553) unknown [murine herpesvirus 68]	0.006
222	L13600	Rattus norvegicus glycine transporter mRNA, complete cds.	1.7	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	0.003
223	AJ224150	Plasmodium berghei EF-1alpha A-gene	1.7	2072290	(U95094) XL-INCENP [Xenopus laevis]	0.001
224	S80642	butyrophilin [mice, lactating mammary gland, mRNA Partial, 3193 nt]	1.7	2695746	(AJ223010) Pmt2 [Schizosaccharomyces pombe]	9e-04
225	M22363	C.elegans unc-86 gene encoding two alternative proteins, complete cds.	1.7	2224683	(AB002369) KIAA0371 [Homo sapiens]	1e-04
226	X92123	M.musculus cgt gene exon 1	1.7	3874232	(Z49909) similar to Prokaryotic ribonuclease PH [Caenorhabditis elegans]	3e-05
227	AB016000	Ipomoea nil PKn2 (knotted-like gene) mRNA, complete cds	1.7	2183083	(AF000422) TTF-I interacting peptide 5 [Homo sapiens]	1e-05
228	D14133	Bovine mRNA for synaptocanalin I	1.7	3925277	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	2e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
229	L01991	Mus musculus TAFG-1-like neuronal glycoprotein (PCS) mRNA, complete cds.	1.7	3006139	(AL022299) hypothetical protein	4e-07
230	X63016	Tomato yellow leaf curl virus Thailand isolate complete genome (TYLCV-TH B-DNA)	1.7	3643608	(AC005395) hypothetical protein [Arabidopsis thaliana]	1e-07
231	Z22802	H.sapiens microsatellite repeat. > :: gb G34562 G34562 human STS SHGC-51834	1.7	100210	extensin precursor (clone Tom L 4) - tomato esculentum]	4e-09
232	K02765	Human complement component C3 mRNA, alpha and beta subunits, complete cds.	1.7	2984320	(AE000773) acetoin utilization protein [Aquifex aeolicus]	1e-09
233	Z74818	S.cerevisiae chromosome XV reading frame ORF YOL076w	1.7	3873700	(Z73102) predicted using Genefinder; Similarity to Bacillus subtilis DNAJ protein gene; cDNA EST EMBL:C12520 comes from this gene; cDNA EST EMBL:D71409 comes from this ge...	7e-11
234	D21871	Pig mRNA for thimet oligopeptidase	1.7	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	8e-13
235	Y14344	Gallus gallus gene encoding neurofascin, exons 9,10,11 & 12	1.7	3876421	(Z81070) cDNA EST EMBL:C12730 comes from this gene; cDNA EST yk200b6.5 comes from this gene; cDNA EST yk349a12.5 comes from this gene [Caenorhabditis elegans]	3e-14
236	Z73608	S.cerevisiae chromosome XVI reading frame ORF YPL252c	1.7	1439663	(U64605) C05D9.6 gene product [Caenorhabditis elegans]	6e-18

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
237	AG000518	Homo sapiens genomic DNA, 21q region, clone: T171N23	1.7	1174468	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG >gi 529357 (U13019) No definition line found [Caenorhabditis elegans]	6e-18
238	D17716	Human mRNA for N-acetylglucosaminyltransferase V, complete cds	1.7	961446	(D63877) KIAA0157 gene product is novel.	5e-19
239	AF102512	Cheilodactylus vittatus country USA: Midway Island cytochrome c oxidase subunit I gene, mitochondrial gene encoding mitochondrial protein, partial cds	1.7	1572756	(U70848) C43G2.1 gene product [Caenorhabditis elegans]	5e-40
240	L30107	Rattus norvegicus liver-specific transporter gene, promoter region.	1.7	4176443	(AL022238) dJ1042K10.4 (novel protein)	3e-49
241	X91220	H.sapiens mRNA for Na-Cl electroneutral thiazide-sensitive cotransporter	1.7	3478637	(AC005546) R29425_1 [Homo sapiens]	6e-54
242	U97146	Rattus norvegicus calcium-independent phospholipase A2 mRNA, complete cds	1.6	<NONE>	<NONE>	<NONE>
243	Z48508	Pea seed-borne mosaic virus RNA for coat protein and polymerase (partial)	1.6	<NONE>	<NONE>	<NONE>
244	M18349	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5.	1.6	<NONE>	<NONE>	<NONE>
245	M13158	Yeast (S.pombe) cdc25+ gene (mitosis initiation), complete cds.	1.6	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mycoplasma				
246	U39712	genitalium section 34 of 51 of the complete genome	1.6	<NONE>	<NONE>	<NONE>
247	M17922	Mouse Murine urokinase-type plasminogen activator protein gene, complete cds.	1.6	3875750	(Z81499) predicted using Genefinder; cDNA EST yk410e3.3 comes from this gene; cDNA EST yk410e3.5 comes from this gene [Caenorhabditis elegans]	8.0
248	M89986	Human polymorphic loci in Xq28.	1.6	3261710	(Z84724) psd [Mycobacterium tuberculosis]	6.4
249	M89986	Human polymorphic loci in Xq28.	1.6	2143805	inositol-polyphosphate 4-phosphatase - rat	6.2
250	U68725	Rattus norvegicus Deleted in colorectal Cancer	1.6	1256804	(U51449) RING3 protein [Xenopus laevis]	5.8
251	X95199	P.platessa GSTA, GSTA1, GSTA2, and PPTN genes	1.6	3915113	MALEYLACETATE REDUCTASE Pseudomonas cepacia >gi 643636 (U19883) maleylacetate reductase [Burkholderia cepacia]	4.9
252	Y09103	D.melanogaster RPA1 gene	1.6	3916021	HYPOTHETICAL 91 KD PROTEIN IN COB INTRON >gi 2654230 gnl PID e1192341 (X02819) unidentified reading frame [Schizosaccharomyces pombe]	4.8
253	Z14078	T.aestivum mitochondrion fMet, 18S, 5S repeat unit DNA	1.6	2501668	DYSTROPHIN-RELATED PROTEIN 2 sapiens]	3.6
254	AB002314	Human mRNA for KIAA0316 gene, complete cds	1.6	130997	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 1 PRECURSOR >gi 81809 pir A29324 proline-rich protein precursor - soybean >gi 170049 (J02746) proline-rich protein [Glycine max]	2.8
255	M21488	Human muscle creatine kinase gene (CKMM), exon 2.	1.6	119399	ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP40]	2.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
256	AE001164	Borrelia burgdorferi (section 50 of 70) of the complete genome	1.6	4050089	(AF109907) hypothetical protein [Homo sapiens]	1.5
257	X61757	M.musculus rearranged T-cell receptor beta variable region (Vb17a)	1.6	3377766	(AF080090) semaphorin IV isoform b [Mus musculus]	1.2
258	M15346	T.cruzi tandemly repeated gene encoding an 85 kDa antigen with homology to heat shock proteins.	1.6	2804437	(AF043695) similar to zinc metalloprotease family of peptidases [Caenorhabditis elegans]	0.41
259	L39018	Rattus norvegicus sodium channel protein 6 (SCP6) mRNA, complete cds	1.6	2920535	(AF018081) type XVIII collagen [Homo sapiens]	0.037
260	M29483	Human leukocyte adhesion protein p150.95 alpha subunit gene, exons 7 - 15.	1.6	1840045	(U49082) transporter protein [Homo sapiens]	2e-09
261	L06844	Aspergillus niger beta-D-fructofuranosidase (suc1) gene, one exon.	1.6	4206210	(AF071527) putative calcium channel [Arabidopsis thaliana]	9e-10
262	M10946	Chicken aldolase B gene, complete cds, clones lambda-C(11.1.4).	1.6	2746775	(AF040640) similar to peptidase family C19 (ubiquitin carboxyl-terminal hydrolase) [Caenorhabditis elegans]	1e-31
263	X07881	Human gene PRB3L for proline-rich protein G1	1.5	<NONE>	<NONE>	<NONE>
264	U22260	Nicotiana tabacum UMP synthase (pyr5-6) mRNA, partial cds	1.5	3880923	(Z99271) similar to Reverse transcriptase comes from this gene [Caenorhabditis elegans]	0.50
265	U76759	Mus musculus nuclear protein NIP45 mRNA, complete cds	1.4	1330394	(U58761) C01F1.6 gene product [Caenorhabditis elegans]	8.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					POTASSIUM-	
266	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	1.4	1703461	TRANSPORTING ATPASE BETA CHAIN (PROTON PUMP) (GASTRIC H ⁺ /K ⁺ ATPASE BETA SUBUNIT) 3.6.1.36) beta chain - human >gi 184105 (M75110) H,K-ATPase beta subunit [Homo sapiens]	8.9
267	X64659	C.jacchus interferon gene for interferon gamma	1.4	1486485	(U28832) US10 [Gallid herpesvirus 1] >gi 1486497	6.8
268	U11825	Schistosoma japonicum structural muscle protein paramyosin mRNA, complete cds.	0.88	<NONE>	<NONE>	<NONE>
269	D84278	Human DNA for CD38, exon 1	0.68	3766363	(AL031907) hypothetical serine rich protein [Schizosaccharomyces pombe]	3.0
270	M59755	Bovine lens aldose reductase pseudogene, 3' end.	0.67	<NONE>	<NONE>	<NONE>
271	M81758	Homo sapiens skeletal muscle voltage-dependent sodium channel alpha subunit (SkM1) mRNA, complete cds.	0.65	2437819	(Z86105) 1,4-beta-glucanase [Anaerocellum thermophilum]	3.6
272	L01965	Human type IV sodium channel alpha polypeptide	0.64	2437819	(Z86105) 1,4-beta-glucanase [Anaerocellum thermophilum]	3.5
273	U90122	Danio rerio bone morphogenetic protein-4 (bmp4) mRNA, partial cds	0.63	2983532	(AE000720) formate dehydrogenase alpha subunit [Aquifex aeolicus]	7.9
274	L41624	Hylobates lar mucin (MUC1) gene, exons 1-6.	0.63	1517808	(D79215) FGF-10 [Rattus norvegicus]	0.91

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
275	AF030881	Fugu rubripes sushi retrotransposon gag polyprotein (gag) and pol polyprotein (pol) genes, complete cds	0.63	1519696	(U67956) coded for by C. elegans cDNA yk126f9.5; coded for by C. elegans cDNA yk159h6.3; coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.5 [Caenorhabditis elegans]	0.38
276	U52909	Arabidopsis thaliana U1 snRNP 70K protein gene, complete cds	0.62	<NONE>	<NONE>	<NONE>
277	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA, complete cds	0.62	3800934	(AF100655) contains similarity to ser/thr protein kinases [Caenorhabditis elegans]	9.7
278	U17081	Human fatty acid binding protein (FABP3) gene, complete cds	0.62	3617848	(AF049709) tyrosylprotein sulfotransferase-A; TPST-A	7.7
279	AB018340	Homo sapiens mRNA for KIAA0797 protein, partial cds	0.62	424044	VP5 protein - porcine rotavirus >gi 61355	7.7
280	Y00093	H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.62	1054945	(U38621) polyprotein [Tobacco vein mottling virus]	4.5
281	M63138	Human cathepsin D (catD) gene, exons 7, 8, and 9.	0.62	136810	GLYCOPROTEIN M >gi 73791 pir WMBE51 UL10 protein - human herpesvirus 1 1-473 [Human herpesvirus 1] >gi 221732 gnl PID d1002131	3.5
282	X76056	N. sylvestris DNA for spacer region between 25S and 18S ribosomal RNA genes	0.62	2661176	(U76671) putative cds [Rhodobacter sphaeroides]	2.0
283	X74501	B.taurus mRNA for ACTH receptor	0.62	4249552	(AB001075) galectin-2 related protein	2.0
284	M57634	Rat F1-ATPase beta subunit mRNA, 3' end.	0.62	2119692	transforming growth factor-beta type III receptor - chicken >gi 511843 (L01121) transforming growth factor-beta type III receptor [Gallus gallus]	1.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
285	Y15724	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	0.62	2498164	ASPARTYL/ASPARAGINYL BETA-HYDROXYLASE (ASPARTATE BETA-HYDROXYLASE) (ASP BETA-HYDROXYLASE) (PEPTIDE-ASPARTATE BETA-DIOXYGENASE) beta-dioxygenase (EC 1.14.11.16) - bovine >gi 162694 taurus]	0.52
286	AL010142	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-72, complete sequence	0.62	3183206	HYPOTHETICAL PROTEIN KIAA0009 sapiens]	4e-07
287	AB008160	Mus musculus Stat3 gene, 5'-flanking region and exon 1 partial sequence	0.62	466097	HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III >gi 1078903 pir S44654 ZK353.1 protein - Caenorhabditis elegans >gi 289757 (L15313) putative [Caenorhabditis elegans] (Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4...	1e-35
288	AB018795	Halomonas marina gene for alginate lyase, complete cds	0.62	3877493		3e-46
289	Z69906	Human DNA sequence from cosmid E141E2, on chromosome 22, complete sequence [Homo sapiens]	0.61	<NONE>	<NONE>	<NONE>
290	U18259	Human clone CIITA-8 MHC class II transactivator CIITA mRNA, complete cds.	0.61	1483567	(X79983) viral proteinase [Pseudorabies virus]	9.8
291	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.61	475724	(U08884) protein VIII precursor [Bovine adenovirus type 3]	7.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
292	U70825	Rattus norvegicus 5-oxo-L-prolinase mRNA, complete cds	0.61	733543	(U23448) similar to genome polyprotein (SP:POLG_BVDVN, P19711); alternative splicing to C04A2.7a	4.4
293	L81667	Homo sapiens (subclone 2_a9 from P1 H49) DNA sequence	0.61	2565087	(U80759) CAGH4 alternate open reading frame [Homo sapiens]	3.3
294	AE000760	Aquifex aeolicus section 92 of 109 of the complete genome	0.61	2811092	HOMEBOX PROTEIN HOX-A3 (HOX-1.5) homeobox-containing transcription factor [Mus musculus]	2.6
295	U58512	Mus musculus Rho-associated, coiled-coil forming protein kinase p160 ROCK-1 mRNA, complete cds	0.61	295671	(L11275) selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III	1.5
296	U27459	Human origin. recognition complex protein 2 homolog hORC2L mRNA, complete cds	0.61	200285	(M97900) putative open reading frame [Mus musculus]	0.66
297	L36680	Pisum sativum S-adenosylmethionine synthase mRNA, 3' end.	0.61	2285790	(AB002086) p47 [Rattus norvegicus]	4e-12
298	AE000673	Aquifex aeolicus section 5 of 109 of the complete genome	0.61	3395782	(AF058446) histone macroH2A1.2 [Gallus gallus]	6e-27
299	AF086310	Homo sapiens full length insert cDNA clone ZD51F08	0.61	3646450	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]	8e-29
300	AJ009675	Agrotis ipsilon mRNA for 3-hydroxy-3-methylglutaryl coenzyme A reductase	0.61	4176370	(AC005058) similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	2e-73
301	AC005577	Homo sapiens chromosome 19, cosmid F18382B, centromeric end, complete sequence [Homo sapiens]	0.60	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Candida albicans				
302	U40454	topoisomerase type I (CATOP1) gene, complete cds	0.60	<NONE>	<NONE>	<NONE>
303	J01390	Emericella nidulans mtDNA between h2/h5 and bh2/b2 junctions. genes for ATPase subunit 6, cytochrome oxidase subunit 3, seven. unidentified proteins, twentyfour tRNA's and L-rRNA.	0.60	<NONE>	<NONE>	<NONE>
304	L11172	Plasmodium falciparum RNA polymerase I gene, complete cds.	0.60	<NONE>	<NONE>	<NONE>
305	Z81079	Caenorhabditis elegans cosmid F39H11, complete sequence [Caenorhabditis elegans]	0.60	<NONE>	<NONE>	<NONE>
306	Z49627	S.cerevisiae chromosome X reading frame ORF YJR127c	0.60	118751	MAJOR DNA-BINDING PROTEIN herpesvirus 1 (strain 11) >gi 60327 (X64346) major ssDNA-binding protein [Saimiriine herpesvirus 2]	9.6
307	U94911	Rattus norvegicus H-K-ATPase alpha 2 gene, alternatively spliced products and partial cds	0.60	2213862	(AF003086) PfSNF2L [Plasmodium falciparum]	7.4
308	U67476	Methanococcus jannaschii section 18 of 150 of the complete genome	0.60	1749688	(D89240) unnamed protein product	5.7
309	U67513	Methanococcus jannaschii section 55 of 150 of the complete genome	0.60	3327421	(U97068) zonadhesin [Mus musculus]	4.3
310	U57817	Haemophilus ducreyi lipoprotein gene, complete cds	0.60	4008577	(AL034491) conserved hypothetical protein [Schizosaccharomyces pombe]	2.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					probable protein-tyrosine kinase (EC 2.7.1.112) RTK - Pacific electric ray >gi 290858	1.5
311	X80700	H.sapiens G17 gene	0.60	422541		
312	L42167	Mus musculus (clone R24) rds gene, partial cds	0.60	4220848	(AF033823) moira [Drosophila melanogaster]	0.51
313	U54777	Human hMSH6 mRNA, complete cds	0.60	2665637	(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07
314	D86985	Human mRNA for KIAA0232 gene, complete cds	0.60	1938462	(U97006) No definition line found [Caenorhabditis elegans]	2e-07
315	D43964	Rat liver mRNA for Kan-1, complete cds	0.60	1280135	(U55376) coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II)	5e-15
316	U49058	Rattus norvegicus CTD-binding SR-like protein rA4 mRNA, partial cds	0.60	2145091	(U37500) RNA polymerase II largest subunit [Mus musculus]	1e-19
317	X84388	U.ruddi mitochondrial 12S ribosomal RNA	0.60	3874247	(Z70205) predicted using Genefinder	2e-37
318	AF125447	Caenorhabditis elegans cosmid Y14H12B	0.59	<NONE>	<NONE>	<NONE>
319	U20189	Hyoscyamus muticus clone cVS2 vetispiradiene synthase mRNA, partial cds.	0.59	<NONE>	<NONE>	<NONE>
320	M63962	Human gastric H,K-ATPase catalytic subunit gene, complete cds.	0.59	<NONE>	<NONE>	<NONE>
321	AJ132366	Helicobacter pylori (strain P1) comB and pmrA (partial) genes, and partial ORF1 and ORF2	0.59	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
322	U17289	transcription factor AP-2 (AP-2) gene, alternative exon 1a, and isoform 2, partial cds.	0.59	2459419	(AC002332) hypothetical protein [Arabidopsis thaliana]	9.4
323	Z71466	S.cerevisiae chromosome XIV reading frame ORF YNL190w	0.59	3875542	(Z67990) Similarity to Rat amiloride-sensitive sodium channel beta-subunit	7.3
324	Z66493	Beet soil-borne virus genes for 13K, 22K and 48K proteins	0.59	2119867	cryV465 protein - Bacillus thuringiensis thuringiensis]	7.2
325	L41351	Homo sapiens prostatic mRNA, complete cds	0.59	729212	CRYSTALLIN J1C crystallin [Tripedalia cystophora]	4.2
326	X79854	S.lincolnensis gene for 16S ribosomal RNA	0.59	3702828	(AF056577) high mobility group protein 1.2	3.2
327	AJ223356	Strongylocentrotus purpuratus mRNA for SuDp98 protein	0.59	2495704	HYPOTHETICAL PROTEIN KIAA0129 product is novel. [Homo sapiens]	2.5
328	X86019	H.sapiens mRNA for PRPL-2 protein	0.59	1743341	(Y10027) transcription factor TEF-1 [Mus musculus]	2.5
329	U75528	Xiphias gladius creatine kinase gene, partial cds	0.59	1845995	(U69477) envelope glycoprotein [Human immunodeficiency virus type 1]	2.4
330	AC005573	Homo sapiens chromosome 5, PAC clone 202e13	0.59	2506366	DNA POLYMERASE EPSILON SUBUNIT B DNA-directed DNA polymerase (EC 2.7.7.7) II chain B - yeast. (Saccharomyces cerevisiae) >gi 786319 (U25842) DNA Polymerase epsilon, subunit B (Swiss Prot. accession number P24482) [Saccharomyces cerevisiae]	1.4
331	L19180	Rat receptor-linked protein tyrosine phosphatase	0.59	1235974	(X96713) collagen [Globodera pallida]	1.1
332	L32090	Listeria monocytogenes secA gene, complete cds.	0.59	2291129	(AF016415) No definition line found [Caenorhabditis elegans]	0.83

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Xenopus laevis</i>			(AL031124) hypothetical	
333	U24433	syndecan-2 mRNA, complete cds.	0.59	3355692	protein SC1C2.25c [Streptomyces coelicolor]	0.64
334	M23412	<i>Drosophila</i> muscarinic acetylcholine receptor mRNA, complete cds.	0.59	168237	(M76546) hydroxyproline-rich protein [Helianthus annuus]	0.22
335	AF060729	<i>Synaphea media</i> chloroplast atpB-rbcL intergenic spacer region, partial sequence	0.59	731596	HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION >gi 626567 pir S46825 hypothetical protein YHL010c - yeast (Saccharomyces cerevisiae) >gi 2289881 (U11582) No definition line found [Saccharomyces cerevisiae]	0.16
336	AF029734	<i>Xanthobacter autotrophicus</i> transcriptional activator AldR (aldR) gene, partial cds; and NAD-dependent chloroacetaldehyde dehydrogenase (aldB) gene, complete cds	0.59	2498801	PERIAXIN >gi 2143901 pir I58157 periaxin - rat >gi 505297 (Z29649) periaxin [Rattus norvegicus]	0.13
337	X95307	<i>C.reinhardtii</i> LI818r-1 gene	0.59	1723781	HYPOTHETICAL 34.3 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION >gi 2131717 pir S64612 hypothetical protein YGR277c - yeast (Saccharomyces cerevisiae) >gi 1323505 gnl PID e243248 (Z73062) ORF YGR277c [Saccharomyces cerevisiae]	1e-04
338	M24572	<i>Dictyostelium discoideum</i> tRNA-Glu-GAA gene, clone yGluGAA8.	0.59	1176186	HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION >gi 606121 coli]	3e-06
339	U73733	Human hMSH6 gene, exon 2	0.59	2665637	(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07

3460

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Escherichia coli				
340	D90747	genomic DNA. (25.2 - 25.6 min)	0.59	134286	DOLICHOL KINASE	6e-08
341	J05211	Human desmoplakin mRNA, 3' end.	0.59	246796	major centromere protein, CENP-B [human, Peptide, 594 aa]	4e-08
342	L24441	Loligo pealii kinesin light chain mRNA, complete cds.	0.59	547800	KINESIN LIGHT CHAIN (KLC) sea urchin (Strongylocentrotus purpuratus) >gi161530	5e-14
343	M25140	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4.	0.58	<NONE>	<NONE>	<NONE>
344	L81932	Homo sapiens (subclone 9_h2 from P1 H21) DNA sequence	0.58	<NONE>	<NONE>	<NONE>
345	AF087966	Homo sapiens full length insert cDNA clone YU51G04	0.58	<NONE>	<NONE>	<NONE>
346	Z78574	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10G11	0.58	<NONE>	<NONE>	<NONE>
347	AF068061	Blattella germanica allatostatin neuropeptide precursor, gene, complete cds	0.58	<NONE>	<NONE>	<NONE>
348	AF015592	Homo sapiens Cdc7 (CDC7) mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
349	AF028006	Methanosarcina barkeri atp operon: ATP synthase beta subunit (atpD), ATP synthase epsilon subunit (atpC), ATP synthase gene 1 (atpI), ATP synthase a subunit subunit (...)	0.58	3184291	(AC004136) putative DNA polymerase III gamma subunit	9.4
350	AB017032	Mus musculus gene for pancreatic trypsin, complete cds	0.58	3170561	(AF056704) synapsin IIIa [Rattus norvegicus]	9.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Dictyostelium discoideum developmental protein DG1110 (DG1110) gene, partial cds	0.58	105417	basic proline-rich peptide IB-8a human	9.2
351	AF081585					
352	AF086322	Homo sapiens full length insert cDNA clone ZD53E01	0.58	93026	hypothetical protein - African swine fever virus (strain Malawi Lil-20/1) >gi 450758 (X71982) myeloid differentiation antigen homologue [African swine fever virus] >gi 903686 (M95672) unknown protein	7.1
353	AF088025	Homo sapiens full length insert cDNA clone ZC19C04	0.58	2384644	(U92805) thrombospondin-3 [Xenopus laevis]	7.0
354	AB002339	Human mRNA for KIAA0341 gene, partial cds	0.58	2135587	M130 antigen (cytosolic variant 2) - human	5.4
355	U67548	Methanococcus jannaschii section 90 of 150 of the complete genome	0.58	2911094	(AL021957) hypothetical protein Rv2174	4.2
356	L07868	Homo sapiens receptor tyrosine kinase (ERBB4) gene, complete cds.	0.58	461922	PYRUVATE DECARBOXYLASE (8-10 NM CYTOPLASMIC FILAMENT-ASSOCIATED PROTEIN) (P59NC) 4.1.1.1) - Neurospora crassa >gi 293948 (L09125) pyruvate decarboxylase [Neurospora crassa] >gi 1655909	4.2
357	X03897	Bacillus subtilis sigma 43 operon with P23-dnaE-rpoD genes (dnaE for DNA primase, rpoD for RNA polymerase)	0.58	1323704	(U55387) similar to C. elegans F38E1.9 gene product encoded by GenBank Accession Number U41996 [Cricetulus griseus]	4.1
358	D76419	Desulfovibrio vulgaris rbo gene for desulfoferrodoxin and rub gene for rubredoxin, complete cds	0.58	3420047	(AC004680) putative protein kinase [Arabidopsis thaliana]	2.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
359	Z82174	sequence from cosmid B20F6 on chromosome 22, complete sequence [Homo sapiens]	0.58	2145455	(Y07866) catalase-peroxidase	2.4
360	M33642	F.solani STI35 protein gene, complete cds.	0.58	2896706	(AL021897) hypothetical protein Rv1069c	2.4
361	U64873	Mus musculus transforming growth factor alpha (TGF alpha) gene, partial cds	0.58	3874437	(Z81038) predicted using Genefinder; cDNA EST yk488a2.5 comes from this gene [Caenorhabditis elegans]	1.8
362	AB002132	Macrophthalmus banzai mitochondrial DNA for 12S and 16S rRNA, partial and complete sequence	0.58	2960022	(AJ224676) rho type GEF [Drosophila melanogaster]	1.8
363	AF070070	Caenorhabditis elegans MutS homolog (msh-5) mRNA, partial cds	0.58	4098205	(U75869) Omp22 [Helicobacter pylori]	1.8
364	AF045240	Staphylococcus epidermidis plasmid pIP1629 mobilization protein (mobC1), (orf69-1), (mobA1),	0.58	4218117	(AL035353) protein (fragment)	0.62
365	X61637	H.sapiens Wilms tumor gene 1, exons 8 and 9	0.58	2331059	(U88211) unknown [Gallus gallus]	0.62
366	AF039312	Moraxella catarrhalis strain 4223 transferrin binding protein A (tbpA) and transferrin binding protein B (tbpB) genes, complete cds; and unknown gene	0.58	120155	FIBER PROTEIN >gi 74229 pir ERADFM fiber protein - mouse adenovirus 1 >gi 209758 (M30594) fiber protein [Mastadenovirus mus1]	0.27
367	D87463	Human mRNA for KIAA0273 gene, complete cds	0.58	3861477	(U94177) androgen receptor [Pan troglodytes]	0.12
368	U40342	Mus musculus ninein mRNA, complete cds.	0.58	4115936	(AF118223) No definition line found [Arabidopsis thaliana]	0.004

209

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
369	S57235	CD68=110kda transmembrane glycoprotein [human, promonocyte cell line U937, mRNA, 1722 nt]	0.58	2072501	(U96113) WWP1 [Homo sapiens]	1e-04
370	U39391	Mus musculus serotonin1A receptor mRNA, complete cds.	0.58	1469876	(D63481) The KIAA0147 gene product is related to adenylyl cyclase. [Homo sapiens]	1e-07
371	D00056	Monkey B-lymphotropic papovavirus genes for VP-1, 2, 3 and large T antigen, complete and partial cds, strain LPV-76 > :: gb M14494 PPMVP1 M Monkey B-lymphotropic papovavirus mutant (LPV-76) PstI B fragment encoding VP1, VP2, VP3 and T-antigen.	0.58	2462069	(AJ001774) vanadium chloroperoxidase	1e-08
372	M77182	Amsacta entomopoxvirus spheroidin gene, complete cds, and four vaccinia related orfs. > :: gb I16670 I16670 Sequence 1 from patent US 5476781	0.58	1730722	HYPOTHETICAL 43.8 KD PROTEIN IN NCE3-HHT2 INTERGENIC REGION >gi 2131871 pir S62957 hypothetical protein YNL035c - yeast (Saccharomyces cerevisiae) >gi 1301880 gnl PID e239670 (Z71311) ORF YNL035c [Saccharomyces cerevisiae]	8e-14
373	S72579	igloo-S=growth-associated protein GAP-43 homolog	0.58	2689720	(AF037168) DnaJ homologue [Arabidopsis thaliana]	7e-14
374	AF018165	Tetraodon fluviatilis amyloid precursor protein mRNA, complete cds	0.58	3219938	HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I >gi 2058378 gnl PID e314002 pombe]	5e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
375	U81803	Filobasidiella neoformans translation elongation factor EF1-alpha (CnTEF1) mRNA, complete cds	0.57	<NONE>	<NONE>	<NONE>
376	U09781	Candida albicans ATCC 18804, CBS 562 peptide transporter gene, complete cds.	0.57	<NONE>	<NONE>	<NONE>
377	AC002143	Homo sapiens (subclone 4_b10 from BAC H102) DNA sequence	0.57	<NONE>	<NONE>	<NONE>
378	U23442	Tetrahymena thermophila RR internal deletion sequence.	0.57	<NONE>	<NONE>	<NONE>
379	U17289	Mus musculus transcription factor AP-2 (AP-2) gene, alternative exon 1a, and isoform 2, partial cds.	0.57	<NONE>	<NONE>	<NONE>
380	X70844	Buzura suppressaria nuclear polyhedrosis virus gene for polyhedrin protein	0.57	<NONE>	<NONE>	<NONE>
381	AJ012159	Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene	0.57	<NONE>	<NONE>	<NONE>
382	X76571	H.sapiens simple DNA sequence region clone wgl1a8.	0.57	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
383	AF034434	Vibrio cholerae pathogenicity island, putative transposase, aldehyde dehydrogenase (aldA), toxR-activated gene A protein (tagA), putative inner membrane protein, and putative zinc metalloprotease genes, complete cds; and...	0.57	<NONE>	<NONE>	<NONE>
384	AB017031	Mus musculus gene for TESP4, complete cds	0.57	<NONE>	<NONE>	<NONE>
385	X89788	S.hispidus mitochondrial DNA for SSU ribosomal RNA gene	0.57	<NONE>	<NONE>	<NONE>
386	L16921	Rat progesteron receptor gene, 5' untranslated region.	0.57	3323116	(AE001251) femA protein, putative [Treponema pallidum] (S48157) DNA polymerase-primase 180 kda subunit [Drosophila melanogaster, Peptide, 1490 aa]	8.9
387	AF027292	Homo sapiens interferon regulatory factor 6	0.57	259790	hypothetical protein YDR446w - yeast CAI: 0.11 [Saccharomyces cerevisiae]	6.7
388	AJ012581	Cicer arietinum mRNA for cytochrome P450	0.57	2131498	(AF070935) GABA receptor subunit [Musca domestica] (U97008) weak similarity to family 1 of G-protein coupled receptors [Caenorhabditis elegans]	5.3
389	L15363	Human transfer RNA-Met (TRMEP1) pseudogene, complete gene	0.57	3228680	(U94875) p40 [Borna disease virus]	5.2
390	AE000525	Helicobacter pylori 26695 section 3 of 134 of the complete genome	0.57	1938478		4.0
391	AF020189	Amblyomma americanum ecdysteroid receptor (AamEcR) mRNA, 3'UTR, region 1	0.57	2072224		4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human UbA52 gene				
392	X56997	coding for ubiquitin-52 amino acid fusion protein	0.57	2960113	(AL022121) hypothetical protein Rv3689	4.0
393	AL010260	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-81, complete sequence	0.57	117233	CYTOCHROME P450 2C14 (CYPIIC14) phenobarbital-inducible, hepatic - rabbit P-450 [Oryctolagus cuniculus] >gi 358265 prf 1306317A cytochrome P450 [Oryctolagus cuniculus]	3.9
394	M99581	Xenopus laevis gamma-crystallin (gcry3) gene, complete cds.	0.57	141647	GASTRULA ZINC FINGER PROTEIN XLCGF44.2 >gi 85736 pir S06571 finger protein (clone XlcGF44-2) - African clawed frog (fragment)	3.0
395	M38384	Drosophila melanogaster seven in absentia mRNA, complete cds.	0.57	1707127	(U80454) T16A1.1 [Caenorhabditis elegans]	3.0
396	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome	0.57	1173433	IRON(III)-TRANSPORT SYSTEM PERMEASE PROTEIN SFUB >gi 152861 (M33815) protein (sufB)	2.3
397	X12600	Klebsiella pneumoniae nifX, nifU, nifS, nifV and nifW genes	0.57	2909562	(AL021925) hypothetical protein Rv2256c	1.4
398	AB014526	Homo sapiens mRNA for KIAA0626 protein, complete cds	0.57	482390	insect-stage-specific protein - Trypanosoma cruzi >gi 162099 (M65021) insect stage-specific antigen	0.61
399	AF063587	Rhodococcus fascians strain NRRL-B-15096 hypothetical protein gene, complete cds	0.57	4104321	(AF034582) vesicle associated protein [Rattus norvegicus]	0.46
400	L11117	Guinea pig estrone sulfotransferase gene.	0.57	82584	alpha/beta-gliadin precursor (clone A212) - wheat	0.35

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
401	V00829	Mouse complete gene for a mouse kallikrein gene. Genes are mGK1 (complete gene) and mGK-2 of hormones, e.g., grow... > :: gb J00390 MUSKAL07 Mouse pseudo-kallikrein 2, exons 4 and 5, and kallikrein 1 gene, complete cds.	0.57	2500916	NUCLEAR HORMONE RECEPTOR NOR-2 receptor [Rattus norvegicus] >gi 1583604 prf 2121281A NOR-2 protein [Rattus norvegicus]	0.20
402	X53092	Chicken mRNA for beta-2 subunit of neuronal nicotinic acetylcholine receptor	0.57	1072256	(U40953) similar to matrin F/G (SP:Q00910) containing C4-type zinc-fingers [Caenorhabditis elegans]	0.031
403	L07939	Ovis ovis granulocyte colony stimulating factor	0.57	3874345	(Z81035) predicted using Genefinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes f...	3e-07
404	U18061	Colletotrichum gloeosporioides CAP20 (cap20) gene, complete cds.	0.57	2914695	(AC003974) putative ubiquitin specific protease	9e-08
405	Z73955	L.japonicus mRNA for small GTP-binding protein, RAB11G	0.57	112894	TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) >gi 107549 pir A35797 probable DNA-binding protein A20 - human >gi 177866 (M59465) A20	7e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
406	X04335	Petunia grp-1 gene for glycine-rich protein	0.57	3876901	(Z77660) Similarity to Human enoyl-CoA hydratase (SW:ECHM_HUMAN); cDNA EST EMBL:T00611 comes from this gene; cDNA EST yk203d10.3 comes from this gene; cDNA EST yk203d10.5 comes from this gene; cDNA EST yk457h5.3 comes from t...	1e-27
407	U40718	Rattus norvegicus S-adenosylmethionine decarboxylase (AMDP2) pseudogene	0.56	<NONE>	<NONE>	<NONE>
408	M60318	S.cerevisiae SSD1 protein gene, complete cds. > :: gb AR013983 AR013983 Sequence 8 from patent US 5773245	0.56	<NONE>	<NONE>	<NONE>
409	X60057	Nicotiana tabacum blp4 mRNA for luminal binding protein (BiP)	0.56	<NONE>	<NONE>	<NONE>
410	AF085930	Homo sapiens full length insert cDNA clone YR55A09	0.56	<NONE>	<NONE>	<NONE>
411	AL010189	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-102, complete sequence	0.56	<NONE>	<NONE>	<NONE>
412	X05402	Murine G-CSF gene for granulocyte colony stimulating factor precursor	0.56	<NONE>	<NONE>	<NONE>
413	U92280	Rattus norvegicus regulator of G-protein signalling 12 (RGS12) mRNA, complete cds	0.56	<NONE>	<NONE>	<NONE>
414	U85660	Human papillomavirus strain RTRX7 complete genome	0.56	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
415	X57626	M. javanica mitochondrion ATPase 6, and putative tRNA-f-Met and tRNA-His genes	0.56	<NONE>	<NONE>	<NONE>
416	AB003363	Sus scrofa S100C gene, complete cds	0.56	<NONE>	<NONE>	<NONE>
417	L42291	Danio rerio DANA element, intron 4.	0.56	2650002	(AE001062) conserved hypothetical protein [Archaeoglobus fulgidus]	8.7
418	AF031826	Mus musculus leukocystatin gene, complete cds	0.56	462493	L-LACTATE DEHYDROGENASE (IMMUNOGENIC PROTEIN P36) >gi 479296 pir S33362 L-lactate dehydrogenase (EC 1.1.1.27) - Mycoplasma hyopneumoniae	6.7
419	U17068	Pennisetum glaucum Ac-like element, AcL2.	0.56	399449	ESCARGOT/SNAIL PROTEIN HOMOLOG	6.7
420	Z48042	H.sapiens mRNA encoding GPI-anchored protein p137	0.56	141232	HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D) >gi 76316 pir QQSA7C hypothetical protein E-74	6.7
421	AF027657	Choristoneura fumiferana entomopoxvirus nucleotide triphosphate phosphohydrolase I (NPHI) gene, complete cds	0.56	464999	PUTATIVE ACETYLCHOLINE REGULATOR UNC-18 >gi 480359 pir S36747 acetylcholine regulator unc-18 - Caenorhabditis elegans >gi 247392 bbs 100294 putative acetylcholine regulator unc-18	5.1
422	AB011540	Homo sapiens mRNA for MEGF7, partial cds	0.56	1718033	URACIL-DNA GLYCOSYLASE (UDG) herpesvirus 2 >gi 695219 (U20824) uracil DNA glycosylase	5.1
423	X59941	X.maculatus NGF gene for nerve growth factor	0.56	1169081	COMMON PLANT REGULATORY FACTOR CPRF-1 >gi 515621 (X58575) light-inducible protein CPRF-1 [Petroselinum crispum] >gi 1498301 (U46217) CPRF1	3.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
424	M72711	Rat transcriptional repressor of myelin-specific genes (SCIP) mRNA, complete cds.	0.56	501027	(U01849) ORF2 [Trypanosoma brucei]	2.3
425	AL023850	Caenorhabditis elegans cosmid Y67D11A, complete sequence [Caenorhabditis elegans]	0.56	266771	CHORISMATE MUTASE (CM) / PREPHENATE DEHYDRATASE (PDT) (P-PROTEIN) >gi 281791 pir S26053 chorismate mutase (EC 5.4.99.5) P / prephenate dehydratase (EC 4.2.1.51) - Erwinia herbicola >gi 43344	2.3
426	U47862	Schistosoma mansoni gynecophoral canal protein mRNA, complete cds	0.56	2147138	ATP synthase chain 6 - Platymonas subcordiformis mitochondrion >gi 633582 (Z47797) ATP synthase subunit 6 [Platymonas subcordiformis]	2.3
427	V00574	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-ras-1) with four exons.	0.56	1518672	(U60289) receptor protein tyrosine phosphatase psi [Homo sapiens]	1.7
428	Z71502	X.laevis H1(0)-1 gene	0.56	1651674	(D90899) ferrichrome-iron receptor	1.3
429	M37278	R.norvegicus renin gene, exons 1-9.	0.56	2853019	(AF045141) putative serine proteinase [Scirpophaga incertulas]	1.0
430	D28878	Thermus thermophilus polA gene for thermostable DNA polymerase I, complete cds	0.56	3659692	(AF068748) sphingosine kinase [Mus musculus]	0.77
431	Z15027	H.sapiens HLA class III DNA	0.56	1304141	(D43758) fibrinogen A-alpha-chain	0.76
432	M14362	Human T-cell surface antigen CD2 (T11) mRNA, complete cds.	0.56	2462979	(Y11915) Tenascin-X [Bos taurus]	0.59
433	Z50801	Z.mays mRNA for chlorophyll a/b-binding protein CP29	0.56	109677	collagen alpha 1(I) chain - mouse >gi 50487	0.50

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
434	Z38114	S.cerevisiae chromosome XIII cosmid 9745	0.56	140372	HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi 83159 pir S19367 hypothetical protein YCL039w - yeast (Saccharomyces cerevisiae)	0.35
435	AF052254	Escherichia coli DNA gyrase A (gyrA) gene, partial cds	0.56	2724126	(AF038535) synaptotagmin VII [Homo sapiens]	0.12
436	AF080649	Tegula pulligo 12S small subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.56	3913223	CYCLIN-DEPENDENT KINASE INHIBITOR 1 p21/WAF1 [Felis catus]	0.11
437	AJ005690	Danio rerio mRNA for protein tyrosine kinase	0.56	2623830	(AF030962) unknown [Schistosoma mansoni]	7e-06
438	U31202	Human noggin (NOGGIN) gene, complete cds.	0.56	3875475	(Z78411) F02D8.3 [Caenorhabditis elegans]	1e-06
439	X51695	Ovis sp. trichohyalin mRNA, partial	0.56	3386622	(AC004665) unknown protein [Arabidopsis thaliana]	1e-10
440	U28938	Rattus norvegicus protein tyrosine phosphatase D30 mRNA, complete cds	0.56	3293547	(AF072709) putative oxidoreductase [Streptomyces lividans]	1e-14
441	AE001171	Borrelia burgdorferi (section 57 of 70) of the complete genome	0.56	2315521	(AF016452) similar to the beta transducin family	4e-16
442	AF036685	Caenorhabditis elegans cosmid C05B10	0.56	1519671	(U67951) contains similarity to ATP/GTP-binding site motif (PS:PS00017) [Caenorhabditis elegans]	6e-20
443	X01173	Xenopus laevis vitellogenin gene A1 5' flanking region	0.56	1118102	(U41558) K02B2.3 gene product [Caenorhabditis elegans]	2e-31
444	D10911	Mus musculus DNA for MS2 protein, complete cds	0.55	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rice mRNA EN117,				
445	D30010	partial sequence	0.55	<NONE>	<NONE>	<NONE>
446	U51991	Escherichia coli phosphoprotein phosphatase	0.55	<NONE>	<NONE>	<NONE>
447	M18858	Mouse T cell receptor C-gamma-7.1 mRNA, 3' end.	0.55	<NONE>	<NONE>	<NONE>
448	U95218	Homo sapiens T cell-death associated protein gene, complete cds	0.55	<NONE>	<NONE>	<NONE>
449	M14948	Human R-ras gene, exon 1.	0.55	<NONE>	<NONE>	<NONE>
450	AB002353	Human mRNA for KIAA0355 gene, complete cds	0.55	<NONE>	<NONE>	<NONE>
451	L81689	Homo sapiens (subclone 1_d6 from P1 H54) DNA sequence	0.55	<NONE>	<NONE>	<NONE>
452	M68955	Human myristoylated alanine-rich C-kinase substrate (MACS) gene, 5' end.	0.55	3322710	(AE001220) V-type ATPase, subunit B (atpB-1) [Treponema pallidum]	5.0
453	X62953	R.norvegicus mRNA (pJG116) with repetitive elements	0.55	1076802	extensin-like protein - maize >gi 600118 mays]	5.0
454	L34630	Synechocystis sp. mntABC transporter system: periplasmic-binding protein (mntC), complete cds; (mntA) gene, complete cds; membrane protein (mntB) gene, complete cds.	0.55	2117632	hydrogen dehydrogenase (EC 1.12.1.2) - Clostridium acetobutylicum >gi 557064 (U15277) hydrogenase I [Clostridium acetobutylicum]	5.0
455	U43521	Plasmodium berghei merozoite surface protein-1 gene, complete cds	0.55	127654	MYOGLOBIN	4.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
456	Z64937	H.sapiens CpG DNA, clone 17g7, reverse read cpg17g7.r1a.	0.55	417298	MFS18 PROTEIN PRECURSOR	3.8
457	U10914	Macaca mulatta clone irh83 T-cell receptor alpha chain mRNA, partial cds.	0.55	310406	(L09212) tat protein [Simian immunodeficiency virus] virus]	3.8
458	AF022838	Homo sapiens multidrug resistance protein	0.55	1585251	traB gene [Amycolatopsis methanolica]	2.8
459	M35603	Mouse Hox-3.1 gene and Hox-3.2-Hox-3.1 intergenic region.	0.55	818849	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]	2.0
460	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
461	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
462	U59736	Human transcription factor (NFATc.b) mRNA, complete cds	0.55	3327144	(AB014565) KIAA0665 protein [Homo sapiens]	0.096
463	U34860	Saccharomyces cerevisiae origin recognition complex large subunit (ORC1) gene, complete cds	0.55	140372	HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi 83159 pir S19367 hypothetical protein YCL039w - yeast (Saccharomyces cerevisiae)	0.017
464	AF012341	Homo sapiens glutaryl-CoA dehydrogenase (GCDH) gene, exons 6, 7, 8, 9, and 10	0.55	1166611	(U46674) coded for by C. elegans cDNA yk27d9.5; coded for by C. elegans cDNA yk27d9.3; short region of weak homology to drosophila suppressor of sable protein	0.008

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HIV-1 isolate Q98-				
465	AF004891	CxA from Kenya, envelope glycoprotein C2V3 region (env) gene, partial cds	0.54	<NONE>	<NONE>	<NONE>
466	Y10159	D.discoideum racGAP gene	0.54	<NONE>	<NONE>	<NONE>
467	AB001895	Homo sapiens mRNA for B120, complete cds	0.54	<NONE>	<NONE>	<NONE>
468	X12357	Bovine gene for aspartyl protease NM1 exons 3 and 4 > :: lcl X12357 Bovine aspartyl protease NM1 gene, exons 3 and 4.	0.54	<NONE>	<NONE>	<NONE>
469	AE001151	Borrelia burgdorferi (section 37 of 70) of the complete genome	0.54	<NONE>	<NONE>	<NONE>
470	X92052	H.sapiens mRNA for T cell receptor alpha chain	0.54	<NONE>	<NONE>	<NONE>
471	U00938	Mus musculus ileal lipid-binding protein gene, complete cds	0.54	1009712	(U27698) calreticulin [Arabidopsis thaliana]	4.9
472	X68367	M.thermoformicum complete plasmid pFZ1 DNA	0.54	125272	CASEIN KINASE II, ALPHA CHAIN (CK II) >gi 419938 pir A43297 casein kinase II (EC 2.7.1.-) alpha chain - Theileria parva >gi 161871 (M92084) casein kinase II alpha subunit [Theileria parva]	4.7
473	Z61098	H.sapiens CpG DNA, clone 44c4, reverse read epG44c4.r1a .	0.54	4191274	(AJ131094) Xvent-1B protein [Xenopus laevis]	3.7
474	M63962	Human gastric H,K-ATPase catalytic subunit gene, complete cds.	0.54	3881648	(Z70757) similar to serine protease inhibitor [Caenorhabditis elegans]	3.7
475	X86019	H.sapiens mRNA for PRPL-2 protein	0.54	1648828	(D87963) ETF-related factor-1 (ETFR-1)	2.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>S. glaucescens</i> genes				
476	X89010	strU, strX, strV and strW for 5'-hydroxystreptomycin production and transport polypeptides	0.54	3550345	(AF084524) cellular repressor of E1A-stimulated genes CREG [Mus musculus]	0.25
477	AB007836	Homo sapiens mRNA for Hic-5, partial cds	0.54	1097213	ORF 1 [Streptomyces lavendulae]	0.15
478	U32622	Comamonas testosteroni TsaR (tsaR), toluenesulfonate methyl-monoxygenase oxygenase component component (tsaB), toluenesulfonate zinc-independent alcohol dehydrogenase...	0.54	3875351	(Z96047) DY3.6 [Caenorhabditis elegans]	0.006
479	D61394	Arabidopsis thaliana gene for beta-VPE, complete cds	0.53	<NONE>	<NONE>	<NONE>
480	D61394	Arabidopsis thaliana gene for beta-VPE, complete cds	0.53	<NONE>	<NONE>	<NONE>
481	Z33072	M. capricolum DNA for CONTIG MC097	0.53	<NONE>	<NONE>	<NONE>
482	U45975	Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA, partial cds.	0.53	<NONE>	<NONE>	<NONE>
483	Z71324	S. cerevisiae chromosome XIV reading frame ORF YNL048w	0.53	2135586	M130 antigen (cytosolic variant 1) - human	2.1
484	L32090	Listeria monocytogenes secA gene, complete cds.	0.53	2291129	(AF016415) No definition line found [Caenorhabditis elegans]	0.70

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus mRNA				
485	D86423	for HGT keratin, partial cds	0.53	1235974	(X96713) collagen [Globodera pallida]	0.41
486	Y15969	Mus musculus V kappa 21-6 gene, partial	0.52	<NONE>	<NONE>	<NONE>
487	M27480	Mus musculus (clone 3F9) transcribed germline T cell receptor gamma chain (Tcr-g) mRNA, VJ4 C4 region.	0.52	3875542	(Z67990) Similarity to Rat amiloride-sensitive sodium channel beta-subunit	4.6
488	D87004	Human (lambda) DNA for immunoglobulin light chain	0.52	1766073	(U37272) winged helix protein CWH-1 [Gallus gallus]	3.5
489	Z99704	Human DNA sequence from cosmid E75B8 on chromosome 22, complete sequence [Homo sapiens]	0.51	<NONE>	<NONE>	<NONE>
490	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
491	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome	0.50	<NONE>	<NONE>	<NONE>
492	M14602	Human myoglobin gene, exon 2.	0.49	478384	helicase homolog g10L protein - African swine fever virus >gi 414091 (X72951) G10L 125 KDa protein (U97002) similar to Schizosaccharomyces pombe 4-nitrophenylphosphatase (PNPPASE) (SP:Q00472, NID:g5004) [Caenorhabditis elegans]	7.0
493	D87075	Human mRNA for KIAA0238 gene, partial cds	0.24	1938429		2.5
494	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.23	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		N.crassa				
495	J05254	mitochondrial small (19S) rRNA and Cys-tRNA.	0.23	192150	(L05670) clustrin [Mus musculus]	5.1
496	X16399	Gene for glutamate dehydrogenase (EC 1.4.1.4), put. bacterial origin	0.23	790933	(L07867) invariant surface glycoprotein [Trypanosoma brucei]	0.030
497	AE001251	Treponema pallidum section 67 of 87 of the complete genome	0.22	<NONE>	<NONE>	<NONE>
498	AF026919	Homo sapiens amyloid lambda light chain variable region mRNA, partial cds	0.21	<NONE>	<NONE>	<NONE>
499	Z27247	D.melanogaster mRNA for defensin	0.21	<NONE>	<NONE>	<NONE>
500	Y15608	Candida albicans UBI3 gene	0.21	<NONE>	<NONE>	<NONE>
501	V00598	Human beta-tubulin pseudogene.	0.21	<NONE>	<NONE>	<NONE>
502	X79426	A.thaliana microsatellite [repeated motif (gat)7]	0.21	<NONE>	<NONE>	<NONE>
503	X75772	A.caerulescens mitochondrial genes for cytochrome b and NADH dehydrogenase 5	0.21	139626	PROTEIN T1 PRECURSOR	7.8
504	AF028736	Serratia marcescens site specific recombinase	0.21	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.6
505	X97545	S.cerevisiae OST5 gene	0.21	2275631	(AF014940) No definition line found [Caenorhabditis elegans]	2.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
506	M24543	Human prostate-specific antigen (PA) gene, complete cds.	0.21	1938527	(U97012) C04E6.2 gene product [Caenorhabditis elegans]	2.7
507	M62470	Mouse thrombospondin (THBS1) gene, complete cds.	0.21	548563	RNA REPLICASE POLYPROTEIN 2.7.7.48) - Erysimum latent virus >gi 3892232 (AF098523) replicase protein [Erysimum latent virus]	2.1
508	Y13544	Homo sapiens cosmid C1	0.21	1235710	(L40584) polyprotein [Infectious pancreatic necrosis virus]	2.0
509	M24193	Chicken MHC B complex protein (C12.3) mRNA, complete cds.	0.21	3600102	(AF090441) extracellular reelin [Gallus gallus]	0.52
510	X97161	H.sapiens TFE3 gene, exon 4,5 & 6	0.21	854065	(X83413) U88 [Human herpesvirus 6]	0.30
511	X67649	R.norvegicus DNA sequence for LFB1/HNF1 promoter	0.21	3913114	TRANSCRIPTION FACTOR COUP 2 COUP-TFII - chicken >gi 392817 (U00697) orphan receptor COUP-TFII [Gallus gallus]	0.004
512	U63807	Fugu rubripes growth hormone (GH) gene, complete cds	0.21	3510505	(AF030881) pol polyprotein [Fugu rubripes]	3e-04
513	Z95636	H.sapiens mRNA for laminin alpha 5 chain	0.21	400350	NAM7 PROTEIN (NONSENSE MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1) factor NAM7 - yeast (Saccharomyces cerevisiae) >gi 4023	1e-07
514	U91907	Mirounga leonina major histocompatibility complex class II (DQA) gene, partial cds	0.20	<NONE>	<NONE>	<NONE>
515	Z35758	Transmissible gastroenteritis virus TFI virion protein genes	0.20	<NONE>	<NONE>	<NONE>
516	X00334	Drosophila virilis simple DNA sequence (pDv-19)	0.20	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
517	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	0.20	<NONE>	<NONE>	<NONE>
518	D78515	Mus musculus rae28 gene, exon 1 and 5'flanking region	0.20	<NONE>	<NONE>	<NONE>
519	M62975	Drosophila melanogaster RNA polymerase II second largest subunit upstream (DmRP 140) gene, exons 1-4.	0.20	<NONE>	<NONE>	<NONE>
520	M27260	Chicken 78-kD glucose-regulated protein, complete cds.	0.20	<NONE>	<NONE>	<NONE>
521	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	0.20	<NONE>	<NONE>	<NONE>
522	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	0.20	<NONE>	<NONE>	<NONE>
523	U04636	Human cyclooxygenase-2 (hCox-2) gene, complete cds.	0.20	<NONE>	<NONE>	<NONE>
524	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.20	<NONE>	<NONE>	<NONE>
525	AF043514	Mus musculus phosphomannomutase (Pmm2) mRNA, complete cds	0.20	3025006	HYPOTHETICAL 15.5 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION >gi 1787009 (AE000181) orf, hypothetical protein [Escherichia coli]	9.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
526	U23144	Xenopus laevis FTZ-F1-related nuclear orphan receptor variant (xFF1rAshort) mRNA, complete cds.	0.20	3184402	(AB014477) period protein [Chymomyza costata]	9.6
527	U14621	Paracentrotus lividus Pax-6 (suPax-6) mRNA, complete cds.	0.20	465894	PROBABLE MICROSOMAL SIGNAL PEPTIDASE 23 KD SUBUNIT (SPC22/23) >gi 630688 pir S44854 K12H4.4 protein - Caenorhabditis elegans >gi 289708 (L14331) homology with signal peptidase; coded for by C. elegans cDNAs GenBank: M79661, M79662 and M79663; putative	7.7
528	AF030511	Actinobacillus pleuropneumoniae MRP ATPase homolog (mrp) gene, partial cds; ApxIVA var3 (apxIVA) gene, complete cds; and beta-galactosidase (lacZ) gene, partial cds	0.20	1175966	HYPOTHETICAL 45.3 KD PROTEIN IN THIS 5'REGION >gi 1084720 pir S56193 probable membrane protein YFL062w - yeast (Saccharomyces cerevisiae)	7.2
529	AF070581	Homo sapiens clone 24540 mRNA sequence	0.20	542394	glyoxal oxidase (EC 1.2.3.-) precursor - basidiomycete (Phanerochaete chrysosporium) >gi 1050302	5.8
530	X75437	T.maritima pgK gene for 3-phosphoglycerate kinase	0.20	825648	(Z34531) coproporphyrinogen oxidase [Homo sapiens]	5.8
531	U32686	Haemophilus influenzae Rd section 1 of 163 of the complete genome	0.20	3309593	(AF072878) ciliary outer arm dynein beta heavy chain	5.6
532	Z28081	S.cerevisiae chromosome XI reading frame ORF YKL081w	0.20	2507201	CARBON CATABOLITE DEREPRESSING PROTEIN KINASE >gi 1469803 (L78129) serine/threonine kinase [Candida albicans]	5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Hordeum vulgare				
533	AF022725	limit dextrinase (HvLD99) gene, complete cds	0.20	3139154	(AF064077) adrenocorticotrophic hormone receptor [Sus scrofa]	4.3
534	AL021726	Drosophila melanogaster cosmid 171E4	0.20	3885334	(AC005623) putative argonaute protein [Arabidopsis thaliana]	2.6
535	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.20	4008334	(Z92824) B0413.4 [Caenorhabditis elegans]	1.5
536	Z46606	H.sapiens HLTF gene for helicase-like transcription factor	0.20	132946	60S RIBOSOMAL PROTEIN L30B (RP29) cytosolic - yeast (Saccharomyces cerevisiae) >gi 171821 not determined [Saccharomyces cerevisiae] >gi 1045254 cerevisiae] >gi 1323250 gnl PID e243708 (Z72933) ORF YGR148c [Saccharomyces cerevisiae]	1.5
537	X87193	H.sapiens mRNA for 2.19 gene	0.20	139820	DNA-REPAIR PROTEIN XRCC1	1.5
538	L77965	Clostridium perfringens C beta 2 toxin gene, complete cds	0.20	1175950	HYPOTHETICAL 33.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION >gi 1084703 pir S56211 probable membrane protein YFL044c - yeast (Saccharomyces cerevisiae) >gi 836711 gnl PID d1009835 (D50617) YFL044C	1.4
539	M15938	Chicken neural cell-adhesion molecule (NCAM) gene, exon 18.	0.20	2133082	regulatory protein MSR1 - yeast	1.1
540	AJ003220	Solanum tuberosum mRNA for extensin-like protein, partial	0.20	2496932	HYPOTHETICAL 55.9 KD PROTEIN C56G2.1 IN CHROMOSOME III >gi 726413 (U23177) C56G2.1 gene product [Caenorhabditis elegans]	1.1
541	X98108	A.thaliana psbP gene	0.20	119227	EPIDERMAL GROWTH FACTOR PRECURSOR precursor - mouse >gi 309210 (J00380) prepro-egf [Mus musculus]	0.49

368

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
542	AB011179	Homo sapiens mRNA for KIAA0607 protein, partial cds	0.20	2143753	gene VGF protein - rat >gi 205690 (M60525) nerve growth factor inducible protein [Rattus norvegicus] >gi 205701 (M60522) nerve growth factor-inducible protein [Rattus norvegicus] >gi 207651	0.39
543	X75318	H.sapiens ITIH1 gene (exon 22) and ITIH3 gene	0.20	629557	RNA-binding protein rnpD - Arabidopsis thaliana (fragment) >gi 510240 (X61108) RNA binding protein [Arabidopsis thaliana]	0.38
544	AB008374	Oncorhynchus mykiss mRNA for alpha 3 type I collagen, partial cds	0.20	1082610	muf1 protein - human >gi 762953 (X86018) muf1 [Homo sapiens]	0.37
545	U09809	Limulus polyphemus arginine kinase mRNA, complete cds.	0.20	3882016	(AJ012650) CP [Papaya ringspot virus]	0.37
546	AB020671	Homo sapiens mRNA for KIAA0864 protein, partial cds	0.20	2674350	(U93121) M-phase phosphoprotein-1 [Homo sapiens]	0.18
547	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.20	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.043
548	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.20	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.042

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cdk5=cyclin-dependent kinase 5 regulatory subunit p35 [mice, brain, 129/SvJ, C57BL/6, Genomic/mRNA, 5528 nt]	0.20	3413870	(AB007923) KIAA0454 protein [Homo sapiens]	0.020
549	S82819	Streptomyces griseus DNA for serine/threonine protein kinases, complete cds	0.20	861405	(U29154) T07F12.2 gene product [Caenorhabditis elegans]	0.019
550	D31792	Homo sapiens butyrophilin (BT3.2) gene, exons 5-10, and complete cds	0.20	2773341	(AF040954) putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]	0.008
551	U97499	Rattus norvegicus nonmuscle myosin heavy chain-A mRNA, complete cds.	0.20	3880111	(Z81130) predicted using Genefinder	0.002
552	U31463	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13	0.20	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	4e-04
553	X78401	Nocardia lactamdurans pcbAB and pcbC genes for alpha-aminoadipyl-L-cysteiny-D-valine synthetase and isopenicillin N synthase	0.20	1723511	PUTATIVE ENDONUCLEASE C1F12.06C yeast (Schizosaccharomyces pombe) >gi 1217980 (Z69944) unknown [Schizosaccharomyces pombe]	4e-09
554	X57310	S.epidermidis genes epiY', epiY, epiA, epiB, epiC, epiD, epiQ, epiP	0.20	3874927	(Z73424) C44B9.1 [Caenorhabditis elegans]	3e-10
555	X62386					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
556	X59000	Epizootic haemorrhagic disease virus gene segment 6 for NS1	0.20	3879755	(Z80220) similar to nucleotide binding protein; cDNA EST EMBL:M75897 comes from this gene; cDNA EST EMBL:M89054 comes from this gene; cDNA EST EMBL:D26713 comes from this gene; cDNA EST EMBL:D26718 comes from this gene; cDNA...	8e-16
557	M98776	Human keratin 1 gene, complete cds	0.20	1086900	(U41278) contains similarity to G beta repeats	2e-30
558	AF011446	Mus musculus granzyme K gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
559	AF074708	Macaca mulatta clone MMU1.5 FRG1-like pseudogene, exons 7 and 8, partial sequence	0.19	<NONE>	<NONE>	<NONE>
560	X13287	Medicago sativa nodulin-25 gene	0.19	<NONE>	<NONE>	<NONE>
561	Z49509	S.cerevisiae chromosome X reading frame ORF YJR009c	0.19	<NONE>	<NONE>	<NONE>
562	D89041	Bovine DNA for prostaglandin F2alpha receptor, partial cds	0.19	<NONE>	<NONE>	<NONE>
563	D29644	Streptococcus salivarius DNA for dextranase	0.19	<NONE>	<NONE>	<NONE>
564	AE001461	Helicobacter pylori, strain J99 section 22 of 132 of the complete genome	0.19	<NONE>	<NONE>	<NONE>
565	L38559	Homo sapiens galactocerebrosidase (GALC) gene, exon 17.	0.19	<NONE>	<NONE>	<NONE>
566	Z82628	R.prowazekii genomic DNA fragment (clone A405F)	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
567	U25641	Tetrahymena thermophila telomerase component p80 mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
568	AB002343	Human mRNA for KIAA0345 gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
569	D10064	Erwinia carotovora gene for pectate lyase III, complete cds	0.19	<NONE>	<NONE>	<NONE>
570	U31734	Homo sapiens clone MF118 A4A10 hypoxanthine phosphoribosyltransferase (hprt) 130 kb deletion mutant mRNA, partial cds, contains human Alu element	0.19	<NONE>	<NONE>	<NONE>
571	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	0.19	<NONE>	<NONE>	<NONE>
572	M95623	Homo sapiens hydroxymethylbilane synthase gene, complete cds.	0.19	<NONE>	<NONE>	<NONE>
573	S67478	(GC*IS)=vitamin D-binding protein/group specific component [human, peripheral blood leukocytes, Genomic, 794 nt, segment 4 of 9]	0.19	<NONE>	<NONE>	<NONE>
574	X99075	H.sapiens NRGN gene, exon 1	0.19	<NONE>	<NONE>	<NONE>
575	AF044775	Homo sapiens breakpoint cluster region BCRder14 sequence	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for KIAA0335 gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
576	AB002333					
577	U53566	Macaca mulatta pit-1/GHF-1 transcription factor mRNA, complete cds	0.19	1078068	probable membrane protein YLR311c - yeast	9.2
578	U73664	Human t(11;14)(q13;q32) breakpoint junction sequence	0.19	116734	COAT PROTEIN (CAPSID PROTEIN) virus >gi 58901 (X62133) CyMV coat protein gene product	8.8
579	AF004054	Heterophyllaea pustulata rps16 gene, chloroplast gene, partial intron sequence	0.19	1928991	(U92815) heat shock protein 70 precursor [Citrullus lanatus]	8.7
580	Z27081	Caenorhabditis elegans cosmid M01A8, complete sequence [Caenorhabditis elegans]	0.19	2496247	HYPOTHETICAL ATP-BINDING PROTEIN MJ0625 >gi 2128413 pir A64378 hypothetical protein MJ0625 - Methanococcus jannaschii >gi 1591336 (U67510) M. jannaschii predicted coding region MJ0625	8.6
581	Z74145	S.cerevisiae chromosome IV reading frame ORF YDL097c	0.19	1174425	TYROSINE-PROTEIN KINASE SPK-1	6.7
582	D38547	Small round structured virus genomic RNA, 3'terminal sequence containing ORF2 and ORF3	0.19	971318	(Z48053) putative protein [Bovine herpesvirus 1]	5.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
583	D88000	Ralstonia eutropha DNA 16S ribosomal RNA > :: dbj D88002 D88002 Ralstonia eutropha DNA for 16S ribosomal RNA > :: dbj D88003 D88003 Ralstonia eutropha DNA for 16S ribosomal RNA > :: dbj D88004 D88004 Ralstonia eutropha DNA for 16S ribosomal RNA	0.19	3800952	(AF100657) No definition line found [Caenorhabditis elegans]	5.1
584	U67462	Methanococcus jannaschii section 4 of 150 of the complete genome	0.19	3183617	(AJ005586) MYB-related transcription factor [Antirrhinum majus]	4.0
585	L23906	Gallus domesticus microsatellite DNA marker.	0.19	1947094	(U93074) voltage-gated sodium channel homolog BdNa1	3.9
586	AE001462	Helicobacter pylori, strain J99 section 23 of 132 of the complete genome	0.19	1730177	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) ISOMERASE (PHI) >gi 2118333 pir I48073 glucose phosphate isomerase - Chinese hamster >gi 987046 griseus] (Z82256) cDNA EST yk251g7.3 comes from this gene; cDNA EST yk251g7.5 comes from this gene; cDNA EST EMBL:D68223 comes from this gene; cDNA EST EMBL:C12737 comes from this gene; cDNA EST yk389c8.5 comes from this gene; cDNA E...	3.9
587	M19460	P.putida catBC operon encoding cis,cis-muconate lactonizing enzyme I and muconolactone isomerase genes, complete cds.	0.19	3873843		3.9
588	U22349	Tetrahymena australis telomerase RNA gene, complete sequence	0.19	4105782	(AF049922) PGP169-12 [Petunia x hybrida]	3.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
589	L27745	Homo sapiens voltage operated calcium channel, alpha-1 subunit mRNA, complete cds.	0.19	3763926	(AC004450) unknown protein [Arabidopsis thaliana]	3.0
590	AF049588	Canis familiaris synapsin I gene, partial cds	0.19	4104931	(AF042196) auxin response factor 8 [Arabidopsis thaliana]	3.0
591	X06627	Staphylococcus aureus plasmid pS194 sequence	0.19	137927	PRE-NECK APPENDAGE PROTEIN (LATE PROTEIN GP12) >gi 75856 pir WMBP22 gene 12 protein - phage phi-29 >gi 215330 (M14782) pre-neck appendage protein [Bacteriophage phi-29] >gi 225367 prf 1301270G gene 12 [Bacteriophage phi-29]	2.3
592	X61597	M.musculus gene for kallikrein-binding protein	0.19	2982874	(AE000675) cobalamin synthesis related protein CobW	1.7
593	AF016242	Dictyostelium discoideum protein synthesis elongation factor 1-alpha (tef2) gene, partial cds	0.19	133659	PUTATIVE RNA-DIRECTED RNA POLYMERASE	1.4
594	AF004447	Venezuelan equine encephalitis virus strain 1327 polyprotein gene, partial cds > :: gb AF004460 AF004460 Venezuelan equine encephalitis virus strain 1385 polyprotein gene, partial cds	0.19	4096173	(U25968) early embryogenesis protein [Oryza sativa]	1.3
595	J04821	Human elastin (ELN) gene, exon 1, clones HELC-5 and HELC-6.	0.19	1170523	INHIBIN BETA B CHAIN PRECURSOR inhibin precursor - bovine >gi 563753 (U16241) betaB inhibin/activin precursor [Bos taurus]	1.3
596	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.19	3024881	PROBABLE TRANSPORT PROTEIN CY21C12.11 >gi 2078066 gnl PID e315171 (Z95210) betP	0.83

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
597	M69053	D.melanogaster calcium-activated K+ channel subunit	0.19	1707984	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE I (FD-GOGAT) >gi 2126524 pir S60228 glutamate synthase (ferredoxin) (EC 1.4.7.1) gltB - Synechocystis sp. (PCC 6803) >gi 515938 (X80485) glutamate synthase	0.80
598	AF076279	Dictyostelium firmibasis plasmid Dfp1, complete plasmid sequence	0.19	453986	(U00008) yejA [Escherichia coli]	0.79
599	D28873	Mouse MCNP gene for C-type natriuretic peptide, complete cds (exon1, exon2)	0.19	2650444	(AE001092) acetyl-CoA synthetase (acs-1) [Archaeoglobus fulgidus]	0.63
600	U06071	Oxytricha nova macronuclear actin II gene, complete cds.	0.19	1584024	complement control protein [Botryllus schlosseri]	0.48
601	L54057	Homo sapiens CLP mRNA, partial cds.	0.19	3036883	(AL022374) putative ABC transporter	0.46
602	X89806	P.lividius cDNA for COLL2alpha gene	0.19	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	0.41
603	AE001104	Archaeoglobus fulgidus section 3 of 172 of the complete genome	0.19	2315192	(Y11739) transcription factor [Homo sapiens]	0.35
604	U54501	Rattus norvegicus microsatellite sequence D0Mco22	0.19	228951	D-MeAsp receptor:ISOTYPE=epsilon3 [Mus musculus]	0.32
605	X74468	Human papillomavirus type 15 genomic DNA	0.19	3695390	(AF096371) contains similarity to Rattus norvegicus cyclin G-associated kinase (SW:P97874) [Arabidopsis thaliana]	0.28
606	U20285	Human Gps1 (GPS1) mRNA, complete cds	0.19	2582659	(AJ002527) glucitol-6-phosphate dehydrogenase [Clostridium beijerinckii]	0.27
607	D49408	Human gene for interleukin 3 receptor alpha subunit, exon 10	0.19	2522368	(AF008596) alpha1,3-fucosyltransferase [Helicobacter pylori]	0.16

374

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
608	AF041141	Homo sapiens pituitary specific homeodomain protein (PROP1) gene, exon 3 and complete cds	0.19	37403	(X03541) trk gene product (aa 1-641) [Homo sapiens]	0.091
609	L12531	Discopyge ommata Ca2+ channel alpha 1 subunit gene sequence.	0.19	3618274	(AJ223219) hypothetical protein	0.069
610	AF052445	Yellow fever virus clone HONG9 polyprotein gene, complete cds	0.19	1932822	(U15928) KH-domain putative RNA binding protein	0.001
611	Z36946	B.anthraxis sap gene encoding S-layer protein	0.19	173241	(L06487) ZIP1 protein [Saccharomyces cerevisiae]	2e-04
612	AF087984	Homo sapiens full length insert cDNA clone YW29A12	0.19	3786014	(AC005499) hypothetical protein [Arabidopsis thaliana]	1e-06
613	AE001010	Archaeoglobus fulgidus section 97 of 172 of the complete genome	0.19	3135493	(AF060248) unknown [Arabidopsis thaliana]	7e-08
614	L08965	Trichosporon cutaneum carbamoyl phosphate synthetase large subunit (argA) gene, partial cds.	0.19	1086901	(U41278) F33G12.3 gene product [Caenorhabditis elegans]	2e-08
615	M91466	Rattus norvegicus A2b-adenosine receptor mRNA, complete cds.	0.19	2984320	(AE000773) acetoin utilization protein [Aquifex aeolicus]	6e-09
616	X95971	S.lividans groEL2 gene	0.19	3925277	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	7e-10
617	U12539	Schizosaccharomyces pombe sed2 (sed2) gene, complete cds.	0.19	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	3e-14

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
618	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete cds.	0.19	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	9e-15
619	Z68327	Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.	0.19	3875774	EMBL:D32434 comes from this gene; cDNA EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; ... >gi 3878710 gnl PID e1348373 EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; ...	6e-15
620	U66525	Dictyostelium discoideum ORFveg114 mRNA, complete cds	0.19	3540281	(AF056116) All-1 related protein [Fugu rubripes]	2e-17
621	U25830	Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds	0.19	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	1e-18
622	U89407	Mus musculus strain BALB/c delta-aminolevulinic acid dehydratase (Lv) mRNA, partial cds	0.19	1825764	(U88314) C46H11.11 gene product [Caenorhabditis elegans]	3e-25
623	AF095598	Bison bison athabasca microsatellite BBJ 2	0.18	<NONE>	<NONE>	<NONE>
624	AF064260	Strongylocentrotus purpuratus SRC8 mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
625	U69533	Arabidopsis thaliana AtKAP alpha mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>
626	D89041	Bovine DNA for prostaglandin F2alpha receptor, partial cds	0.18	<NONE>	<NONE>	<NONE>
627	M24571	Dictyostelium discoideum tRNA-Glu-GAA gene, clone yGluGAA7.	0.18	<NONE>	<NONE>	<NONE>
628	X59772	D.melanogaster ovo gene required for female germ line development	0.18	<NONE>	<NONE>	<NONE>
629	AL010209	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-104, complete sequence	0.18	<NONE>	<NONE>	<NONE>
630	U67575	Methanococcus jannaschii section 117 of 150 of the complete genome	0.18	111839	inositol 1,4,5-triphosphate receptor 2 - rat	8.5
631	U28730	Caenorhabditis elegans cosmid K10B2	0.18	1787604	(AE000232) orf, hypothetical protein [Escherichia coli]	8.3
632	X99798	L.lactis pepF1 & pepF2 genes	0.18	3406624	(AF079110) glycosomal malate dehydrogenase [Trypanosoma brucei]	8.1
633	AF025306	Danio rerio band 4.1-like protein 4 (nbl4) mRNA, complete cds	0.18	465445	PROBABLE NUCLEAR ANTIGEN herpesvirus 1 (strain Kaplan) >gi 334072 (M34651) ORF-3 protein [Pseudorabies virus]	7.9
634	AF059251	Mus musculus lipoyxygenase (alox) mRNA, complete cds	0.18	1655667	(Z81368) hypothetical protein Rv2393	6.6
635	Z22605	G.domesticus CTCF protein mRNA.	0.18	481864	3-methyl-2-oxobutanoate dehydrogenase	6.6
636	AB011086	Homo sapiens mRNA for KIAA0514 protein, complete cds	0.18	3874158	(Z81464) predicted using Genefinder	6.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
637	Z78536	Caenorhabditis elegans cosmid C07A4, complete sequence [Caenorhabditis elegans]	0.18	3702121	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]	6.4
638	U67530	Methanococcus jannaschii section 72 of 150 of the complete genome	0.18	3877946	(Z81094) Weak similarity to 65 KDA heat shock protein (TR:G602231); cDNA EST EMBL:D71705 comes from this gene; cDNA EST EMBL:D74382 comes from this gene [Caenorhabditis elegans] (Z69634) cDNA EST EMBL:D71510 comes from this gene; cDNA EST EMBL:C08449 comes from this gene; cDNA EST yk266b12.3 comes from this gene; cDNA EST yk266b12.5 comes from this gene; cDNA EST yk461h7.3 comes from this gene; cDNA...	6.3
639	M63781	Influenza A/Duck/England/1/62 (H4N6) nucleoprotein mRNA, complete cds.	0.18	3873663	(Z69634) cDNA EST EMBL:D71510 comes from this gene; cDNA EST EMBL:C08449 comes from this gene; cDNA EST yk266b12.3 comes from this gene; cDNA EST yk266b12.5 comes from this gene; cDNA EST yk461h7.3 comes from this gene; cDNA...	6.2
640	M73781	Oryctolagus cuniculus integrin beta-8 subunit mRNA, complete cds. > :: gb I44828 I44828 Sequence 3 from patent US 5635601	0.18	1362129	major allergen OLE17 - common olive	5.8
641	X67219	D.melanogaster Rop gene	0.18	3449286	(AB011527) MEGF1 [Rattus norvegicus]	4.8
642	AF106941	Homo sapiens beta-arrestin 2 mRNA, complete cds	0.18	548353	[PROTEIN-PII] URIDYLTRANSFERASE vinelandii >gi 39257 (X59610) uridylyl transferase	3.7
643	AF052602	Danio rerio huntingtin (HD) mRNA, complete cds	0.18	241058	potential IGF binding protein [chickens, Peptide Partial, 77 aa, segment 2 of 3]	3.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
644	AB020709	Homo sapiens mRNA for KIAA0902 protein, complete cds	0.18	3875570	(Z68314) predicted using Genefinder; cDNA EST EMBL:M75775 comes from this gene; cDNA EST EMBL:M89255 comes from this gene; cDNA EST EMBL:M89127 comes from this gene; cDNA EST EMBL:T00141 comes from this gene; cDNA EST EMBL:T...	2.1
645	AF096883	HIV-1 isolate patient 3 country USA pol polyprotein (pol) gene, partial cds	0.18	3250696	(AL024486) putative protein	1.7
646	L39928	Pyrocoelia miyako (clone pB-PmL41) luciferase mRNA, complete cds	0.18	2914702	(AC003974) unknown protein [Arabidopsis thaliana]	0.73
647	M17082	Human carcinoembryonic nonspecific crossreacting antigen (CEA; NCA) gene, exons 1 and 2.	0.18	1351833	REGULATORY PROTEIN ABAA	0.72
648	X75318	H.sapiens ITIH1 gene (exon 22) and ITIH3 gene	0.18	629557	RNA-binding protein rnpD - Arabidopsis thaliana (fragment) >gi 510240 (X61108) RNA binding protein [Arabidopsis thaliana]	0.41
649	AF011908	Mus musculus apoptosis associated tyrosine kinase (AATYK) mRNA, complete cds	0.18	330442	(K03332) nuclear antigen 2 [Epstein-Barr virus]	5e-04
650	U04004	Simian immunodeficiency virus SIVagm VER-2 envelope protein gene, partial cds.	0.18	135102	ASPARTYL-tRNA SYNTHETASE aspartate--tRNA ligase (EC 6.1.1.12) - Escherichia coli coli] >gi 1736513 gnl PID d1016401 (D90829) Aspartate--tRNA ligase (EC 6.1.1.12) [Escherichia coli]	6e-11
651	U88155	Xenopus laevis RanGTPase activating protein	0.18	995714	(X91258) pid:e198503 [Saccharomyces cerevisiae]	2e-13

381

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
652	Z18921	B.oleracea gene for S-receptor kinase-like protein	0.18	3875535	(Z66511) similar to ribokinase; cDNA EST EMBL:D69553 comes from this gene; cDNA EST EMBL:D65938 comes from this gene; cDNA EST yk280h9.3 comes from this gene; cDNA EST yk280h9.5 comes from this gene; cDNA EST yk223d11.3 come...	1e-19
653	M60650	S.cerevisiae STA2 gene, complete cds.	0.16	<NONE>	<NONE>	<NONE>
654	U80912	Eucalyptus globulus NADP-isocitrate dehydrogenase (EgICDH) mRNA, complete cds	0.16	3766172	(AF057298) ornithine decarboxylase antizyme 2 [Mus musculus]	4.2
655	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.16	76749	hypothetical protein 4 - fowl adenovirus 1	4.0
656	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.16	3044086	(AF055904) unknown [Myxococcus xanthus]	0.60
657	AF030231	Glycine max sucrose synthase (SS) mRNA, complete cds	0.078	<NONE>	<NONE>	<NONE>
658	M19183	Woodchuck hepatitis virus (WHV), complete genome, clone WHV 59.	0.072	1076190	cell wall glycoprotein, 75K, precursor - diatom (Cylindrotheca fusiformis) >gi 515363 (X80394) P75K gene product [Cylindrotheca fusiformis]	6.3
659	U31557	Ovine adenovirus IVa2 protein gene, DNA polymerase gene, terminal protein gene and 52.55 kDa protein gene, partial cds	0.072	3511143	(AF061244) unknown [Agrocye aegerita]	6.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
660	AL021491	Caenorhabditis elegans cosmid Y44A6B, complete sequence [Caenorhabditis elegans]	0.070	<NONE>	<NONE>	<NONE>
661	M33874	X.laevis Xotch protein mRNA, complete cds.	0.070	1654096	(Y09076) RAD3 [Schizosaccharomyces pombe]	0.23
662	AB012725	Mus musculus ZAN75 mRNA for zinc finger protein, complete cds	0.069	1350800	MITOCHONDRIAL RIBOSOMAL PROTEIN S5	2.0
663	AL021491	Caenorhabditis elegans cosmid Y44A6B, complete sequence [Caenorhabditis elegans]	0.068	<NONE>	<NONE>	<NONE>
664	Z60318	H.sapiens CpG DNA, clone 1e1, reverse read cpg1e1.r1a .	0.068	1280134	(U55376) F16H11.2 gene product [Caenorhabditis elegans]	2.6
665	Z35973	S.cerevisiae chromosome II reading frame ORF YBR104w	0.068	2493000	PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR EMBL:Z14816 comes from this gene; cDNA EST EMBL:Z14946 comes from this gene; cDNA EST EMBL:D69746 comes from this gene; cDNA EST yk219b6.3 comes from this gene; cDNA ES...	0.68
666	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames	0.068	1235974	(X96713) collagen [Globodera pallida]	4e-04
667	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.068	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	1e-59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
668	M34161	Rat tachykinin (PPT) gene, exons 5 and 6.	0.067	<NONE>	<NONE>	<NONE>
669	L03811	Aspergillus niger zinc finger protein (creA) gene, complete cds.	0.067	<NONE>	<NONE>	<NONE>
670	M64983	Human fibrinogen beta chain gene, complete mRNA. >gb I47706 I47706 Sequence 3 from patent US 5639940	0.067	<NONE>	<NONE>	<NONE>
671	AF014051	Nicotiana tabacum Mg chelatase subunit (ChlH) mRNA, partial cds	0.067	<NONE>	<NONE>	<NONE>
672	Y07540	H.sapiens sil gene	0.067	92331	glycoprotein GP330, renal - rat (fragments)	7.5
673	AJ000347	Rattus norvegicus mRNA for 3'(2'),5'-bisphosphate nucleotidase	0.067	129238	25 KD OOKINETE SURFACE ANTIGEN PRECURSOR (PRS25) >gi 320962 pir A44966 25k ookinete surface antigen precursor - Plasmodium reichenowi reichenowi]	7.4
674	L19979	Squid sodium channel mRNA, complete cds.	0.067	2128473	hypothetical protein MJ0750 - Methanococcus jannaschii >gi 1592304 (U67521) ferredoxin-type protein	1.5
675	X08050	Yeast tRNA-Glu(3) gene and flanking regions	0.067	1334398	(X15081) MURF2 protein (AA 1-348)	0.65
676	X17115	Human mRNA for IgM heavy chain complete sequence	0.067	1731331	HYPOTHETICAL 51.6 KD PROTEIN CY49.14C >gi 1370241 gnl PID e247089 (Z73966) hypothetical protein Rv2075c [Mycobacterium tuberculosis]	0.51
677	AF032871	Homo sapiens uncoupling protein 3 (UCP3) gene, exon 1 and partial exon 2	0.067	112900	ALPHA-2C-1 ADRENERGIC RECEPTOR human >gi 178194 (J03853) kidney alpha-2-adrenergic receptor [Homo sapiens] >gi 1628638 (U72648) alpha2-C4-adrenergic receptor [Homo sapiens]	0.50

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DYNAMIN 3 (DYNAMIN, TESTICULAR) rat	
678	X05319	Mouse class II MHC E-beta 2 (d) gene exon 3	0.067	585074	>gi 391872 gnl PID d1003668 (D14076) testicular dynamin [Rattus norvegicus]	3e-04
679	AB006362	Candida albicans CaSLN1 gene, complete cds	0.067	3417296	(AC003007) Unknown gene product (partial) [Homo sapiens]	9e-56
680	AF021236	African horse sickness virus capsid VP3 (L3) mRNA, complete cds	0.066	<NONE>	<NONE>	<NONE>
681	AE001507	Helicobacter pylori, strain J99 section 68 of 132 of the complete genome	0.066	<NONE>	<NONE>	<NONE>
682	AF039717	Caenorhabditis elegans cosmid R13H8	0.066	<NONE>	<NONE>	<NONE>
683	AF029027	Syncerus caffer isolate Queen Elizabeth Mweya 14 mitochondrial DNA control region	0.066	<NONE>	<NONE>	<NONE>
684	AF087967	Homo sapiens full length insert cDNA clone YU51G05	0.066	2982476	(X97203) C1 protein [Beet curly top virus]	9.5
685	J02037	Baboon endogenous virus proviral long terminal repeat DNA.	0.066	972767	(L37868) POU-domain transcription factor [Homo sapiens]	7.3
686	AF000141	Lycopersicon esculentum class I knotted-like homeodomain protein (LeT6) mRNA, complete cds	0.066	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	5.6
687	AB001746	Bensingtonia sp. OK255 gene for 18S rRNA > :: dbj AB001747 AB001747 Bensingtonia sp. OK259 gene for 18S rRNA	0.066	3859889	(AF070064) cap 'n' collar isoform C [Drosophila melanogaster]	0.38

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
688	AE001461	Helicobacter pylori, strain J99 section 22 of 132 of the complete genome	0.065	<NONE>	<NONE>	<NONE>
689	M30821	Chicken erythroid transport proteins c1 and c2	0.065	<NONE>	<NONE>	<NONE>
690	AB009802	Homo sapiens gene for osteonidogen, intron 3	0.065	<NONE>	<NONE>	<NONE>
691	AF086062	Homo sapiens full length insert cDNA clone YZ06B11	0.065	<NONE>	<NONE>	<NONE>
692	AB002369	Human mRNA for KIAA0371 gene, complete cds	0.065	2500884	SIGNAL SEQUENCE BINDING PROTEIN binding protein [Synechococcus sp.]	5.5
693	AF086864	Cyclopodia sp. large subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNAs, partial sequence > :: gb AF086866 AF086866 Penicillidia sp. large subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNAs, partial sequence	0.065	3721684	(AB012957) probable glycosyl transferase [Vibrio cholerae]	5.5
694	L44593	Bacteriophage BK5-T ORF410, 3' end pf cds, 20 ORFs, repressor protein, and Cro repressor protein genes, complete cds, ORF70' gene, 5' end of cds.	0.065	1172067	PEPTIDASE T (AMINOTRIPEPTIDASE) influenzae Rd]	3.2
695	U80079	Ciona intestinalis MyoD-family protein (CiMDFa) mRNA, complete cds	0.065	4218110	(AL035353) contains EST gb:F15281	2.5

3460

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
696	AB020718	Homo sapiens mRNA for KIAA0911 protein, complete cds	0.065	1722734	MINOR CAPSID PROTEIN L2 >gi 1020192 type 23]	1.9
697	AF082137	Zea mays copia-like retrotransposon Stl-14 leader region, partial sequence	0.065	1877501	(U89278) polyhomeotic 2 homolog [Homo sapiens]	1.1
698	X64053	R.norvegicus ZnBP gene for zinc binding protein	0.065	464963	TRYPSIN PRECURSOR	0.36
699	U67065	Mus musculus butyrophilin (BTN) gene, promoter region and complete cds	0.065	2132252	hypothetical protein YPL263c - yeast	3e-10
700	M64862	Rat matrix F/G mRNA, complete cds.	0.065	3420183	(AF041105) organic anion transporter protein 3 [Rattus norvegicus]	4e-19
701	K02205	Yeast (S.cerevisiae) transcriptional activator of amino acid-biosynthetic genes (GCN4) gene, complete cds.	0.064	<NONE>	<NONE>	<NONE>
702	X58282	Maize mRNA for a high mobility group protein	0.064	<NONE>	<NONE>	<NONE>
703	AC001545	Homo sapiens (subclone 1_f3 from P1 H69) DNA sequence	0.064	<NONE>	<NONE>	<NONE>
704	AF023461	Homo sapiens FRA3B region sequence	0.064	<NONE>	<NONE>	<NONE>
705	U50307	Caenorhabditis elegans cosmid F43H9.	0.064	<NONE>	<NONE>	<NONE>
706	U46542	Streptococcus crista HmpA gene, partial cds, putative adhesin/ABC transport system protein (scbA) gene, complete cds	0.064	1209391	(D83659) TPR protein pombe] >gi 2894282 gnl PID e1251103 (AL021838) pre-mrna splicing factor. [Schizosaccharomyces pombe]	9.2
707	X57564	A.rusticana mRNA for neutral peroxidase	0.064	1492037	(U60315) MC094R [Mollusum contagiosum virus subtype 1]	6.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
708	U06986	Human alpha-2-macroglobulin receptor/lipoprotein receptor protein (A2MR/LRP) gene, exons 39-41.	0.064	100800	rab15B protein - wheat >gi 21853 (X62476) rab protein [Triticum aestivum]	5.3
709	D85773	Human CpG island sequence, clone Q28B8	0.064	2245382	(U88325) suppressor of cytokine signalling-1 [Mus musculus]	5.3
710	L06178	Apis mellifera ligustica complete mitochondrial genome	0.064	3695379	(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana]	3.2
711	Y16242	Triticum aestivum mRNA for beta-amylase	0.064	1175958	HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REGION >gi 1084712 pir S56201 probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae) >gi 836701 gnl PID d1009825 (D50617) YFL054C	3.1
712	L81779	Homo sapiens (subclone 2_a2 from P1 H25) DNA sequence	0.064	3845169	(AE001391) phosphatase (acid phosphatase family)	0.81
713	X13826	C.reinhardtii psb1 mRNA for OEE1 protein of photosystem II (oxygen-evolving enhancer protein)	0.064	171040	(M94535) ATPase [Saccharomyces cerevisiae] cerevisiae, Peptide, 377 aa [Saccharomyces cerevisiae]	0.054
714	X06487	H.sapiens mRNA for bcl2-Ig fusion gene	0.064	2429362	(AF020261) proline rich protein [Santalum album]	0.016
715	U79638	Mus musculus cyclin-dependent kinase inhibitor protein (p15(INK4b)) gene, exon 2 and partial cds	0.064	3929221	(AF082557) TRF1-interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]	1e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human T cell				
716	U39099	receptor alpha chain mRNA, partial cds	0.063	<NONE>	<NONE>	<NONE>
717	U39673	Clostridium acetobutylicum KdpC (kdpC) gene, partial cds, sensor histidine kinase homolog (kdpD) and response regulator homolog (kdpE) genes, complete cds	0.063	<NONE>	<NONE>	<NONE>
718	AL022317	Human DNA sequence from clone 140L1 on chromosome 22q13.1-13.31, complete sequence [Homo sapiens]	0.063	1931640	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]	5.2
719	U28972	Spiroplasma citri orfA and orfB genes, partial cds, orfC, orfD, and orfE genes and Spiroplasma virus SpV1-derived ORF1 and ORF3 genes, complete cds, and SpV1-derived ORF14 gene, partial cds.	0.063	4091939	(AF070704) envelope glycoprotein [Human immunodeficiency virus type 1]	5.2
720	U15159	Mus musculus limk kinase (limk) mRNA, complete cds	0.063	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	5.1
721	AF058416	Homo sapiens lipoprotein receptor-related protein (LRP1), exons 39, 40, and 41	0.063	1788123	(AE000276) orf, hypothetical protein [Escherichia coli]	4.0
722	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.063	2244849	(Z97337) hypothetical protein	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Streptococcus			(Z70203) cDNA EST	
723	L29323	pneumoniae methyl transferase gene cluster, complete sequence	0.063	3874022	EMBL:D72339 comes from this gene; cDNA EST EMBL:D75197 comes from this gene [Caenorhabditis elegans]	2.3
724	X72631	H.sapiens mRNA encoding Rev-ErbAalpha > :: emb[X72632]HSREV ERB2 H.sapiens mRNA encoding Rev-ErbAalpha (internal fragment)	0.063	3979878	(Z73105) predicted using Genefinder; cDNA EST EMBL:T01277 comes from this gene; cDNA EST EMBL:T01796 comes from this gene; cDNA EST EMBL:D32545 comes from this gene; cDNA EST EMBL:D33060 comes from this gene; cDNA EST EMBL:D...	1.7
725	U17969	Human initiation factor eIF-5A gene, complete cds.	0.063	2429509	(AF025467) contains similarity to drosophila DNA-binding protein K10 (NID:g8148) [Caenorhabditis elegans]	1.4
726	AE001000	Archaeoglobus fulgidus section 107 of 172 of the complete genome	0.063	3462802	(AF082486) nef protein [Human immunodeficiency virus type 1]	0.35
727	S80986	svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3876 nt]	0.063	1326288	(U58734) weak similarity to ankyrin G [Caenorhabditis elegans]	0.093
728	AF109134	Homo sapiens 7-60 mRNA, complete cds	0.063	1083764	proline-rich proteoglycan 2 precursor, parotid - rat >gi 310200 (L17318) proline-rich proteoglycan [Rattus norvegicus]	0.001
729	D87466	Human mRNA for KIAA0276 gene, partial cds	0.063	2879865	(AL021816) SPBC24E9.03c, unknown, len:251aa [Schizosaccharomyces pombe]	6e-05
730	AB018269	Homo sapiens mRNA for KIAA0726 protein, complete cds	0.063	2995865	(AF053455) tetraspan TM4SF [Homo sapiens]	2e-16
731	D86954	Cricetulus griseus mRNA for Cytochrome P-450 2A14, complete cds	0.063	2496896	HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III >gi 3874383 gnl PID e1344077 type (RING finger) [Caenorhabditis elegans]	1e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium				
732	AL010232	falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-58, complete sequence	0.062	<NONE>	<NONE>	<NONE>
733	U90714	Mycoplasma gallisepticum haemagglutinin precursor genes, complete cds	0.062	<NONE>	<NONE>	<NONE>
734	AF107044	Homo sapiens clone pCL4 DNA-binding protein SOX21 (SOX21) gene, complete cds	0.062	<NONE>	<NONE>	<NONE>
735	L41729	Caenorhabditis elegans Ro ribonucleoprotein autoantigen mRNA, complete cds	0.062	2983060	(AE000687) putative protein [Aquifex aeolicus]	8.6
736	Z99287	Caenorhabditis elegans cosmid Y7A9D, complete sequence [Caenorhabditis elegans]	0.062	1176542	PUTATIVE SERINE/THREONINE- PROTEIN KINASE D1044.3 IN CHROMOSOME III >gi 495684 (U00065) contains EGF-like repeats; highly similar to ZC84.1; 3' exons similar to protein kinase [Caenorhabditis elegans]	5.8
737	AB014514	Homo sapiens mRNA for KIAA0614 protein, partial cds	0.062	4033395	DNA GYRASE SUBUNIT B subunit [Myxococcus xanthus]	3.9
738	L29165	Human germline immunoglobulin light chain variable region (lambda-IIIb subgroup) from IgM rheumatoid factor.	0.062	1914685	(Y12014) RAD23 protein, isoform II	1.3
739	U09364	Schistosoma japonicum Chinese clone pY6 paramyosin mRNA, partial cds.	0.062	1350800	MITOCHONDRIAL RIBOSOMAL PROTEIN S5	1.3
740	Y16242	Triticum aestivum mRNA for beta- amylase	0.062	79834	hypothetical protein 1246 (uvrA region) - Micrococcus luteus (fragment)	0.59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Leishmania pifanoi			TROPOMYOSIN I (TMI)	
741	M97695	cysteine proteinase (cys2) gene, complete cds.	0.062	1174754	(POLYPEPTIDE 49) >gi 320989 pir A60607 tropomyosin - fluke	0.018
742	U67526	Methanococcus jannaschii section 68 of 150 of the complete genome	0.062	1330345	(U58755) coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	1e-40
743	Z78414	Caenorhabditis elegans cosmid W09D12, complete sequence [Caenorhabditis elegans]	0.061	<NONE>	<NONE>	<NONE>
744	Y13606	Mus musculus gene encoding filensin, exons 6, 7	0.061	2314715	(AE000651) H. pylori predicted coding region HP1527	4.9
745	J04374	Eggplant mosaic virus genome.	0.061	141449	HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556 >gi 80759 pir JQ0431 hypothetical 35.5K protein - Streptomyces fradiae transposon Tn4556	3.8
746	AB022200	Marine obligately oligotrophic bacterium POO-10 DNA for 16S ribosomal RNA, partial sequence	0.061	3983593	(AB000307) transcarboxylase-beta	2.2
747	X54250	Rat mRNA for zinc finger protein AT-BP2, partial cds	0.061	1377886	(L46815) DNA binding protein Rc [Mus musculus]	0.98
748	X69942	M.musculus mRNA of enhancer-trap-locus 1	0.061	2983969	(AE000748) putative protein [Aquifex aeolicus]	0.57
749	AJ223206	Mus musculus mRNA for scrapie responsive protein 1	0.061	4204265	(AC005223) 45643 [Arabidopsis thaliana]	5e-31
750	Y10205	H.sapiens mRNA for CD88 protein	0.060	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
751	U79260	Human clone 23745 mRNA, complete cds	0.060	<NONE>	<NONE>	<NONE>
752	X07453	Plasmodium falciparum 11-1 gene part 1	0.060	<NONE>	<NONE>	<NONE>
753	U57502	Rattus norvegicus protein tyrosine phosphatase delta gene, catalytic domain, partial cds.	0.060	3452285	(AF044915) polar tube protein PTP55 precursor	0.28
754	X68359	M.fascicularis gene for apolipoprotein C-III	0.060	730843	SHUTTLE CRAFT PROTEIN >gi 487400	2e-04
755	X51634	Pseudomonas braB gene for branched chain amino acid transport carrier (LIV-II)	0.059	1835622	(U85718) CCML [Pseudomonas putida GB-1]	8.1
756	AF072405	Gossypium hirsutum cotton fiber expressed protein 2 (CFE2) mRNA, complete cds	0.059	423766	alkaline phosphatase, 145K - Synechococcus sp.	4.7
757	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.056	2662481	(AF034859) juvenile hormone resistance protein	3.3
758	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.054	547847	LECTIN PRECURSOR	7.0
759	X61046	Hydra N-COL 2 mRNA for mini-collagen, partial cds	0.053	<NONE>	<NONE>	<NONE>
760	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.052	<NONE>	<NONE>	<NONE>
761	S79843	{random amplified hybridization microsatellite RAHM} [Beta vulgaris=sugar beets, Genomic, 537 nt]	0.025	1730145	GAMETOGENESIS EXPRESSED PROTEIN GEG-154 >gi 2137331 pir I48361 gene GEG-154 protein - mouse >gi 550123 (X71642) pid:g550123 [Mus musculus]	2e-16

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mouse mRNA for				
762	AB000096	GATA-2 protein, complete cds	0.023	<NONE>	<NONE>	<NONE>
763	Z62366	H.sapiens CpG DNA, clone 67h7, forward read cpg67h7.ft1a	0.023	3123312	ZINC FINGER PROTEIN 142 (KIAA0236) to Human zinc finger protein(ZNF142) [Homo sapiens]	5.9
764	L11670	Human transmembrane glycoprotein (CD53) gene, exons 2 through 8.	0.023	80636	hypothetical 67K protein - Mycobacterium fortuitum plasmid pAL5000 >gi 149986 (M60875) ORF2	3.4
765	D83984	Sulculus diversicolor DNA for IDO-like myoglobin, complete cds	0.023	3114665	(AF061267) inner membrane component HtxE [Pseudomonas stutzeri]	3.4
766	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.023	683532	(X02155) thyroglobulin [Bos taurus]	1.1
767	U58835	Dissostichus mawsoni preprotrypsin gene, complete cds	0.022	<NONE>	<NONE>	<NONE>
768	AJ009630	Glomus versiforme chitin synthase gene (clone Gvchs3)	0.022	<NONE>	<NONE>	<NONE>
769	J04040	Human glucagon mRNA, complete cds.	0.022	<NONE>	<NONE>	<NONE>
770	X74908	L.esculentum Asr3 gene	0.022	<NONE>	<NONE>	<NONE>
771	L07293	Shigella dysenteriae O-antigen polysaccharide biosynthesis rfbX, O-antigen polymerase (rfc), rhamnosyl transferase I and II (rfbR and rfbQ) and rfbD genes, complete cds.	0.022	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
772	AF040094	inositol polyphosphate 5-phosphatase II (INPP5P) mRNA, complete cds	0.022	<NONE>	<NONE>	<NONE>
773	X76776	H.sapiens HLA-DMB gene	0.022	<NONE>	<NONE>	<NONE>
774	AE001521	Helicobacter pylori, strain J99 section 82 of 132 of the complete genome	0.022	<NONE>	<NONE>	<NONE>
775	X16004	A.longa rbcL, rpl5, rps8, rpl36, rps14, rps2, trnI, trnF, trnC and rpoB (partial) genes > :: emb[X75651]ALRIBP A.longa plastid genes for ribosomal proteins, tRNAs, RNA polymerase subunit beta and rubisco large subunit	0.022	<NONE>	<NONE>	<NONE>
776	Y12707	Lactococcus lactis cremoris plasmid pHW393 DNA, rlladii, mlladii genes	0.022	<NONE>	<NONE>	<NONE>
777	U27118	Arabidopsis thaliana glutamyl-tRNA reductase	0.022	<NONE>	<NONE>	<NONE>
778	Z96622	H.sapiens telomeric DNA sequence, clone 5PTEL002, read 5PTELOO002.seq	0.022	191333	(J05503) carbamoyl-phosphate synthetase (E.C.6.3.5.5)	9.8
779	D83984	Sulculus diversicolor DNA for IDO-like myoglobin, complete cds	0.022	1078509	probable membrane protein YDR018c - yeast	9.7
780	Z77952	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA4A3	0.022	4204206	(AB022786) N-acetyl-beta-D-glucosaminidase [Enterobacter sp.]	7.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis				
781	M10217	mitochondrial DNA, complete genome.	0.022	2145763	B2168_C2_205 protein - Mycobacterium leprae	7.3
782	M55147	Pea chloroplast glyceraldehyde-3-phosphate dehydrogenase (Gpb1) gene, complete cds.	0.022	417308	PROBABLE HELICASE MOT1 Mot1p is a probable helicase essential for vegetative growth on rich glucose medium at 30 degree C: Swiss-Prot Accession number P32333; similar to S. cerevisiae RAD26 gene product: Swiss-Prot Accession number P40352	4.2
783	X58839	Acholeplasma virus MV-L1 DNA for complete circular genome	0.022	3273189	(AB008757) subunit II of c(o/b)3-type cytochrome c oxidase [Bacillus stearothermophilus]	4.1
784	M26185	Mouse c-myb oncogene, exon 1 and exon 2 (partial).	0.022	138592	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) >gi 72270 pir VJFF1 vitellogenin I precursor unnamed protein product [Drosophila melanogaster]	2.5
785	AF061195	Streptomyces albus valine dehydrogenase (Vdh) gene, complete cds	0.022	2088768	(AF003145) B0414.8 gene product [Caenorhabditis elegans]	0.86
786	AF053622	Homo sapiens alpha 1,2-mannosidase IB gene, exon 9	0.022	1352361	EARLY GROWTH RESPONSE PROTEIN 1 fish >gi 531456 (U12895) egr1 [Danio rerio] rerio]	0.36
787	Z71500	S.cerevisiae chromosome XIV reading frame ORF YNL224c	0.022	1708875	PUTATIVE TUMOR SUPPRESSOR LUCA15 sapiens]	0.16
788	D10471	Herpes simplex virus type 2 genomic DNA for 0.74-0.84 region, complete cds	0.022	3132276	(AB011486) short ORF [TT virus]	0.13
789	U43082	Zea mays T cytoplasm male sterility restorer factor 2 (rf2) mRNA, complete cds	0.022	3319720	(AL031035) putative aldehyde dehydrogenase [Streptomyces coelicolor]	0.011

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens simple				
790	X86913	tandem repeat DNA (clone wg3a6)	0.021	<NONE>	<NONE>	<NONE>
791	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
792	U34016	Nannostomus sp. large subunit rRNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.	0.021	<NONE>	<NONE>	<NONE>
793	X00845	Yeast mitochondrial genes for 15S rRNA and tRNA-Trp	0.021	<NONE>	<NONE>	<NONE>
794	AB012113	Homo sapiens gene for CC chemokine PARC precursor, complete cds	0.021	<NONE>	<NONE>	<NONE>
795	U62395	Daucus carota globulin-like protein (Gea8) gene, complete cds	0.021	<NONE>	<NONE>	<NONE>
796	M22718	P.falciparum actin II gene, complete cds.	0.021	2623773	(AF004835) tyrocidine synthetase 3 [Brevibacillus brevis]	8.8
797	U27118	Arabidopsis thaliana glutamyl-tRNA reductase	0.021	3549885	(AJ006631) cysteine-rich secretory protein-1 [Equus caballus]	8.8
798	X99832	H.sapiens CLN3 gene, complete CDS	0.021	262249	(S52010) orf1 5' of EpoR [mice, Peptide. 85 aa] [Mus sp.]	8.7
799	AF016266	Homo sapiens TRAIL receptor 2 mRNA, complete cds	0.021	729048	SUCCINYL-COA:COENZYME A TRANSFERASE transferase [Clostridium kluyveri]	8.7
800	Z92541	Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-13 contains lactase-phlorizin hydrolase (LCT)	0.021	585820	LIPOPOLYSACCHARIDE 1,2-N-ACETYLGLUCOSAMINETRANSFERASE >gi 466761 (U00039) rfaK [Escherichia coli] >gi 1790053 (AE000440) probably hexose transferase; lipopolysaccharide core biosynthesis	5.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		dopamine D2				
801	S58588	receptor [human, brain, Genomic, 3794 nt, segment 4 of 5]	0.021	2677620	(Y08029) NAD(P)(+)-arginine ADP-ribosyltransferase [Oryctolagus cuniculus]	5.1
802	M60522	Rat nerve growth factor-inducible protein (VGF) gene, complete cds.	0.021	4103934	(AF030050) replication factor C [Rattus norvegicus]	3.1
803	AF045654	Gallus gallus neuregulin beta-1a mRNA, complete cds	0.021	2746829	(AF040647) No definition line found [Caenorhabditis elegans]	3.0
804	M69023	Human globin gene.	0.021	3880259	(Z82056) T26H5.8 [Caenorhabditis elegans] >gi 3880787 gnl PID e1350288 (AL032620) T26H5.8	2.4
805	Z65960	H.sapiens CpG DNA, clone 69d2, reverse read cpg69d2.rt1b .	0.021	1707245	(U80845) similar to family 1 of G-protein coupled receptors [Caenorhabditis elegans]	0.79
806	X97073	A.oligospora gene encoding lectin	0.021	116949	CORE ANTIGEN >gi 73601 pir NKVLC2 core antigen - woodchuck hepatitis virus 2 >gi 336135	0.47
807	X56491	D. melanogaster mRNA for gene containing opa repetitive element	0.021	2842750	HOMEODOMAIN PROTEIN DLX-7 >gi 1620520	0.16
808	L78760	Homo sapiens (subclone 1_f6 from P1 H31) DNA sequence	0.021	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.15
809	AB007864	Homo sapiens KIAA0404 mRNA, partial cds	0.021	118144	CYSTEINE SYNTHASE A (O-ACETYL SERINE SULFHYDRYLASE A) (O-ACETYL SERINE (THIOL)-LYASE A) (CSASE A) >gi 68323 pir SYEBAC cysteine synthase (EC 4.2.99.8) A - Salmonella typhimurium >gi 153935 (M21450) cysK protein [Salmonella typhimurium]	0.12
810	AL021932	Mycobacterium tuberculosis H37Rv complete genome; segment 22/162	0.021	2909514	(AL021932) hypothetical protein Rv0439c	7e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
811	U89991	Hypocrea jecorina mannose-1-phosphate guanylyltransferase (MPG1) mRNA, complete cds	0.021	3581924	(AL031538) mannose-1-phosphate guanylyltransferase [Schizosaccharomyces pombe]	6e-20
812	X00641	Sugar beet mitochondrial minicircle pO sequence	0.020	<NONE>	<NONE>	<NONE>
813	Z50097	D.melanogaster mRNA for hdc protein.	0.020	<NONE>	<NONE>	<NONE>
814	AF044866	Phoebe sennae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs	0.020	<NONE>	<NONE>	<NONE>
815	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
816	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
817	AE001405	Plasmodium falciparum chromosome 2, section 42 of 73 of the complete sequence	0.020	2196776	(AF003342) bunched gene product [Drosophila melanogaster]	8.4
818	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	627071	histidine-rich protein - Plasmodium lophurae	2.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
819	Y13304	Hylobates hooleck mitochondrial DNA for cytb gene, Horace	0.020	285580	(D10043) ORF [Acetobacter pasteurianus] (U80439) coded for by C. elegans cDNA yk7c8.5; coded for by C. elegans cDNA yk133b3.5; coded for by C. elegans cDNA yk65a4.5; coded for by C. elegans cDNA yk7c8.3; coded for by C. elegans cDNA CEESQ66F; coded for by C. elegans cDNA yk65a4.3;...	2.1
820	Z66539	H.sapiens creatine transporter gene	0.020	1703594	EARLY GROWTH RESPONSE PROTEIN 1 fish >gi 531456 (U12895) egr1 [Danio rerio] rerio]	0.98
821	AF053622	Homo sapiens alpha 1,2-mannosidase IB gene, exon 9	0.020	1352361	HYPOTHETICAL 38.1 KD PROTEIN IN SBCB-HISL INTERGENIC REGION >gi 405956 (U00009) ORF_ID:o349#4; similar to [SwissProt Accession Number P33015] [Escherichia coli] >gi 1736693 gnl PID d1016570 Number P33015] [Escherichia coli] >gi 1788323 (AE000292) putative transport system permease protein [Escherichia coli]	0.72
822	M20555	Human MHC class II HLA-DRw53-beta (DR4,w4) gene, exons 2,3,4,5,6.	0.020	465569	COENZYME PQQ SYNTHESIS PROTEIN F synthesis F - Pseudomonas fluorescens >gi 929802	0.43
823	M20555	Human MHC class II HLA-DRw53-beta (DR4,w4) gene, exons 2,3,4,5,6.	0.020	1709751		0.42

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
824	AJ005015	Homo sapiens mRNA for putative SMC-like protein, partial	0.020	267449	HYPOTHETICAL 12.5 KD PROTEIN ZK637.2 IN CHROMOSOME III >gi 102507 pir S15787 hypothetical protein 1 (cosmid ZK637) - Caenorhabditis elegans Genefinder; cDNA EST yk217b5.3 comes from this gene; cDNA EST yk217b5.5 comes from this gene; cDNA EST yk340g12.3 comes from this gene; cDNA EST yk340g12.5 comes from this gene; cDNA EST yk428c5.5 co...	1e-12
825	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.020	1109847	(U41538) No definition line found [Caenorhabditis elegans]	1e-22
826	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.019	132836	60S RIBOSOMAL PROTEIN L28 protein L28 [Rattus norvegicus]	5.7
827	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.019	2633401	(Z99109) similar to DNA exonuclease	4.5
828	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.019	2492604	MULTIDRUG RESISTANCE PROTEIN CDR2 albicans]	4.4
829	U67538	Methanococcus jannaschii section 80 of 150 of the complete genome	0.019	1723566	PUTATIVE GLUCOSYLTRANSFERASE C17C9.07 >gi 1314159 gnl PID e241760 (Z73099) SPAC17C9.07, putative glucosyl transferase len: 501, similar to SW:ALG8_YEAST P40351 glucosyltransferase ALG8 pombe]	2.7
830	U56088	Human periodic tryptophan protein 2 (PWP2) gene, exons 3 to 14	0.019	2144804	collagen alpha 1(II) chain - bovine	0.040
831	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.018	1916976	(U91682) vitelline membrane protein homolog [Aedes aegypti]	7.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
832	AF026258	Onobrychis viciifolia chalcone synthase (CHS) mRNA, complete cds	0.018	763076	(Z48799) ZP3 [Cyprinus carpio] >gi 777724 (L41637) egg membrane protein [Cyprinus carpio]	5.2
833	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.009	3955011	(AJ005438) beta adrenoreceptor B	0.60
834	X71603	C.jejuni VST DNA >:: emb A39603 A39603 Sequence 2 from Patent WO9417205 >:: gb I76090 I76090 Sequence 2 from patent US 5691138	0.008	<NONE>	<NONE>	<NONE>
835	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.008	138116	HEAD FIBER PROTEIN (LATE PROTEIN GP8.5) >gi 75846 pir WMBP8H gene 8.5 protein - phage PZA >gi 216057 (M11813) head fiber protein	8.1
836	X91751	Bovine herpesvirus type 1 UL7 gene	0.008	1711436	SUPEROXIDE DISMUTASE (FE) 1.15.1.1 (Fe) - Pseudomonas aeruginosa >gi 409767	5.9
837	M95594	Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate synthase (ACS2) gene, complete cds.	0.008	683698	(Z48229) orf1 gene product [Saccharomyces cerevisiae]	1e-06
838	U67465	Methanococcus jannaschii section 7 of 150 of the complete genome	0.008	3874664	(Z68493) predicted using Genefinder	1e-07
839	X72388	B.taurus mRNA for filensin	0.008	100174	1-aminocyclopropane-1-carboxylate synthase	7e-09
840	U22398	Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.	0.008	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	2e-18
841	L42546	Xenopus laevis LIM class homeodomain protein	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
842	AF041428	ribosomal protein s4 X isoform gene, complete cds	0.007	<NONE>	<NONE>	<NONE>
843	AF000227	Secale cereale omega secalin gene, complete cds	0.007	<NONE>	<NONE>	<NONE>
844	D86254	Human MHC (HLA) DRB intron 1 DNA, partial sequence	0.007	<NONE>	<NONE>	<NONE>
845	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
846	Y07738	M.musculus gene for vimentin	0.007	<NONE>	<NONE>	<NONE>
847	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.007	<NONE>	<NONE>	<NONE>
848	AF055119	Homo sapiens alpha-tectorin (TECTA) gene, exon 6	0.007	<NONE>	<NONE>	<NONE>
849	M61195	Zucchini 1-aminocyclopropane-1-carboxylate synthase	0.007	<NONE>	<NONE>	<NONE>
850	Y11050	Homo sapiens DSG3 gene, partial intron and partial exon 6, 140 bp	0.007	<NONE>	<NONE>	<NONE>
851	X61204	M.voltae vhuD, vhuG, vhuA, vhuU & vhuB genes	0.007	<NONE>	<NONE>	<NONE>
852	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.007	<NONE>	<NONE>	<NONE>
853	S43882	telomere: {minichromosome, repeats} [Trypanosoma brucei, Genomic, 1170 nt]	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
854	L32674	Geomydoecus nadleri mitochondrial cytochrome oxidase I gene, partial cds.	0.007	<NONE>	<NONE>	<NONE>
855	U58732	Caenorhabditis elegans cosmid F48D6.	0.007	<NONE>	<NONE>	<NONE>
856	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
857	Z35284	H.sapiens mRNA for MDR3 P-glycoprotein	0.007	1730696	HYPOTHETICAL 121.1 KD PROTEIN IN BIO3-HXT17 INTERGENIC REGION PRECURSOR YNR067c - yeast (Saccharomyces cerevisiae)	9.5
858	X15217	Human sno oncogene mRNA for snoA protein, ski-related	0.007	902455	(U24203) membrane protein [Escherichia coli]	8.8
859	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	1684636	(Y09454) ORF3 [Lactobacillus casei bacteriophage A2]	8.3
860	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	3878803	(Z48795) R05H5.7 [Caenorhabditis elegans]	8.3
861	S76317	119=180-200 kda membrane protein scavenger receptor homolog {clone 18, intron and flanking exons 14 and 15} [sheep, lymph node, lymphocytes, Genomic, 308 nt, segment 2 of 2]	0.007	294747	(L08174) ORF2 [Romanomermis culicivorax]	7.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
862	D88084	Pedicularis verticillata chloroplast DNA, intergenic region between trnT(UGU) and trnL(UAA)5'exon	0.007	2555187	(AF026789) vitellogenin [Pimpla nipponica]	6.9
863	X58869	Chicken mRNA for aldehyde dehydrogenase	0.007	115978	CD30L RECEPTOR PRECURSOR (LYMPHOCYTE ACTIVATION ANTIGEN	6.5
864	D87120	Homo sapiens mRNA for GS3786, complete cds	0.007	3879589	(Z50875) From the non dominant, cDNA EST EMBL:D35637 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes fr... >gi 3880965 gnl PID e1350578 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes ...	5.1
865	X68793	H.sapiens gene for antithrombin III	0.007	2358285	(AF010403) ALR [Homo sapiens]	3.8
866	AJ001596	Danio rerio mRNA for opioid receptor homologue	0.007	2507509	HYPOTHETICAL 29.8 KD PROTEIN IN HOLB-PTSG INTERGENIC REGION >gi 1787342 (AE000210) orf, hypothetical protein [Escherichia coli] protein in holB 3'region . [Escherichia coli]	1.9
867	AF061195	Streptomyces albus valine dehydrogenase (Vdh) gene, complete cds	0.007	2088768	(AF003145) B0414.8 gene product [Caenorhabditis elegans]	1.9
868	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.007	1710105	UDP-N-ACETYLGLUCOSAMINE 2-EPIMERASE UDP-N-acetylglucosamine 2-epimerase [Plasmid pWQ799]	1.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Zebrafish retinoic acid receptor alpha 2.A	0.007	2239219	(Z97210) hypothetical protein	0.77
869	L03398	Human mRNA for KIAA0150 gene, partial cds	0.007	19917	(Z14014) Pistil extensin like protein, partial CDS only	0.61
870	D63484	Maize glyceraldehyde 3-phosphate dehydrogenase, 3' end.	0.007	543068	mucin, tracheobronchial - dog >gi 402558	0.45
871	M31483	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.007	2494941	ALPHA-2B ADRENERGIC RECEPTOR adrenoceptor [Cavia porcellus] >gi 1587159 prf 2206293B adrenoceptor alpha2B [Cavia porcellus]	0.42
872	AF090115	Helianthus tuberosus lectin 1 mRNA, complete cds	0.007	1110587	(S79410) nuclear localization signals Peptide, 140 aa [Mus sp.]	0.26
873	AF064029	H.sapiens PAL2A gene	0.007	1706176	CUTINASE TRANSCRIPTION FACTOR 1 ALPHA >gi 1262912 (U51671) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]	0.21
874	X88931	zRAR alpha =retinoic acid receptor alpha [zebrafish, embryos, mRNA, 1773 nt]	0.007	2239219	(Z97210) hypothetical protein	0.11
875	S74155	Petromyzon marinus plasma albumin mRNA, complete cds.	0.007	730888	OCTAPEPTIDE-REPEAT PROTEIN T2	0.011
876	M74193	Saccharomyces cerevisiae Spp41p (SPP41) gene, complete cds.	0.007	3820885	(AL033126) 65G3.k [Drosophila melanogaster]	0.001
877	U03673	Homo sapiens mRNA for Laminin-5 beta3 chain, complete cds	0.007	1235974	(X96713) collagen [Globodera pallida]	3e-06
878	D37766					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Caenorhabditis elegans putative transcription factor MAB-3 (mab-3) gene, complete cds	0.007	3747107	(AF095741) unknown [Rattus norvegicus]	5e-09
879	AF022388					
		Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds	0.007	1890281	(U89984) transformation-sensitive protein homolog	2e-09
880	U89984					
		Homo sapiens mRNA for KIAA0882 protein, partial cds	0.007	3880809	(AF021465) similar to RhoGAP rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA ... Probable rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA ...	1e-23
881	AB020689					
		Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
882	AF100694					
		Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
883	AF027173					
		Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
884	U76524					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
885	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
886	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	<NONE>	<NONE>	<NONE>
887	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	<NONE>	<NONE>	<NONE>
888	M80529	Rattus norvegicus ceruloplasmin gene, exon 1 and 5' flank	0.006	<NONE>	<NONE>	<NONE>
889	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.006	99408	hypothetical protein 6 - Chlamydomonas reinhardtii transposon >gi 1360717 gnl PID e33461 reinhardtii]	9.6
890	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.006	4039024	(AF039110) polyprotein [Rubella virus]	9.3
891	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	160533	(M94428) merozoite surface antigen 1 [Plasmodium vivax]	7.5
892	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	4019458	(AF093984) envelope glycoprotein [Human immunodeficiency virus type 1]	7.0
893	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	1916976	(U91682) vitelline membrane protein homolog [Aedes aegypti]	6.8
894	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	102059	promastigote surface antigen-2 (clone 4.6) - Leishmania major (fragment) >gi 9583 (X57135) surface antigen P2 [Leishmania major]	2.4
895	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	3171241	(AF067204) transcription factor BF-1 [Danio rerio]	1.0
896	X99384	M.musculus mRNA for paladin gene	0.003	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
897	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.003	<NONE>	<NONE>	<NONE>
898	AE001148	Borrelia burgdorferi (section 34 of 70) of the complete genome	0.003	4160388	(AJ011856) ORF Q0255 [Saccharomyces cerevisiae]	7.6
899	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.003	1709213	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)	1.5
900	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
901	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
902	AF104631	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
903	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
904	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
905	M21339	Human non-histone chromosomal protein HMG-14 gene, complete cds.	0.002	<NONE>	<NONE>	<NONE>
906	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human h-lys gene for lysozyme (upstream region)				
907	X57103		0.002	<NONE>	<NONE>	<NONE>
908	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
909	U01066	Human CD4 promoter, partial sequence.	0.002	<NONE>	<NONE>	<NONE>
910	L28094	Barley mRNA sequence.	0.002	<NONE>	<NONE>	<NONE>
911	AD000833	Homo sapiens DNA from chromosome 19-cosmid f19399 (~17 kb EcoRI restriction fragment)	0.002	<NONE>	<NONE>	<NONE>
912	AJ011701	Homo sapiens TRHR gene promoter and exons 1-2, partial	0.002	<NONE>	<NONE>	<NONE>
913	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
914	AF037062	Homo sapiens retinol dehydrogenase gene, complete cds	0.002	<NONE>	<NONE>	<NONE>
915	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
916	U67608	Methanococcus jannaschii section 150 of 150 of the complete genome	0.002	<NONE>	<NONE>	<NONE>
917	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
918	Z46736	H.sapiens DNA for repeat region (ABM-C82)	0.002	<NONE>	<NONE>	<NONE>
919	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
920	Z85983	X.laevis mRNA for NOVA protein	0.002	<NONE>	<NONE>	<NONE>
921	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
922	S61977	medium-chain acyl-CoA dehydrogenase {exon 10, intron 10} [human, Genomic, 1407 nt]	0.002	<NONE>	<NONE>	<NONE>
923	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	<NONE>	<NONE>	<NONE>
924	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	<NONE>	<NONE>	<NONE>
925	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.002	<NONE>	<NONE>	<NONE>
926	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>
927	X51646	H.sapiens DNA for dopamine D2 receptor gene	0.002	3329125	(AE001337) Yop C/Gen Secretion Protein D [Chlamydia trachomatis]	9.5
928	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	465762	HYPOTHETICAL 112.1 KD PROTEIN C06G4.1 IN CHROMOSOME III >gi 630524 pir S44748 C06G4.1 protein - Caenorhabditis elegans >gi 409292 (L25598) homology with vigilin; coded for by C. elegans cDNA GenBank:M88954 (CEL12C9); putative [Caenorhabditis	8.9
929	U48478	Human skeletal muscle ryanodine receptor gene	0.002	2137221	co-repressor protein - mouse >gi 642619	6.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
930	AF100694	Pontin52 mRNA, complete cds	0.002	806536	(Z22520) membrane protein [Bacillus acidopullulyticus]	6.3
931	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	3881055	(AL023844) Y48A6B.1 [Caenorhabditis elegans]	5.8
932	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.002	3878330	(Z81097) K07A1.4 [Caenorhabditis elegans]	4.8
933	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	137640	REPLICATION PROTEIN E1 papillomavirus	4.0
934	AF019660	Mus musculus nuclear orphan receptor RORgamma	0.002	1330365	(U58757) similar to nucleotide pyrophosphatases	3.9
935	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.002	1785972	(U46951) ORF5; Method: conceptual translation supplied by author	3.7
936	V00508	Human gene for epsilon-globin.	0.002	1333804	(X56082) protease [Ruminococcus flavefaciens]	3.5
937	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	4153876	(AC005531) similar to mouse homeodomain-interacting protein kinase 2; similar to AF077659 (PID:g3702958)	3.0
938	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.002	1070461	ornithine carbamoyltransferase (EC 2.1.3.3) - yeast (Saccharomyces cerevisiae) >gi 929866 (X83502) pid:e130025 [Saccharomyces cerevisiae] >gi 1008256	2.8
939	S41458	rod cGMP phosphodiesterase beta-subunit [human, mRNA, 3231 nt]	0.002	3450883	(AF083334) fibroin [Antheraea pernyi]	1.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
940	X06286	Drosophila melanogaster Gart locus with genes for GARS=phosphoribosylamineglycine ligase, AIRS=phosphoribosylformylglycinamide cyclo-ligase, GART=glycinamide ribotide transformylase > :: gb J02527 DROGART D.melanogaster Gart gene encoding two polypeptides with GAR synthase, AIR synthase, and GAR transformylase enzyme activities and a pupal cuticle gene nested within intron A of the Gart gene.	0.002	2662054	(AB004651) isocitrate lyase	1.5
941	AF015812	Homo sapiens RNA helicase p68 (HUMP68) gene, complete cds	0.002	3641659	(AB008374) alpha 3 type I collagen	1.1
942	X78925	H.sapiens HZF2 mRNA for zinc finger protein	0.002	141624	ZINC FINGER PROTEIN ZFP-37 (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN)	1.0
943	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	3879997	(Z49071) weak similarity with mu-type opioid receptor (Swiss Prot accession number (P33535)	1.0
944	Z69639	Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.	0.002	3523162	(AF076292) TGF-beta/activin signal transducer FAST-1p	0.81

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
945	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.002	2984161	(AE000761) hypothetical protein [Aquifex aeolicus]	0.80
946	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.002	101830	hypothetical protein B - chestnut blight fungus	0.72
947	AF017307	Homo sapiens Ets-related transcription factor (ERT) mRNA, complete cds	0.002	200531	(M18071) prion protein [Mus musculus]	0.72
948	U11383	Drosophila melanogaster Ovo-1028aa (ovo) mRNA, complete cds.	0.002	2465207	(AF016045) OVO-like 1 binding protein [Homo sapiens]	0.35
949	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.002	3834294	(U80846) No definition line found [Caenorhabditis elegans]	0.29
950	AF086315	Homo sapiens full length insert cDNA clone ZD52F10	0.002	545067	(S68356) action potential broadening potassium channel=Shab [Aplysia, bag cell neurons, head ganglia, Peptide, 905 aa] [Aplysia] >gi 743110 prf 2011375A K channel [Aplysia californica]	0.15
951	X53096	S.aureus genes encoding Sau96I DNA methyltransferase and Sau96I restriction endonuclease	0.002	2529575	(AF018164) kinesin-like protein 3C [Homo sapiens]	0.11
952	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.002	729918	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)	0.092
953	X73973	G.gallus RAR-gamma2 mRNA for retinoic acid receptor	0.002	586122	TRICHOHYALIN >gi 423321 pir A40691 trichohyalin - sheep >gi 295941 (Z18361) trichohyalin	0.073
954	S41458	rod cGMP phosphodiesterase beta-subunit [human, mRNA, 3231 nt]	0.002	1017427	(X90569) elastic titin [Homo sapiens]	0.013

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		D.melanogaster			(U88169) similar to	
955	M35887	defective chorion-1 fc125 (dec-1) gene, complete cds.	0.002	1825606	molybdoterin biosynthesis MOEB proteins [Caenorhabditis elegans]	0.008
956	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.002	1825593	(U88167) D2092.2 gene product [Caenorhabditis elegans]	1e-06
957	AF033929	Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence	9e-04	<NONE>	<NONE>	<NONE>
958	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-04	<NONE>	<NONE>	<NONE>
959	AF029062	Homo sapiens DEAD-box protein (BAT1) gene, partial cds	8e-04	<NONE>	<NONE>	<NONE>
960	U70671	Human ataxin-2 related protein mRNA, partial cds	8e-04	<NONE>	<NONE>	<NONE>
961	AF051709	Dendrocopos leucopterus clone 2 microsatellite HrU2 repeat region	8e-04	<NONE>	<NONE>	<NONE>
962	X14077	Pea phy gene for phytochrome apoprotein	8e-04	<NONE>	<NONE>	<NONE>
963	AC004497	Homo sapiens chromosome 21, P1 clone LBNL#6	8e-04	457146	(L27838) rhoptry protein [Plasmodium yoelii]	9.6
964	AF077344	Homo sapiens cartilage-derived C-type lectin	8e-04	3702123	(AJ011707) TraD protein [Escherichia coli]	8.5
965	X85117	H.sapiens epb72 gene exons 2,3,4,5,6,7	8e-04	2570059	(AJ004687) N-4 cytosine-specific methyltransferase [Neisseria gonorrhoeae]	6.8
966	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1345859	COPPER TRANSPORT PROTEIN CTR1 transport protein - yeast (Saccharomyces cerevisiae) gene product [Saccharomyces cerevisiae]	6.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
967	AF031403	MLL/AF4 translocation breakpoint t(4;11)(q21;23)	8e-04	2498926	SMALL PROTEIN B HOMOLOG A43259, from E. hirae [Mycoplasma pneumoniae]	6.6
968	L29252	Human (clone D13-2) L-iditol-2 dehydrogenase gene, exon 4, exon 5, exon 6 and exon 7.	8e-04	1488070	(U63997) putative transposase [Enterococcus faecium]	5.2
969	X16995	Mouse N10 gene for a nuclear hormonal binding receptor	8e-04	1493833	(U47323) stromal cell protein [Mus musculus]	3.2
970	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds	8e-04	1346101	4-AMINO BUTYRATE AMINOTRANSFERASE TRANSAMINASE) (GABA AMINOTRANSFERASE) homolog - smut fungus (Ustilago maydis) >gi 881562 Emericella nidulans gamma-amino-n-butyrate transaminase Swiss-Prot Accession Number P14010 [Ustilago maydis]	0.83
971	U37452	Human Down Syndrome region of chromosome 21 genomic sequence, clone A31D6-1C5.	8e-04	4164069	(AF111093) latrophilin 3 splice variant bbah [Bos taurus]	0.26
972	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-04	1352877	HYPOTHETICAL 13.0 KD PROTEIN IN RAD26-GEF1 INTERGENIC REGION >gi 1077881 pir S57057 probable membrane protein YJR038c - yeast (Saccharomyces cerevisiae) >gi 1015688 (Z49538) ORF YJR038c putative [Saccharomyces cerevisiae]	0.23
973	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-04	1788557	(AE000312) orf, hypothetical protein [Escherichia coli]	0.19

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
974	X83872	H.vulgaris mRNA for cAMP response element binding protein	8e-04	1175386	HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I >gi 2130289 pir S58305 hypothetical protein SPAC18B11.06 - fission yeast hypothetical protein [Schizosaccharomyces pombe]	0.005
975	M32514	Rat simple sequence DNA, clone 5.	8e-04	2394492	(AF024502) No definition line found [Caenorhabditis elegans]	0.002
976	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-04	2981631	(AB012223) ORF2 [Canis familiaris]	0.001
977	X89211	H.sapiens DNA for endogenous retroviral like element	8e-04	2065210	(Y12713) Pro-Pol-dUTPase polyprotein	3e-04
978	U14391	Human myosin-IC mRNA, complete cds.	8e-04	3142302	(AC002411) Strong similarity to myosin heavy chain gb Z34293 from A. thaliana. [Arabidopsis thaliana]	4e-16
979	L13612	Drosophila melanogaster dead-box protein D.melanogaster DEAD-box gene, complete CDS	8e-04	3776027	(AJ010475) RNA helicase [Arabidopsis thaliana]	9e-24
980	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
981	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
982	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
983	Z73987	Human DNA sequence from cosmid N120B6 on chromosome 22 Contains ESTs, complete sequence [Homo sapiens]	7e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Brassica rapa mRNA for SRK45, complete cds				
984	AB012106		7e-04	<NONE>	<NONE>	<NONE>
985	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
986	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
987	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
988	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	<NONE>	<NONE>	<NONE>
989	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
990	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
991	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
992	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
993	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	<NONE>	<NONE>	<NONE>
994	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	3327230	(AB014608) KIAA0708 protein [Homo sapiens]	9.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
995	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	3327230	(AB014608) KIAA0708 protein [Homo sapiens]	9.3
996	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	3876455	(Z93380) predicted using Genefinder; similar to 7tm receptor protein [Caenorhabditis elegans]	7.1
997	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	2128771	hypothetical protein MJ1293 - Methanococcus jannaschii >gi 1591931 (U67570) M. jannaschii predicted coding region MJ1293 [Methanococcus jannaschii]	6.2
998	U09412	Human zinc finger protein ZNF134 mRNA, complete cds	7e-04	1083336	glutathione transferase (EC 2.5.1.18) piA - mouse	5.4
999	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	473515	(M17619) NADH dehydrogenase subunit ND4 [Asterina pectinifera]	3.7
1000	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	1724097	(U79772) female sex protein [Mercurialis annua]	3.3
1001	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-04	1197103	(D49747) core, env, and part of E2/NS1	3.2
1002	X16995	Mouse N10 gene for a nuclear hormonal binding receptor	7e-04	345372	unc-5 protein, long form - Caenorhabditis elegans >gi 258529 bbs 118648 (S47168) UNC-5=immunoglobulin and thrombospondin type 1 transmembrane protein {alternatively spliced} aa [Caenorhabditis elegans] >gi 2662596 (AF036698) C. elegans UNC-5 (NID:g25852)	2.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1003	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-04	4204220	(AB022866) mobilization protein	2.5
1004	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-04	3201550	(Y17116) fibrinogen-binding protein	2.4
1005	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	7e-04	1174264	(U45966) polyprotein [Hepatitis G virus]	0.73
1006	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-04	135308	TRANSCRIPTION FACTOR JUN-D	0.065
1007	X98745	H.sapiens EWS gene, intron 6, polymorphism	7e-04	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.001
1008	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	7e-04	1633564	(U47924) C8 [Homo sapiens]	9e-09
1009	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	6e-04	284171	Ig epsilon chain C region form 3 - human	1.3
1010	AB012106	Brassica rapa mRNA for SRK45, complete cds	6e-04	3845262	(AE001414) BRAHMA ortholog (DNA helicase superfamily II)	0.25
1011	AL034404	Human DNA sequence from clone 417C12 on chromosome Xp22.1122.2, complete sequence [Homo sapiens]	3e-04	<NONE>	<NONE>	<NONE>
1012	M99701	Homo sapiens (pp21) mRNA, complete cds.	3e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1013	U00227	Ovis aries Merino breed DR beta-chain antigen binding domain, MHC class II DRB (Ovar-DRB24) gene, partial cds.	3e-04	<NONE>	<NONE>	<NONE>
1014	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	3e-04	<NONE>	<NONE>	<NONE>
1015	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3e-04	999418	(L19655) ORF [Tomato ringspot virus]	8.3
1016	AB012106	Brassica rapa mRNA for SRK45, complete cds	3e-04	2367460	(AF011415) putative pheromone receptor [Mus musculus]	7.0
1017	AJ010737	Mus musculus DNA for microsatellite 3kb upstream lbp gene	3e-04	4106549	(AF104411) neuronal-specific septin 3 [Mus musculus]	5.5
1018	AF053137	Homo sapiens histone deacetylase 3 gene, exons 4, 5, 6, 7, 8, 9, and 10	3e-04	416702	NADH-DEPENDENT FLAVIN OXIDOREDUCTASE acid-inducible - Eubacterium sp >gi 1381570 (U57489) NADH:flavin oxidoreductase [Eubacterium sp. VPI 12708]	5.3
1019	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	3e-04	1785789	(Y08502) orf111d [Arabidopsis thaliana]	5.1
1020	AC004173	Homo sapiens clone UWGC:y23x011 from 6p21, complete sequence [Homo sapiens]	3e-04	558521	(D28917) polyprotein [Hepatitis C virus]	1.1
1021	X57025	Human IGF-I mRNA for insulin-like growth factor I	3e-04	4206707	(AF118122) putative outer membrane protein OmpU	0.65
1022	X77090	H.sapiens IL-1Ra gene.	3e-04	1065941	(U40799) F42C5.7 gene product [Caenorhabditis elegans]	0.12

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Pseudorabies virus with upstream and downstream sequences.			(AF040650) contains similarity to sodium-potassium-chloride cotransport proteins	
1023	M34651		3e-04	2746853		7e-05
1024	Z36011	S.cerevisiae chromosome II reading frame ORF YBR142w	3e-04	2500537	PROBABLE ATP-DEPENDENT RNA HELICASE HAS1 >gi 626265 pir S47451 hypothetical protein YMR290c RNA helicase [Saccharomyces cerevisiae]	4e-08
1025	AF020286	Dictyostelium discoideum 2034 gene, partial cds	3e-04	1465834	(U64857) No definition line found [Caenorhabditis elegans]	6e-14
1026	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha (ODA11) gene, exons 2-15, and partial cds.	3e-04	3876775	(Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531)	9e-15
1027	AF020286	Dictyostelium discoideum 2034 gene, partial cds	3e-04	1465834	(U64857) No definition line found [Caenorhabditis elegans]	1e-17
1028	X79811	S.cerevisiae ACT3 gene	3e-04	3876090	(Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-31
1029	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1030	M22970	Human pancreatic phospholipase A-2 (PLA-2) gene, exons 1 to 3.	2e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1031	Z68686	sequence from cosmid N2E9 on chromosome 22. Contains EST, complete sequence [Homo sapiens]	2e-04	<NONE>	<NONE>	<NONE>
1032	X95154	H.sapiens brca2 gene exon 4 > :: emb A62779 A62779 Sequence 20 from Patent WO9719110	2e-04	<NONE>	<NONE>	<NONE>
1033	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<NONE>	<NONE>	<NONE>
1034	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1035	AE001415	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence	2e-04	<NONE>	<NONE>	<NONE>
1036	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1037	AC000958	Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence	2e-04	<NONE>	<NONE>	<NONE>
1038	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	2e-04	2501523	CD59 GLYCOPROTEIN PRECURSOR	7.1
1039	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	2765360	(Y13925) cathepsin L2 [Penaeus vannamei]	6.8

H23

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					RNA POLYMERASE	
1040	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	2e-04	133636	>gi 67126 pir RRXPLC RNA-directed RNA polymerase (EC 2.7.7.48) - lymphocytic choriomeningitis virus (strain Armstrong 53b) >gi 331369	5.2
1041	AB012106	Brassica rapa mRNA for SRK45, complete cds	2e-04	3822155	(AF074613) type II secretion protein [Escherichia coli O157:H7]	4.0
1042	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	1718125	REGULATORY PROTEIN E2 >gi 1020222 type 36]	0.38
1043	X17058	Sus scrofa mRNA for glucose transport protein	2e-04	3341906	(AB009593) xylose transporter	2e-15
1044	AF008216	Homo sapiens candidate tumor suppressor pp32r1	1e-04	<NONE>	<NONE>	<NONE>
1045	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	1e-04	624126	(U42580) a65L [Paramecium bursaria Chlorella virus 1]	7.9
1046	L14930	Glycine max (Rab7p) mRNA, complete cds.	9e-05	<NONE>	<NONE>	<NONE>
1047	AJ009970	Mus musculus thromboxane A2 receptor gene, exon 3, partial	9e-05	<NONE>	<NONE>	<NONE>
1048	Y11896	M.musculus mRNA for Brx gene, partial	9e-05	<NONE>	<NONE>	<NONE>
1049	L10832	Polistes annularis (clone pan48AAT) tandem repeat region.	9e-05	<NONE>	<NONE>	<NONE>
1050	AF055011	Homo sapiens clone 24587 mRNA sequence	9e-05	3880586	(Z79758) cDNA EST EMBL:D28009 comes from this gene; cDNA EST EMBL:D28008 comes from this gene; cDNA EST EMBL:D32478 comes from this gene; cDNA EST EMBL:D34508 comes from this gene; cDNA EST EMBL:D37581 comes from this gene; ...	7.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1051	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-05	3024292	RHODOPSIN >gi 2290717 (AF000947) rhodopsin [Sepia officinalis]	6.7
1052	Z58294	H.sapiens CpG DNA, clone 34d6, forward read cpg34d6.ft1a .	9e-05	3885496	(AF064825) heparin/heparan sulfate N-acetylglucosaminyl N-deacetylase/N-sulfotransferase [Bos taurus]	0.65
1053	D87451	Human mRNA for KIAA0262 gene, complete cds	9e-05	3874739	(Z66495) similar to claustrin like	0.004
1054	L37092	Mus musculus cyclin-dependent kinase homologue	9e-05	3080513	(AL022598) hypothetical protein	4e-09
1055	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1056	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1057	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1058	D10102	Homo sapiens DNA from cosmid clone:844, GT repeat sequence	8e-05	<NONE>	<NONE>	<NONE>
1059	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	8e-05	1176475	HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION >gi 1078237 pir S56849 probable membrane protein YJL073w - yeast (Saccharomyces cerevisiae) >gi 895898 (X88851) hypothetical protein YJL073w [Saccharomyces cerevisiae]	6.0
1060	X71934	H.sapiens XB gene for tenascin-X, repeat XIII	8e-05	285207	microtubule-associated protein, 110K tau - rat >gi 207158 (M84156) big tau [Rattus norvegicus]	3.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1061	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	4049682	(AF063866) ORF MSV092 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	2.1
1062	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	8e-05	3861019	(AJ235271) unknown [Rickettsia prowazekii]	5e-14
1063	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	7e-05	<NONE>	<NONE>	<NONE>
1064	L04193	Human lens membrane protein (mp19) gene, exon 11.	7e-05	<NONE>	<NONE>	<NONE>
1065	X61609	B.napus gene for LHC II Type III chlorophyll a/b binding protein	7e-05	2132314	hypothetical protein YPR174c - yeast similarity to a nuclear lamin from C. elegans (PIR accession number S42257) [Saccharomyces cerevisiae]	8.9
1066	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	7e-05	2979422	(AB006757) PCDH7 (BH-Pcdh)c [Homo sapiens]	5.7
1067	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	7e-05	2493696	HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi 1480440 (U34204) ORF185; hypothetical 21.4 kD protein [Brassica oleracea]	5.2
1068	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	7e-05	2501029	PROBABLE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (LEUCINE--TRNA LIGASE) (LEURS) KIAA0028 [Homo sapiens]	1.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1069	Z68758	sequence from cosmid cN85E10 on chromosome 22q11.2-qter	3e-05	<NONE>	<NONE>	<NONE>
1070	X60653	human Histone H3.3 pseudogene (CIR-456)	3e-05	<NONE>	<NONE>	<NONE>
1071	Z58294	H.sapiens CpG DNA, clone 34d6, forward read cpg34d6.ft1a .	3e-05	1706241	GUANYLYL CYCLASE GC-E PRECURSOR cyclase receptor [Mus musculus]	9.6
1072	AF043251	Homo sapiens mitochondrial outer membrane protein (Tom40) gene, nuclear gene encoding mitochondrial protein, exons 1 through 6	3e-05	113980	AMINE OXIDASE [FLAVIN-CONTAINING] B oxidase (flavin-containing) (EC 1.4.3.4) B - human B [human, platelet, Peptide Partial, 520 aa] [Homo sapiens]	8.9
1073	M31104	Chicken progesterone receptor gene, encoding forms A and B, exons 1 and 2.	3e-05	1170841	IG GAMMA LAMBDA CHAIN V-II REGION	4.8
1074	AF012899	Sambucus nigra ribosomal inactivating protein precursor mRNA, complete cds	3e-05	543684	ribosomal protein S3 - Chlamydomonas humicola chloroplast (fragment)	4.2
1075	L22206	Human vasopressin receptor V2 gene, complete cds.	3e-05	791207	(U20615) Gnot1 homeodomain protein [Gallus gallus]	1.8
1076	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	3e-05	3237340	(AF033361) polypeptide [Hepatitis C virus]	0.94
1077	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2879805	(AL021813) hypothetical protein	0.001
1078	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	3877951	(Z81555) predicted using Genefinder	3e-07

427

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1079	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-05	<NONE>	<NONE>	<NONE>
1080	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	3880197	(Z81132) predicted using Genefinder	2.4
1081	AF087989	Homo sapiens full length insert cDNA clone YX29D10	2e-05	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	1.8
1082	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	474896	(L31967) mating type protein [Coprinus cinereus]	1.4
1083	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	2e-05	2266988	(Y13274) M33 polycomb-like protein [Mus musculus]	0.62
1084	U67415	Equus caballus UCD- E-CA-467 dinucleotide repeat region, complete sequence	1e-05	<NONE>	<NONE>	<NONE>
1085	X67277	H.sapiens BGP gene for biliary glycoprotein, promoter region and exon 1	1e-05	<NONE>	<NONE>	<NONE>
1086	X85117	H.sapiens epb72 gene exons 2,3,4,5,6,7	1e-05	<NONE>	<NONE>	<NONE>
1087	U88328	Mus musculus suppressor of cytokine signalling-3	1e-05	443877	(Z29457) core region; pid:g443877 [Hepatitis C virus] virus]	3.9
1088	Y12853	Homo sapiens P2X7 gene, exon 4-8	1e-05	3878726	(Z66498) similar to cuticle collagen; cDNA EST EMBL:D75584 comes from this gene	0.36
1089	AE001140	Borrelia burgdorferi (section 26 of 70) of the complete genome	1e-05	3860719	(AJ235270) GLUTAMYL- tRNA AMIDOTRANSFERASE SUBUNIT A (gatA) [Rickettsia prowazekii]	4e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1090	AJ224112	Homo sapiens gamma adaptin gene, exon 2 and flanking intronic sequences	9e-06	<NONE>	<NONE>	<NONE>
1091	AB000565	Homo sapiens DNA for repeat sequence Alu	9e-06	72879	translation initiation factor IF-2 - Escherichia coli	5.1
1092	Z78985	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20B4	9e-06	159975	(M65164) 51C surface protein [Paramecium tetraurelia]	4.8
1093	Z21677	Thermotoga maritima DNA for spc operon	9e-06	585879	50S RIBOSOMAL PROTEIN L2 maritima >gi 437926 (Z21677) ribosomal protein L2	7e-14
1094	AF031494	Drosophila hydei Dhc7 (Threads) mRNA, complete cds	9e-06	729377	DYNEIN BETA CHAIN, CILIARY sea urchin (Anthocidaris crassispina) chain [Anthocidaris crassispina]	4e-18
1095	AF051315	Homo sapiens placental protein 17a1 (PP17) mRNA, complete cds	4e-06	<NONE>	<NONE>	<NONE>
1096	AC001460	Homo sapiens (subclone 2_f4 from BAC H107) DNA sequence	4e-06	2648304	(AE000952) ISA1214-6, putative transposase	6.2
1097	X85030	H.sapiens mRNA for skeletal muscle-specific calpain	4e-06	4239857	(AB016726) calpain [Schistosoma japonicum]	0.006
1098	M75162	Human polymorphic arylamine N-acetyltransferase	3e-06	<NONE>	<NONE>	<NONE>
1099	AB009999	Rattus norvegicus mRNA for CDP-diacylglycerol synthase, complete cds	3e-06	3879045	(Z70309) R102.6 [Caenorhabditis elegans]	7.3
1100	Z78985	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20B4	3e-06	266529	MERCURIC REDUCTASE (HG(II) REDUCTASE) >gi 418744 pir S30168 mercury(II) reductase	6.5
1101	AB012190	Homo sapiens mRNA for Nedd8-activating enzyme hUba3, complete cds	3e-06	3877938	(Z79697) F58H10.1 [Caenorhabditis elegans]	6.3

425

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1102	AF041056	WSCR4 gene, exons 3 and 4	3e-06	1568583	(Z80775) hypothetical protein Rv0044c	1.9
1103	X00777	Mouse E(d) beta gene 5' flanking region and exon 1	3e-06	1680722	(U72497) fatty acid amide hydrolase [Rattus norvegicus]	0.008
1104	D21205	Human mRNA for estrogen responsive finger protein, complete cds	3e-06	563127	(U09825) acid finger protein [Homo sapiens]	1e-05
1105	Z47046	Human cosmid QLL2C9 from Xq28	1e-06	<NONE>	<NONE>	<NONE>
1106	L26261	Human MHC class III HLA-RP1 gene.	1e-06	<NONE>	<NONE>	<NONE>
1107	M13402	Rat 5S RNA gene, clone 5S-2.	1e-06	<NONE>	<NONE>	<NONE>
1108	X68793	H.sapiens gene for antithrombin III	1e-06	<NONE>	<NONE>	<NONE>
1109	AF003540	Homo sapiens Krueppel family zinc finger protein	1e-06	2507553	ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (KIAA0065) (HA0946) Kruppel-related. [Homo sapiens]	0.098
1110	L42096	Homo sapiens (subclone 10_d2 from P1 H21) DNA sequence.	1e-06	1330401	(U58762) T27F7.1 gene product [Caenorhabditis elegans]	0.015
1111	Z69925	Human DNA sequence from cosmid cN116A5, between markers D22S280 and D22S86 on chromosome 22q12 contains EST	9e-07	<NONE>	<NONE>	<NONE>
1112	D90217	S. cerevisiae gene for YmL33, mitochondrial ribosomal proteins of large subunit	9e-07	3879097	(Z81109) predicted using Genefinder; similar to sodium/phosphate transporter; cDNA EST yk326f6.3 comes from this gene; cDNA EST yk326f6.5 comes from this gene [Caenorhabditis elegans]	7.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1113	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-07	1330345	(U58755) coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	2e-29
1114	AF086562	Homo sapiens full length insert cDNA clone ZE16C03	4e-07	1072210	(U40945) coded for by C. elegans cDNA yk74b9.3; coded for by C. elegans cDNA yk74b9.5; similar to repeat of calcium channel alpha subunits; similar to tetracycline resistance protein; similar to hypothetical protein in HSP30-PMP1 region (SP...	3.9
1115	L39062	Homo sapiens interleukin 9 receptor IL9R pseudogene, exons 1-9	4e-07	3879983	(Z46795) similar to transforming protein etc2; cDNA EST EMBL:D34137 comes from this gene; cDNA EST EMBL:D37172 comes from this gene; cDNA EST EMBL:D76266 comes from this gene; cDNA EST EMBL:D70493 comes from this gene; cDNA ...	3.3
1116	Z69364	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA. > :: emb Z69365 HSL96F8A Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA.	4e-07	3493176	(AF022889) latent TGF beta binding protein [Mus musculus]	3.0

431

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for KIAA0164 gene, complete cds	4e-07	4038031	(AC005936) hypothetical protein [Arabidopsis thaliana]	0.30
1117	D79986	Human mRNA for KIAA0098 gene, partial cds	3e-07	<NONE>	<NONE>	<NONE>
1118	D43950	Arabidopsis thaliana DnaJ homologue (AtJ6) mRNA, complete cds	3e-07	3881075	(AL032657) predicted using Genefinder; similar to DnaJ domain ; Thioredoxin; cDNA EST yk433f3.5 comes from this gene; cDNA EST EMBL:D32359 comes from this gene; cDNA EST EMBL:D34721 comes from this gene; cDNA EST yk433f3.3 c...	3e-09
1119	AF037168	H.sapiens mRNA for G9a	3e-07	3873414	(U00043) similar to D. melanogaster trithorax protein	3e-29
1120	X69838	Homo sapiens mRNA for KIAA0552 protein, complete cds	2e-07	2618749	(U90880) hypothetical protein 2; predicted using XGrail	2.0
1121	AB011124	Human cellular fms proto-oncogene, partial cds.	1e-07	<NONE>	<NONE>	<NONE>
1122	K03012	Homo sapiens DNA, microsatellite and Alu repeat region	1e-07	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.095
1123	AB016195	Homo sapiens psihHaA pseudogene	4e-08	<NONE>	<NONE>	<NONE>
1124	Y16795	Homo sapiens FLII gene for ERGB transcription factor, intron 4 and partial cds	4e-08	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	3.6
1125	AB012624	Homo sapiens ogg1 gene, exons 1-7	4e-08	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	3e-05
1126	AJ131341	Homo sapiens (subclone 1_c10 from P1 H69) DNA sequence	3e-08	4225950	(AJ132701) centaurin gamma1B (AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g282920S) [Homo sapiens]	1.8
1127	L81902	Gallus gallus mRNA for high mobility group 1 protein	3e-08	3041855		3e-31
1128	Y17968	Homo sapiens FGFR-4 gene	1e-08	<NONE>	<NONE>	<NONE>
1129	Y13901					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1130	L22024	Mesocricetus auratus serum amyloid P component gene, complete cds.	1e-08	<NONE>	<NONE>	<NONE>
1131	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	1e-08	<NONE>	<NONE>	<NONE>
1132	X14034	Human mRNA for phospholipase C > :: gb M37238 HUMPL C Human phospholipase C mRNA, complete cds.	1e-08	<NONE>	<NONE>	<NONE>
1133	Z59381	H.sapiens CpG DNA, clone 152b10, forward read cpg152b10.ft1a .	1e-08	<NONE>	<NONE>	<NONE>
1134	L81839	Homo sapiens (subclone 2_h3 from P1 H43) DNA sequence	1e-08	<NONE>	<NONE>	<NONE>
1135	X14448	Human GLA gene for alpha-D-galactosidase A (EC 3.2.1.22)	1e-08	3334427	HYPOTHETICAL PROTEIN MJ1207 Methanococcus jannaschii >gi 1591837 (U67562) protease synthase and sporulation negative regulator Pai1, putative [Methanococcus jannaschii]	9.1
1136	AL023774	Human DNA sequence from clone 799F15 on chromosome Xq25, complete sequence [Homo sapiens]	1e-08	1354935	(U58330) probable copper-transporting atpase	1.2
1137	X64639	H.sapiens DNA repetitive subtelomeric-like sequence (522 bp)	1e-08	77356	hypothetical 70K protein - eggplant mosaic virus	0.098
1138	U97058	Human HuD gene, 5'UTR	5e-09	3387886	(AF070530) unknown [Homo sapiens]	9.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1139	Z82181	sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	5e-09	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	8.4
1140	AJ006587	Mus musculus mRNA for translation initiation factor eIF2 gamma X	5e-09	1872200	(U22376) alternatively spliced product using exon 13A	0.64
1141	Y11108	H.sapiens WNT8B gene	4e-09	2854198	(AF045646) contains similarity to collagens	4.0
1142	AE001223	Treponema pallidum section 39 of 87 of the complete genome	4e-09	3334189	CELL DIVISION PROTEIN FTSY HOMOLOG	1.5
1143	Z47046	Human cosmid QLL2C9 from Xq28	4e-09	104045	fibroblast growth factor receptor A1 precursor - African clawed frog >gi 214894 (M55163) fibroblast growth factor receptor [Xenopus laevis]	1.3
1144	AG000746	Homo sapiens genomic DNA, 21q region, clone: T171Bm40	4e-09	113666	!!!! ALU CLASS A WARNING ENTRY !!!!	0.33
1145	M74002	Human arginine-rich nuclear protein mRNA, complete cds.	4e-09	3875371	(Z50748) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes f... >gi 3878699 gnl PID e1351700 possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes f...	3e-06
1146	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2e-09	2494337	ENDO-1,4-BETA-XYLANASE PRECURSOR sp.]	4.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1147	U20554	Drosophila melanogaster UDP-glucose:glycoprotein glucosyltransferase mRNA, complete cds.	2e-09	2499087	UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT) glucosyltransferase - fruit fly (Drosophila sp.) glucosyltransferase precursor [Drosophila melanogaster]	4e-24
1148	Z56162	H.sapiens CpG DNA, clone 91c9, forward read cpg91c9.ft1a .	1e-09	<NONE>	<NONE>	<NONE>
1149	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-09	1002424	(U25739) YSPL-1 form 1 [Mus musculus]	8.9
1150	M85276	Homo sapiens NKG5 gene, complete cds.	1e-09	2315436	(AF016447) No definition line found [Caenorhabditis elegans]	8.3
1151	M94065	Human dihydroorotate dehydrogenase mRNA, 3' end.	1e-09	3892656	(AB014464) MGC-24v [Mus musculus]	6.2
1152	AJ131895	Homo sapiens genomic CAG repeat element, clone 60o2(250)	5e-10	<NONE>	<NONE>	<NONE>
1153	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	5e-10	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7.9
1154	AJ224442	Homo sapiens mRNA for putative methyltransferase	5e-10	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.15
1155	AJ010230	Homo sapiens RET finger protein-like 1 antisense transcript, partial	5e-10	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	0.006
1156	AF111116	Homo sapiens silencer of death domains (SODD) mRNA, complete cds	5e-10	4160014	(AF111116) silencer of death domains [Homo sapiens]	2e-08
1157	Z97017	Homo sapiens mRNA for hypothetical protein	4e-10	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens type II integral membrane protein				
1158	AF001298		4e-10	<NONE>	<NONE>	<NONE>
1159	Y11395	H.sapiens mRNA for p40	2e-10	1000340	(U34384) CheW [Borrelia burgdorferi]	2.4
1160	U41096	Human non-coding sequence upstream from DOC-2 gene on chromosome 5	2e-10	728837	!!! ALU SUBFAMILY SQ WARNING ENTRY	0.28
1161	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	6e-11	<NONE>	<NONE>	<NONE>
1162	Z36111	S.cerevisiae chromosome II reading frame ORF YBR242w	6e-11	2213560	(Z97052) hypothetical protein (Z80220) Similarity to yeast protein TREMBL ID E246895); cDNA EST EMBL:T00018 comes from this gene; cDNA EST EMBL:C13908 comes from this gene; cDNA EST EMBL:C11656 comes from this gene; cDNA EST yk234a5.3 comes from this ge...	3e-27
1163	D89174	Schizosaccharomyces pombe mRNA, partial cds, clone: SY 1004	6e-11	3879758		4e-30
1164	Z95437	Human DNA sequence from cosmid A1 on chromosome 6 contains ESTs. HERV like retroviral sequence	5e-11	<NONE>	<NONE>	<NONE>
1165	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	5e-11	3886065	(AF106581) contains similarity to C4-type zinc fingers	4.9
1166	X56997	Human Uba52 gene coding for ubiquitin-52 amino acid fusion protein	2e-11	<NONE>	<NONE>	<NONE>
1167	AF086253	Homo sapiens full length insert cDNA clone ZD40G12	2e-11	2134780	apoptosis inhibitor IAP homolog - human	3.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1168	AB018314	Homo sapiens mRNA for KIAA0771 protein, partial cds	2e-11	3024343	P53-BINDING PROTEIN 53BP2 Bbp/53BP2 [Homo sapiens]	2e-11
1169	Z74972	S.cerevisiae chromosome XV reading frame ORF YOR064c	2e-11	3041855	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	2e-40
1170	Z82181	Human DNA sequence from cosmid E86D10 on chromosome 22. contains ESTs, exontrap, complete sequence	7e-12	<NONE>	<NONE>	<NONE>
1171	X77738	H.sapiens red cell anion exchanger (EPB3, AE1, Band 3) gene, 3' region	7e-12	2135416	hypothetical protein - human >gi288145	0.012
1172	S61977	medium-chain acyl-CoA dehydrogenase {exon 10, intron 10} [human, Genomic, 1407 nt]	6e-12	113666	!!!! ALU CLASS A WARNING ENTRY !!!!	0.100
1173	X66285	M.musculus DNA for HC1 locus	6e-12	854065	(X83413) U88 [Human herpesvirus 6]	2e-06
1174	S78744	protein S=activated protein C cofactor [rats, liver, mRNA, 3315 nt]	6e-12	2338292	(AF009243) proline-rich Gla protein 2 [Homo sapiens]	3e-10
1175	X58474	Bovine OXT gene for oxytocin, 5' noncoding region	2e-12	1296429	(L77967) small proline-rich protein with paired repeat	4.1
1176	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.rt1a .	2e-12	2935221	(AF030154) pVII [bovine adenovirus type 3]	2.8
1177	Z56314	H.sapiens CpG DNA, clone 10h10, reverse read cpg10h10.rt1a .	2e-12	2708659	(AF037440) putative 26 kDa protein [Edwardsiella ictaluri]	2.8
1178	Z19543	M.musculus h2-calponin cDNA	2e-12	2497945	BETA SCRUIIN >gi1015535 (Z47541) beta scruiin [Limulus polyphemus]	2e-04

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		erythropoietin				
1179	S45332	receptor [human, placental, Genomic, 8647 nt]	7e-13	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	0.074
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-13	<NONE>	<NONE>	<NONE>
1181	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-13	<NONE>	<NONE>	<NONE>
1182	Z59509	H.sapiens CpG DNA, clone 15a1, reverse read cpg15a1.r1a .	2e-13	3150251	(AL023634) hypothetical protein	0.66
1183	D10170	Human CYP11B2 gene for steroid 18-hydroxylase	2e-13	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	3e-05
1184	U65416	Human MHC class I molecule (MICB) gene, complete cds	2e-13	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6e-11
1185	AJ006031	Mus musculus IHABP gene, promoter	8e-14	2132223	hypothetical protein YPL186c - yeast	1.1
1186	U34976	Human gamma-sarcoglycan mRNA, complete cds	8e-14	1054903	(U34976) gamma-sarcoglycan [Homo sapiens] >gi 4239660 sapiens]	0.034
1187	D30647	Rat mRNA for very-long-chain Acyl-CoA dehydrogenase, complete cds	8e-14	3183512	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (VLCAD) >gi 2388724 (AF017176) very-long-chain acyl-CoA dehydrogenase [Mus musculus]	8e-23
1188	Z63247	H.sapiens CpG DNA, clone 7g4, forward read cpg7g4.f1a .	6e-14	86285	histone H1.01 - chicken	6.8
1189	U27196	Gallus gallus zinc finger protein (Fzf-1) mRNA, complete cds.	3e-14	2134436	zinc finger protein - chicken (fragment)	4e-10
1190	M26219	African green monkey origin of replication	2e-14	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1191	AF100694	Pontin52 mRNA, complete cds	2e-14	4235641	(AF119040) NL0D [Lycopersicon esculentum]	0.65
1192	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-14	3043728	(AB011174) KIAA0602 protein [Homo sapiens]	0.28
1193	AJ005866	Homo sapiens mRNA for putative Sqv-7-like protein, partial	2e-14	4008517	(AJ005866) Sqv-7-like protein [Homo sapiens]	0.004
1194	U32709	Haemophilus influenzae Rd section 24 of 163 of the complete genome	2e-14	3861056	(AJ235272) POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (pnp) [Rickettsia prowazekii]	6e-28
1195	AF073485	Homo sapiens MHC class I-related protein MR1 precursor (MR1) gene, partial cds	8e-15	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1.0
1196	AF052135	Homo sapiens clone 23625 mRNA sequence	8e-15	4098124	(U73522) AMSH [Homo sapiens]	8e-14
1197	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<NONE>	<NONE>	<NONE>
1198	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	1.7
1199	Z75104	S.cerevisiae chromosome XV reading frame ORF YOR196c	3e-15	3878570	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3...	1e-15

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1200	X70052	S.cerevisiae sof1 gene	3e-15	1125754	(U42833) coded for by C. elegans cDNA cm16f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]	3e-29
1201	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-15	<NONE>	<NONE>	<NONE>
1202	M92295	Gorilla gorilla gamma 1 and gamma-2 globin genes, complete cds.	1e-15	284078	hypothetical protein 2 - human >gi182220	7.4
1203	L34587	Homo sapiens RNA polymerase II elongation factor SIII, p15 subunit mRNA, complete cds. >:: gb AR022286 AR022286 Sequence 7 from patent US 5792634	9e-16	<NONE>	<NONE>	<NONE>
1204	D83649	Xenopus laevis mRNA for xSox7 protein, complete cds	8e-16	2447043	(D83649) xSox7 protein [Xenopus laevis]	4e-06
1205	AC005190	Homo sapiens PAC clone DJ1152D16 from Xq23; complete sequence [Homo sapiens]	3e-16	<NONE>	<NONE>	<NONE>
1206	J03626	Human UMP synthase mRNA, complete cds.	3e-16	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.65
1207	J00083	Human Alu family interspersed repeat; clone BLUR11.	3e-16	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	4e-06
1208	U70674	Mus musculus m-Numb (m-nb) mRNA, complete cds	1e-16	<NONE>	<NONE>	<NONE>

440

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1209	U66619	Human SWI/SNF complex 60 KDa subunit (BAF60c) mRNA, complete cds	1e-16	1549247	(U66619) SWI/SNF complex 60 KDa subunit [Homo sapiens]	0.003
1210	U75467	Drosophila melanogaster Rga and Atu genes, complete cds	1e-16	1658503	(U75467) Atu [Drosophila melanogaster]	5e-32
1211	M72709	Human alternative splicing factor mRNA, complete cds.	3e-17	<NONE>	<NONE>	<NONE>
1212	U26556	Human ferritin H (FTHL13) pseudogene.	3e-17	<NONE>	<NONE>	<NONE>
1213	D32064	Human gene for 2-oxoglutarate dehydrogenase, complete cds	3e-17	2088843	(AF003386) F59E12.9 gene product [Caenorhabditis elegans]	0.12
1214	M76364	Human (Papua New Guinean) Mitochondrial DNA control region, sequence 131.	3e-17	114009	APAG PROTEIN >gi 72927 pir BVECAG apaG protein - Escherichia coli >gi 40918 (X04711) URF hypothetical protein [Escherichia coli]	0.006
1215	AF017466	Homo sapiens genomic sequence from subtelomeric region of chromosome 4q	1e-17	3947985	(U78948) MADS-box protein 2 [Malus domestica]	4.1
1216	AF004876	Homo sapiens 54TMp (54tm) mRNA, complete cds	1e-17	4101574	(AF004876) 54TMp [Homo sapiens]	0.006
1217	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-18	<NONE>	<NONE>	<NONE>
1218	AF086758	Rattus norvegicus Na-K-2Cl cotransporter	4e-18	3892703	(AL033545) putative glycine-rich protein [Arabidopsis thaliana]	0.30
1219	AF020089	Homo sapiens PEN11B mRNA, complete cds	4e-18	2642493	(AF023910) DNA topoisomerase I [Physarum polycephalum]	0.083
1220	X82333	H.sapiens IRLB gene (exon1-3)	4e-18	106837	irlB protein - human (fragment) >gi 33969	2e-11

1441

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for KIAA0385 gene, complete cds	4e-18	3228540	(AF060181) zinc finger protein [Homo sapiens]	6e-25
1221	AB002383					
1222	X98485	P.vivax PV14 gene	1e-18	<NONE>	<NONE>	<NONE>
1223	Z79057	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA21E8	1e-18	2981631	(AB012223) ORF2 [Canis familiaris]	0.001
1224	L01457	Homo sapiens (clone JH4B1) PM-scl autoantigen mRNA, complete cds.	1e-18	346287	nucleolar 100K polymyositis-scleroderma protein - human >gi 35555 (X66113) PM/Sc1 100kD nucleolar protein [Homo sapiens]	0.001
1225	L02897	Dog nonerythroid beta-spectrin mRNA, 3' end.	4e-19	3493358	(AB017037) nonstructural protein precursor [Himetobi P virus]	0.12
1226	AB012162	Homo sapiens mRNA for APCL protein, complete cds	4e-19	3894265	(AB012162) APCL protein [Homo sapiens]	0.002
1227	AB011093	Homo sapiens mRNA for KIAA0521 protein, partial cds	4e-19	3043566	(AB011093) KIAA0521 protein [Homo sapiens]	9e-09
1228	X78454	X.laevis AB21 mRNA for RPD3 homologue	4e-19	3023945	HISTONE DEACETYLASE (HD) thaliana]	5e-34
1229	U88895	Human endogenous retrovirus H D1 leader region/integrase-derived ORF1, ORF2, and putative envelope protein mRNA, complete cds	2e-19	59977	(Z14310) tripartite fusion transcript PLA2L [Human endogenous retrovirus]	1e-04
1230	U34377	Human tyrosine kinase TXK (txk) gene, exon 13.	1e-19	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-05
1231	X72966	M.musculus rab3A gene	1e-19	2408076	(Z99167) putative peroxisomal organisation and biogenesis protein [Schizosaccharomyces pombe]	2e-09
1232	AB007953	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484	4e-20	<NONE>	<NONE>	<NONE>

442

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					(AB001535) similar to	
1233	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	2e-20	3928756	C.elegans hypothetical protein CET01H8.1,CEC05C12.3,CEF54D1.5. similar to trp and trp-like proteins [Homo sapiens]	1e-07
1234	X82126	H.sapiens HOK-2 gene, exon 2	2e-20	2137269	DNA-binding protein - mouse >gi 437444	1e-19
1235	AF093684	Luciferase reporter vector pXP2 *SA, complete sequence	5e-21	2773363	(AF041382) microtubule binding protein D-CLIP-190	5.5
1236	J05272	Human IMP dehydrogenase type 1 mRNA complete cds.	5e-21	124417	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (IMP DEHYDROGENASE 1) (IMPDH-1) (IMPD 1) I - human	2e-04
1237	D86997	Human (lambda) DNA for immunoglobulin light chain	5e-21	3878261	(Z75712) Similarity to S. Pombe BEM1/BUD5 suppressor; cDNA EST EMBL:Z14470 comes from this gene; cDNA EST yk482d4.3 comes from this gene; cDNA EST yk482d4.5 comes from this gene [Caenorhabditis elegans]	6e-46
1238	Z79865	H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 302f3, forward read 302f3.f	2e-21	2739037	(AF024614) ADAM 10 [Caenorhabditis elegans] Zinc-binding metalloprotease domain; cDNA EST CEMSA42F comes from this gene; cDNA EST yk218f3.3 comes from this gene; cDNA EST yk443d9.3 comes from this gene; cDNA EST yk443d9.5 comes from this gene; cDNA...	2.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1239	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-22	3924779	(AF100694) similar to human B; cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi 3924881 gnl PID e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	0.35
1240	U67824	Human primary Alu transcript	6e-22	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	5e-07
1241	AF070636	Homo sapiens clone 24686 mRNA sequence	2e-22	98710	fatty-acid synthase (EC 2.3.1.85) - Brevibacterium ammoniagenes	2.5
1242	D14034	Human gene for Zn-alpha2-glycoprotein, complete cds	2e-22	4185939	(Y17832) pol protein [Human endogenous retrovirus K]	0.29
1243	M61835	Human lactase phlorizin hydrolase (LCT) gene, exon 2.	2e-22	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.006
1244	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-23	1350828	RABPHILIN-3A >gi 477100 pir A48097 rabphilin-3A - bovine >gi 285646 gnl PID d1003285	0.14
1245	AF074985	Homo sapiens full length insert cDNA YH73H06	8e-24	3170548	(AF056116) unknown [Fugu rubripes]	0.24
1246	D14878	Human mRNA for protein D123, complete cds	7e-24	<NONE>	<NONE>	<NONE>
1247	D16917	Human HepG2 3' region cDNA, clone hmd3d07	6e-24	1397345	(U61955) contains multiple region of strong similarity to C2H2-type zinc fingers (PS:PS00028) [Caenorhabditis elegans]	2.4

444

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1248	Z69654	sequence from cosmid L98A6. Huntington's Disease Region, chromosome 4p16.3.	3e-24	4240566	(AF123462) neurexin III [Homo sapiens]	4.5
1249	AB007914	Homo sapiens mRNA for KIAA0445 protein. complete cds	2e-24	3885949	(AF095568) amelogenin [Paleosuchus palpebrosus]	3.2
1250	AF088072	Homo sapiens full length insert cDNA clone ZD93D10	2e-24	323091	immunodominant microneme protein Etp100 - Eimeria tenella >gi 2707733 (AF032905) microneme protein precursor Etmic-1 [Eimeria tenella]	0.34
1251	AF069489	Homo sapiens cAMP specific phosphodiesterase 4A variant pde46 (PDE4A) gene, exons 2 through 13 and alternative splice exons 3a, 6a, 6b, and 9a	2e-24	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	1e-05
1252	Y12853	Homo sapiens P2X7 gene, exon 4-8	9e-25	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-05
1253	M27830	Human 28S ribosomal RNA gene, complete cds.	8e-25	<NONE>	<NONE>	<NONE>
1254	AB007953	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484	8e-25	<NONE>	<NONE>	<NONE>
1255	Z60212	H.sapiens CpG DNA, clone 195c8, forward read cpg195c8.ft1a .	8e-25	158154	(M81959) POU domain protein [Drosophila melanogaster]	3.3
1256	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-25	<NONE>	<NONE>	<NONE>
1257	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-25	<NONE>	<NONE>	<NONE>
1258	Y12851	Homo sapiens P2X7 gene, exon 1 and joined CDS	2e-25	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus Tera				
1259	U64033	(Tera) mRNA, complete cds	9e-26	<NONE>	<NONE>	<NONE>
1260	U19181	Rattus norvegicus Rabin3 mRNA, complete cds.	9e-26	624225	(U19181) Rabin3 [Rattus norvegicus]	1e-13
1261	AF020788	Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds	9e-26	3915881	SEL-10 PROTEIN Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cDNA EST EMBL:D27698 comes from this gene; cDNA EST EMBL:D32793 comes from this gene; cDNA EST EMBL:D33271 comes from this gen...	7e-32
1262	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	8e-26	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	0.045
1263	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-26	3878629	(Z93385) predicted using Genefinder; Similarity to B.subtilis GTP-binding protein	2e-10
1264	X91195	H.sapiens SOM172 mRNA	1e-26	<NONE>	<NONE>	<NONE>
1265	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-26	1360637	(X95995) ENBP1 [Vicia sativa]	3.1
1266	L08237	Human MG21 mRNA, partial cds.	1e-26	950411	(L08237) located at OATL1 [Homo sapiens]	9e-09
1267	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-27	3881080	(AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8....	0.001
1268	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-27	1731324	HYPOTHETICAL PROTEIN >gi 166306	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1269	X89211	H.sapiens DNA for endogenous retroviral like element	8e-27	2065209	(Y12713) Gag polyprotein [Mus musculus]	0.005
1270	U73166	Homo sapiens cosmid clone LUCA15 from 3p21.3, complete sequence [Homo sapiens]	3e-27	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	4e-04
1271	D78255	Mouse mRNA for PAP-1, complete cds	3e-27	1850098	(D78255) PAP-1 [Mus musculus]	2e-10
1272	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.39
1273	AB015202	Homo sapiens gene for hippocalcin, exon 2, 3 and complete cds	1e-27	3877698	(Z83318) predicted using Genefinder; cDNA EST yk369e7.5 comes from this gene [Caenorhabditis elegans]	0.37
1274	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3328188	(AF074902) laminin alpha chain [Caenorhabditis elegans]	0.19
1275	Z29336	H.sapiens gene for Cu/Zn-superoxide dismutase	1e-27	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	6e-05
1276	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	9.2
1277	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.054
1278	AB001636	Homo sapiens mRNA for ATP-dependent RNA helicase #46, complete cds	4e-28	3913425	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]	3e-22
1279	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.066

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1280	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-05
1281	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1282	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1283	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1284	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1285	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1286	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1287	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	140505	PROBABLE INTRON MATURASE liverwort (Marchantia polymorpha) chloroplast >gi 11663	3.0
1288	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	140505	PROBABLE INTRON MATURASE liverwort (Marchantia polymorpha) chloroplast >gi 11663	1.8
1289	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.50
1290	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.087
1291	Z63029	H.sapiens CpG DNA, clone 77b3, forward read cpg77b3.ft1a .	1e-28	2493240	HYPOTHETICAL 29.3 KD PROTEIN pseudotsugata nuclear polyhedrosis virus]	0.014

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1292	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.010
1293	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.007
1294	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1295	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	126363	LAMININ ALPHA-1 CHAIN PRECURSOR precursor - human	3e-04
1296	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-04
1297	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-05
1298	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	2e-05
1299	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05

449

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1300	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	320919	kinetoplast-associated protein - Trypanosoma cruzi >gi 162142 (M25364) kinetoplast-associated protein	1e-07
1301	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-08
1302	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-09
1303	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-10
1304	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-10
1305	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-11
1306	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1307	AF100694	Pontin52 mRNA, complete cds	4e-29	<NONE>	<NONE>	<NONE>
1308	AF079529	Homo sapiens cAMP-specific phosphodiesterase 8B	4e-29	<NONE>	<NONE>	<NONE>
1309	X93334	H.sapiens mitochondrial DNA, complete genome	4e-29	116977	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - human mitochondrion (SGC1) >gi 13006 (V00662) cytochrome oxidase I [Homo sapiens] >gi 506829 (J01415) cytochrome oxidase subunit 1 [Homo sapiens] sapiens]	3e-09
1310	AF020760	Homo sapiens serine protease (Omi) mRNA, complete cds	4e-29	2738915	(AF020760) serine protease [Homo sapiens]	8e-12
1311	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	4e-29	2072294	(U95097) mitotic phosphoprotein 43 [Xenopus laevis]	1e-25
1312	L32162	Homo sapiens transcription factor mRNA, 5' end.	2e-29	2501706	RENAL TRANSCRIPTION FACTOR KID-1 finger protein [Mus musculus]	8e-15
1313	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-29	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-04
1314	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-29	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	1e-05
1315	U50839	Homo sapiens g16 protein (g16) mRNA, complete cds	1e-29	3212101	(AF069517) RNA binding protein DEF-3 [Homo sapiens]	6e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					intercellular adhesion molecule	
1316	X69711	H. sapiens mRNA for ICAM-R	5e-30	299356	3, ICAM-3=lymphocyte function-associated antigen 1 counter-receptor homolog [human, tonsil, Peptide Partial, 518 aa]	3e-08
1317	AF010227	Homo sapiens receptor-associated coactivator 3	5e-30	2331250	(AF012108) Amplified in Breast Cancer [Homo sapiens]	8e-09
1318	AF086395	Homo sapiens full length insert cDNA clone ZD75C01	2e-30	3861241	(AJ235273) CELL SURFACE ANTIGEN (sca5)	4.2
1319	M27830	Human 28S ribosomal RNA gene, complete cds.	2e-30	1730522	PHOSPHOGLYCERATE KINASE 2.7.2.3) - Pyrococcus woesei >gi 1054832 (X73527) phosphoglycerate kinase [Pyrococcus woesei]	3.8
1320	M79307	Mouse GTP-binding protein (Rab17) mRNA sequence.	2e-30	464564	RAS-RELATED PROTEIN RAB-17 Rab17 - mouse (fragment) >gi 297157 (X70804) rab17 [Mus musculus]	9e-11
1321	AL022168	Human DNA sequence from clone U247E12 on chromosome Xq22-23, complete sequence [Homo sapiens]	1e-30	2072967	(U93570) putative p150 [Homo sapiens]	3e-11
1322	X85124	M.musculus paccin gene	1e-30	2217964	(Z50798) p52 [Gallus gallus]	1e-34
1323	U37408	Homo sapiens phosphoprotein CtBP mRNA, complete cds	5e-31	74518	structural polyprotein - Venezuelan equine encephalitis virus (strain TRD) >gi 323710 (J04332) poly-envelope protein [Venezuelan equine encephalitis virus]	1.1
1324	L04193	Human lens membrane protein (mp19) gene, exon 11.	2e-31	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7e-07
1325	M11167	Human 28S ribosomal RNA gene.	6e-32	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1326	M33336	Human cAMP-dependent protein kinase type I-alpha subunit (PRKAR1A) mRNA, complete cds	2e-32	<NONE>	<NONE>	<NONE>
1327	J03060	Human glucocerebrosidase pseudogene, complete cds	2e-32	2144479	glucosylceramidase (EC 3.2.1.45) precursor - human	1e-05
1328	U33053	Human lipid-activated protein kinase PRK1 mRNA, complete cds	7e-33	2137689	protein kinase (EC 2.7.1.37) - mouse	1e-14
1329	J04617	Human elongation factor EF-1-alpha gene, complete cds. > :: dbj E02629 E02629 DNA of human polypeptide chain elongation factor-1 alpha	6e-33	<NONE>	<NONE>	<NONE>
1330	L40396	Homo sapiens (clone s22i71) mRNA fragment	6e-33	124235	INTERMEDIATE FILAMENT PROTEIN B protein B - common roundworm	1.00
1331	Z72813	S.cerevisiae chromosome VII reading frame ORF YGR028w	6e-33	1709135	MSP1 PROTEIN HOMOLOG Yeast MSP1 protein (TAT-binding homolog 4)	8e-50
1332	AB007941	Homo sapiens mRNA for KIAA0472 protein, partial cds	2e-33	1150834	(U42471) Wiscott-Aldrich Syndrome protein homolog [Mus musculus]	2.0
1333	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	2e-34	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	6e-15
1334	D14657	Human mRNA for KIAA0101 gene, complete cds	7e-35	<NONE>	<NONE>	<NONE>
1335	X69910	H.sapiens p63 mRNA for transmembrane protein	7e-35	2136323	trithorax homolog HTX - human (fragment) homolog=MLL {alternative splicing, clone 14p-18B}	0.94

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1336	AF053455	Homo sapiens tetraspan TM4SF (TSPAN-5) gene, complete cds	7e-35	3152703	(AF065389) tetraspan NET-4 [Homo sapiens]	1e-25
1337	X58374	D.melanogaster crn mRNA	3e-35	117478	CROOKED NECK PROTEIN	6e-41
1338	AF086492	Homo sapiens full length insert cDNA clone ZD95D11	9e-36	2909809	(AF031328) aminoglycoside 6'-N-acetyltransferase It	1.9
1339	Z96223	H.sapiens telomeric DNA sequence, clone 12PTEL120, read 12PTELOO120.seq	3e-36	2408068	(Z99165) hypothetical protein	0.61
1340	Z37986	H.sapiens mRNA for phenylalkylamine binding protein.	1e-36	1362793	emopamil-binding protein - human >gi 780263	5e-11
1341	U57847	Human ribosomal protein S27 mRNA, complete cds. end similar to similar to metallopanstimulin 1 > :: gb AA316327 AA316327 EST188061 HCC cell line (matatasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to metallopanstimulin 1	3e-37	1171014	40S RIBOSOMAL PROTEIN S27 growth factor-inducible zinc finger protein MPS-1 - human >gi 431319 (L19739) metallopanstimulin [Homo sapiens] >gi 1373421 (U57847) ribosomal protein S27	1.4
1342	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial	3e-37	3123027	70 KD WD-REPEAT TUMOR-SPECIFIC ANTIGEN >gi 2505957 gnl PID e353992 (Y15054) 70 kD tumor-specific antigen [Rattus norvegicus]	2e-15
1343	AF084205	Rattus norvegicus serine/threonine protein kinase TAO1 mRNA, complete cds	3e-37	3452473	(AF084205) serine/threonine protein kinase TAO1 [Rattus norvegicus]	5e-47
1344	X78604	R.norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5	1e-37	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1345	AJ236644	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49A3, complete read	1e-37	2239219	(Z97210) hypothetical protein	6e-05
1346	U09367	Human zinc finger protein ZNF136	4e-39	2137269	DNA-binding protein - mouse >gi 437444	7e-23
1347	Z69649	Human DNA sequence from cosmid L69F7B, Huntington's Disease Region, chromosome 4p16.3 contains Huntington Disease (HD) gene.	3e-39	3096918	(AL023094) putative cyclase associated protein CAP [Arabidopsis thaliana]	5.6
1348	AF065389	Homo sapiens tetraspan NET-4 mRNA, complete cds	1e-39	3152703	(AF065389) tetraspan NET-4 [Homo sapiens]	6e-29
1349	AF038172	Homo sapiens clone 23923 mRNA sequence	1e-40	1813464	(U60883) CapC [Bacillus firmus]	2.8
1350	Z83095	H.sapiens Fanconi anaemia group A gene, exons 39, 40, 41, 42 and 43	1e-40	2137870	zinc finger protein - mouse (fragment)	3e-23
1351	AF057734	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 16	1e-40	2842416	(AL008730) dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1) [Homo sapiens]	6e-61
1352	AF070567	Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds	4e-41	3133087	(Y15718) dystrobrevin B DTN-B2 [Homo sapiens]	7e-13
1353	AF006088	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16) mRNA, complete cds	2e-41	3121767	ARP2/3 COMPLEX 16 KD SUBUNIT	3e-36
1354	X69942	M.musculus mRNA of enhancer-trap-locus 1	6e-42	2291152	(AF016418) No definition line found [Caenorhabditis elegans]	6.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1355	X87838	H.sapiens mRNA for beta-catenin	5e-42	1373019	(U28811) cysteine-rich fibroblast growth factor receptor	8e-05
1356	AB018268	Homo sapiens mRNA for KIAA0725 protein, partial cds	5e-42	3882171	(AB018268) KIAA0725 protein [Homo sapiens]	2e-33
1357	M84424	Human cathepsin E (CTSE) gene, exon 9 and complete cds.	2e-42	<NONE>	<NONE>	<NONE>
1358	U80776	Human EST clone NIB1543 mariner transposon Hsmar1 orf gene, complete cds	2e-42	2231380	(U80776) orf; encodes putative chimeric protein with SET domain in N-terminus with similarity to several other human, Drosophila, nematode and yeast proteins [Homo sapiens]	3e-11
1359	U55184	Human G protein Golf alpha gene, exon 12 and complete cds	2e-42	3165531	(AF067608) No definition line found [Caenorhabditis elegans]	1e-16
1360	AC005190	Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence [Homo sapiens]	6e-43	2978255	(AB007407) myeloid zinc finger protein-2 [Mus musculus]	2.3
1361	AB018284	Homo sapiens mRNA for KIAA0741 protein, complete cds	5e-43	<NONE>	<NONE>	<NONE>
1362	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	5e-43	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	1e-07
1363	M93651	Human set gene, complete cds.	2e-43	<NONE>	<NONE>	<NONE>
1364	Z47087	H.sapiens mRNA for RNA polymerase II elongation factor-like protein.	2e-43	1872514	(U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [Homo sapiens] >gi 2361031 (AF016708) E6-AP ubiquitin-protein ligase [Homo sapiens]	7.2
1365	U27197	Drosophila melanogaster pelota (pelo) mRNA, complete cds	2e-43	1352736	PELOTA PROTEIN >gi 973224 (U27197) pelota [Drosophila melanogaster]	1e-46

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					RRP5 PROTEIN HOMOLOG	
1366	D80007	Human mRNA for KIAA0185 gene, partial cds	6e-44	2498864	(KIAA0185) hypothetical protein YM9959.11C of <i>S.cerevisiae</i> . [Homo sapiens]	6e-09
1367	AF005039	Homo sapiens secretory carrier membrane protein (SCAMP3) mRNA, complete cds	6e-44	2232243	(AF005039) secretory carrier membrane protein [Homo sapiens]	2e-09
1368	X68101	<i>R.norvegicus</i> trg mRNA	2e-44	550420	(X68101) trg gene product [<i>Rattus norvegicus</i>]	1e-37
1369	AF044206	Homo sapiens cyclooxygenase (COX-2) gene, promoter and exon 1	2e-45	2072953	(U93565) putative p150 [Homo sapiens]	5e-06
1370	L48708	Homo sapiens facio-genital dysplasia (FGD1) gene, 5' end of intron 17	8e-46	<NONE>	<NONE>	<NONE>
1371	X15822	Human COX VIIa-L mRNA for liver-specific cytochrome c oxidase (EC 1.9.3.1.)	3e-46	117121	CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECURSOR >gi 2144370 pir OSHU7L cytochrome-c oxidase (EC 1.9.3.1) chain VIIa precursor, hepatic - human >gi 30147 (X15822) precursor (AA -23 to 60) [Homo sapiens]	5e-13
1372	U47323	Mus musculus stromal cell protein mRNA, complete cds	3e-46	1493833	(U47323) stromal cell protein [Mus musculus]	1e-48
1373	AF059524	Homo sapiens reticulon gene family protein	7e-47	1731169	HYPOTHETICAL 113.1 KD PROTEIN T28D9.7 IN CHROMOSOME II >gi 861264 (U28738) coded for by <i>C. elegans</i> cDNA yk8h5.3; coded for by <i>C. elegans</i> cDNA yk8h5.5; similar to <i>C. elegans</i> deg-1 and mec-4 in exon 2 [<i>Caenorhabditis elegans</i>]	7.8
1374	AJ132583	Homo sapiens mRNA for puromycin sensitive aminopeptidase, partial	3e-47	1777519	(U39123) T cell receptor beta chain [Homo sapiens]	9.7

457

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1375	M97856	Homo sapiens histone-binding protein mRNA, complete cds.	3e-47	2645327	(U83821) NADH dehydrogenase subunit 3 [Oryzomys palustris]	5.7
1376	U53220	Human retinoblastoma-related Rb2/p130 gene, 5' flanking region and partial cds	3e-47	2499225	CMP-SIALIC ACID TRANSPORTER CMP-sialic acid transporter [Cricetulus griseus]	5.3
1377	X87870	H.sapiens mRNA for hepatocyte nuclear factor 4a	1e-47	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	7.3
1378	AF060195	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds	3e-48	478681	limb deformity protein - chicken	0.25
1379	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	1e-48	3122969	TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSGA) >gi 281040 pir S28499 probable zinc finger protein - rat >gi 57504 (X59993) zinc finger protein	1e-30
1380	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase region mRNA, partial cds	4e-49	88558	retroviral proteinase-like protein - human	6e-05
1381	AB007956	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487	1e-49	<NONE>	<NONE>	<NONE>
1382	D86987	Homo sapiens mRNA for KIAA0214 protein, complete cds	1e-49	2497944	ALPHA SCRUIIN >gi 633238 (Z38132) scruiin [Limulus polyphemus] >gi 1093326 prf 2103269A scrulin [Limulus sp.]	9.7
1383	U25826	Human transcription factor (SC1) gene, complete cds.	4e-50	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus ATP-dependent RNA helicase mRNA, partial cds.				
1384	U46690		4e-50	1335873	(U46690) ATP-dependent RNA helicase [Mus musculus]	3e-24
1385	AF072128	Mus musculus claudin-2 mRNA, complete cds	2e-50	3335184	(AF072128) claudin-2 [Mus musculus]	4e-24
1386	AF093593	Homo sapiens snRNA activating protein complex 19kDa subunit (SNAP19) mRNA, complete cds	1e-50	3668416	(AF093593) snRNA activating protein complex 19kDa subunit [Homo sapiens]	0.003
1387	U79745	Homo sapiens monocarboxylate transporter homologue MCT6 mRNA, complete cds	1e-50	1177607	(X92485) pva1 [Plasmodium vivax]	2e-07
1388	L09647	Rattus norvegicus hepatocyte nuclear factor 3a	1e-50	404764	(L10409) fork head related protein [Mus musculus]	2e-21
1389	X61506	Mouse E46 mRNA for E46 protein	4e-51	114909	BRAIN PROTEIN E46	1e-20
1390	M33387	Human debrisoquine 4-hydroxylase (CYP2D8P) and	1e-51	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	5e-15
1391	AF019767	Homo sapiens zinc finger protein (ZPR1) mRNA, complete cds	4e-52	961507	(D63788) anchor protein, LCM	5.9
1392	Z37986	H.sapiens mRNA for phenylalkylamine binding protein.	2e-52	<NONE>	<NONE>	<NONE>
1393	U65416	Human MHC class I molecule (MICB) gene, complete cds	2e-52	3878637	(Z49128) weak similarity with SINR protein (Swiss Prot accession number P06533); cDNA EST EMBL:T00631 comes from this gene; cDNA EST yk293d10.5 comes from this gene [Caenorhabditis elegans]	8.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1394	Z57647	H.sapiens CpG DNA, clone 189a6. forward read cpg189a6.ft1a .	2e-52	111187	beta-globin DNA-binding protein B1, transcription factor PU.1 - mouse >gi 200586 (M32370) PU.1 protein [Mus musculus] >gi 200972 (M38252) transcription factor Pu.1 [Mus musculus]	5.8
1395	L13738	Human activated p21cdc42Hs kinase (ack) mRNA, complete cds.	2e-52	2921447	(AF037260) non-receptor protein tyrosine kinase Ack [Mus musculus]	7e-23
1396	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA, complete cds	7e-53	2801701	(AF042379) spindle pole body protein spc97 homolog GCP2	1e-16
1397	AF047441	Homo sapiens RNA polymerase I 40kD subunit mRNA, complete cds	6e-53	3914807	DNA-DIRECTED RNA POLYMERASE I 40 KD POLYPEPTIDE (RPA40) (RPA39) >gi 2266929 (AF008442) RNA polymerase I subunit hRPA39 [Homo sapiens]	4e-19
1398	AF104670	Homo sapiens cell cycle protein (PA2G4) gene, exons 6 through 13, and complete cds	2e-53	<NONE>	<NONE>	<NONE>
1399	S60754	{ VNTR locus DXZ4, hypervariable tandem repeat cluster } [human, Genomic, 2991 nt] >:: gb L07935 HUMVNT RA Homo sapiens microsatellite VNTR DNA sequence.	2e-53	1209669	(U38810) CAGR1 [Homo sapiens] >gi 3098420 (AF040945) homeotic regulator homolog MAB21 [Mus musculus]	4.6
1400	D86972	Human mRNA for KIAA0218 gene, complete cds	1e-53	3426041	(AC005168) unknown protein [Arabidopsis thaliana]	9.1

H60

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1401	AJ236682	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49E6, complete read	7e-54	3928721	(AL034355) putative cytochrome oxidase subunit I [Streptomyces coelicolor]	0.30
1402	AJ236682	Homo sapiens chromosome 22 CpG island DNA, genomic MseI fragment, clone 22CGIB49E6, complete read	6e-54	3928721	(AL034355) putative cytochrome oxidase subunit I [Streptomyces coelicolor]	0.28
1403	M37583	Human histone (H2A.Z) mRNA, complete cds.	6e-54	70711	histone H2A.F, embryonic - chicken	2e-16
1404	AJ009947	Homo sapiens mRNA for putative ATPase, partial	6e-54	3550295	(AJ009947) putative ATPase [Homo sapiens]	3e-18
1405	Y08459	B.taurus mRNA for novel cytoplasmic protein	2e-54	<NONE>	<NONE>	<NONE>
1406	AF042384	Homo sapiens BC-2 protein mRNA, complete cds	2e-54	2828147	(AF042384) BC-2 protein [Homo sapiens]	2e-14
1407	AF042379	Homo sapiens spindle pole body protein spc97 homolog GCP2 mRNA, complete cds	8e-55	2801701	(AF042379) spindle pole body protein spc97 homolog GCP2	2e-17
1408	AF005355	Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds	7e-55	3253159	(AF005355) translation initiation factor eIF2C	3e-53
1409	AF008442	Homo sapiens RNA polymerase I subunit hRPA39 mRNA, complete cds	3e-55	3335138	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	3e-20
1410	AF047441	Homo sapiens RNA polymerase I 40kD subunit mRNA, complete cds	3e-55	3335138	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	3e-20

461

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1411	X08004	Human mRNA for Rap1B protein > :: emb A08693 A08693 H.sapiens rap1b cDNA	2e-55	539995	transforming protein rap1b - rat (strain Copenhagen)	2e-18
1412	AF010403	Homo sapiens ALR mRNA, complete cds	2e-55	2358285	(AF010403) ALR [Homo sapiens]	1e-49
1413	M77016	Human tropomodulin mRNA, complete cds.	8e-56	262249	(S52010) orf1 5' of EpoR [mice, Peptide, 85 aa] [Mus sp.]	0.027
1414	AB020633	Homo sapiens mRNA for KIAA0826 protein, partial cds	2e-56	<NONE>	<NONE>	<NONE>
1415	X87489	H.sapiens genomic DNA (chromosome 3; clone NL1243D)	2e-56	1814029	(U84501) cuticle collagen [Caenorhabditis briggsae]	0.038
1416	AB007893	Homo sapiens KIAA0433 mRNA, partial cds	2e-56	2887437	(AB007893) KIAA0433 [Homo sapiens]	9e-21
1417	X78925	H.sapiens HZF2 mRNA for zinc finger protein	1e-56	3342002	(AF054180) hematopoietic cell derived zinc finger protein [Homo sapiens]	2e-21
1418	Z56281	H.sapiens mRNA for interferon regulatory factor 3	9e-57	2497442	INTERFERON REGULATORY FACTOR 3 factor 3 [Homo sapiens]	2e-21
1419	U78772	Homo sapiens nuclear VCP-like protein NVLP.1	8e-57	2406565	(U68140) nuclear VCP-like protein NVLP.2 [Homo sapiens]	5e-20
1420	D79994	Human mRNA for KIAA0172 gene, partial cds	3e-57	1136404	(D79994) similar to ankyrin of Chromatium vinosum. [Homo sapiens]	9e-38
1421	AB002342	Human mRNA for KIAA0344 gene, complete cds	1e-57	2224629	(AB002342) KIAA0344 [Homo sapiens]	4e-20
1422	L19437	Human transaldolase mRNA containing transposable element, complete cds	1e-57	1553119	(U63159) transaldolase [Mus musculus]	2e-20
1423	D17532	Human mRNA for RCK, complete cds	9e-58	129376	PROBABLE ATP-DEPENDENT RNA HELICASE P54 (ONCOGENE RCK) (DEAD BOX PROTEIN 6)	1e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1424	X79568	H.sapiens BDPI mRNA for protein-tyrosine-phosphatase	9e-58	1871531	(X79568) protein-tyrosine-phosphatase	1e-22
1425	X79568	H.sapiens BDPI mRNA for protein-tyrosine-phosphatase	9e-58	1871531	(X79568) protein-tyrosine-phosphatase	9e-23
1426	AB012295	Homo sapiens HKE1.5 mRNA for GDS-related protein, complete cds	7e-58	2648021	(Z97184) RGL2 [Homo sapiens]	9e-19
1427	AF086040	Homo sapiens full length insert cDNA clone YX52E07	1e-58	543222	glutamine (Q)-rich factor 1, QRF-1 - mouse factor 1, QRF-1 [mice, B-cell leukemia, BCL1, Peptide Partial, 84 aa]	3e-36
1428	AB018195	Homo sapiens ca xi mRNA for carbonic anhydrase-related protein XI, complete cds	4e-59	<NONE>	<NONE>	<NONE>
1429	AF071777	Mus musculus IRE1 (Ire1) mRNA, complete cds	4e-59	3766209	(AF071777) IRE1 [Mus musculus]	7e-28
1430	AB000462	Homo sapiens mRNA for SH3 binding protein, complete cds, clone:RES4-23A	3e-59	<NONE>	<NONE>	<NONE>
1431	AF038172	Homo sapiens clone 23923 mRNA sequence	3e-59	3758855	(Z98551) MAL3P6.11 [Plasmodium falciparum]	1.3
1432	Z84812	Human DNA sequence from phage pTEL from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs	1e-59	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	2.5
1433	U36484	Human laminin-binding protein gene, partial cds, and E2 small nucleolar RNA gene, complete sequence	1e-59	226005	protein 40kD [Mus musculus]	7e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DUAL SPECIFICITY	
1434	L11285	Homosapiens ERK activator kinase (MEK2) mRNA.	1e-59	2499630	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 2 (MAP KINASE KINASE 2) (MAPKK 2) kinase type 2 [Gallus gallus]	3e-21
1435	AF086555	Homo sapiens full length insert cDNA clone ZE14E04	4e-60	3287674	(AC005239) F23149_1 [Homo sapiens]	2e-04
1436	M24766	Human (clone pHAIIV2-12) alpha-2 collagen type IV	4e-60	29551	(X05610) alpha (2) chain [Homo sapiens]	6e-15
1437	X65550	H.sapiens mki67a mRNA (long type) for antigen of monoclonal antibody Ki-67	4e-60	1170654	ANTIGEN KI-67 >gi 539555 pir A48666 cell proliferation antigen Ki-67, long form - human Ki-67 [Homo sapiens]	3e-15
1438	M27319	Human calmodulin mRNA, complete cds.	4e-60	1345451	(X05949) Calmodulin (AA 2 - 59) (449 is 1st base in codon) [Drosophila melanogaster]	7e-20
1439	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	3e-60	62133	(X06172) put. 134 kD protein (AA 1 - 1187); put. replicase	7.4
1440	AB002383	Human mRNA for KIAA0385 gene, complete cds	1e-60	1001548	(D64000) hypothetical protein	4.4
1441	AF070614	Homo sapiens clone 24732 unknown mRNA, partial cds	2e-61	3283879	(AF070614) unknown [Homo sapiens]	3e-17
1442	AB002326	Human mRNA for KIAA0328 gene, partial cds	6e-62	547891	MICROTUBULE-ASSOCIATED PROTEIN 4 microtubule-associated protein-U [Bos taurus]	5.6
1443	AF086471	Homo sapiens full length insert cDNA clone ZD88A01	5e-62	<NONE>	<NONE>	<NONE>
1444	AB002311	Human mRNA for KIAA0313 gene, complete cds	2e-62	2506357	2,3-DIHYDROXYPHENYLPROPIONATE 1,2-DIOXYGENASE >gi 1657544 (U73857) similar to mcpI gene (catechol 2,3-dioxygenase) of A. eutrophus 3-(2,3-dihydroxyphenylpropionate)1, 2-dioxygenase 2,3-dihydroxyphenylpropionate 1,2-dioxygenase	3.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1445	AF069737	Xenopus laevis notchless (nle) mRNA, complete cds	2e-62	3687833	(AF069737) notchless [Xenopus laevis]	1e-55
1446	AF044209	Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds	5e-63	2137603	nuclear receptor co-repressor N-CoR - mouse musculus] >gi 1583865 prf 2121436A thyroid hormone receptor co-repressor [Mus musculus]	2e-47
1447	M69238	Human aryl hydrocarbon receptor nuclear translocator (ARNT) mRNA, complete cds.	2e-63	2702319	(AF001307) aryl hydrocarbon receptor nuclear translocator; Arnt [Homo sapiens]	5e-19
1448	X80497	H.sapiens PHKLA mRNA	2e-63	1170685	PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN, LIVER ISOFORM (PHOSPHORYLASE KINASE ALPHA L SUBUNIT) >gi 663010 (X80497) phosphorylase kinase phosphorylase kinase alpha subunit [Homo sapiens]	5e-22
1449	AF031141	Homo sapiens ubiquitin conjugating enzyme	2e-63	2623260	(AF031141) ubiquitin conjugating enzyme [Homo sapiens]	1e-23
1450	Z37166	H.sapiens BAT1 mRNA for nuclear RNA helicase	6e-64	2500529	PROBABLE ATP-DEPENDENT RNA HELICASE P47 >gi 2135840 pir I37201 nuclear RNA helicase (DEAD family) BAT1 - human >gi 587146 (Z37166) nuclear RNA helicase (DEAD family) [Homo sapiens]	9e-24
1451	M64240	Human helix-loop-helix zipper protein (max) mRNA, complete cds. > :: gb I41138 I41138 Sequence 1 from patent US 5624818 > :: gb I77062 I77062 Sequence 1 from patent US 5693487	5e-64	88175	Myc-binding factor Max, short form - human	8e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1452	M98252	Homo sapiens lysyl hydroxylase (partial clone 2.2 Kb LH) RNA, complete mature peptide.	2e-64	400205	PROCOLLAGEN-LYSINE 2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE) [Homo sapiens]	7e-22
1453	U09550	Human oviductal glycoprotein mRNA, complete cds.	8e-65	2493676	OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN)	2e-11
1454	X67877	R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein	7e-65	423664	resiniferatoxin-binding protein RBP-26, cytosolic - rat >gi 311660 (X67877) cytosolic resiniferatoxin binding protein RBP-26 [Rattus norvegicus] >gi 1093373 prf 2103310A resiniferatoxin-binding protein [Rattus norvegicus]	2e-40
1455	AB018254	Homo sapiens mRNA for KIAA0711 protein, complete cds	6e-65	92298	glutamine/glutamic acid-rich protein	0.98
1456	J03607	Human 40-kDa keratin intermediate filament precursor gene.	3e-65	1070608	keratin 19, type I, cytoskeletal - human sapiens]	4e-07
1457	U65896	Human gamma-glutamyl carboxylase gene, complete cds	2e-65	<NONE>	<NONE>	<NONE>
1458	U07681	Human NAD(H)-specific isocitrate dehydrogenase alpha subunit precursor mRNA, complete cds.	2e-65	1708399	ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) dehydrogenase alpha chain precursor - human >gi 706839 subunit precursor [Homo sapiens]	4e-26
1459	U88080	Human zinc finger protein (LD5-1) gene, exons 4, 5 and 6, and complete cds	2e-65	1373394	(U57796) zinc finger protein [Homo sapiens] >gi 2306773	2e-39

466

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1460	M96625	Gallus domesticus tensin mRNA sequence.	3e-66	2134419	tensin - chicken (fragment) >gi 63805 (Z18529) tensin [Gallus gallus] >gi 212755 (L06662) tensin [Gallus gallus]	1e-51
1461	U13262	Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.	1e-70	536926	(U13262) myelin gene expression factor [Mus musculus]	9e-42
1462	U64033	Mus musculus Tera (Tera) mRNA, complete cds	5e-72	1575505	(U64033) Tera [Mus musculus]	9e-34
1463	X78989	M.musculus mRNA for testin	6e-74	1351218	TESTIN 2 (TES2) [CONTAINS: TESTIN 1]	8e-31
1464	U64033	Mus musculus Tera (Tera) mRNA, complete cds	2e-74	1575505	(U64033) Tera [Mus musculus]	5e-37
1465	AF057365	Canis familiaris UDP N-acetylglucosamine transporter mRNA, complete cds	9e-79	3298605	(AF057365) UDP N-acetylglucosamine transporter [Canis familiaris]	9e-10
1466	AJ006064	Rattus norvegicus mRNA for coronin-like protein	1e-82	3757680	(AJ006064) coronin-like protein [Rattus norvegicus]	3e-62
1467	U91582	Macaca fascicularis UDP-glucuronosyltransferase mRNA, complete cds	4e-89	140396	KARYOGAMY PROTEIN KAR4 yeast (Saccharomyces cerevisiae)	1e-08
1468	X06762	Mouse Hox2.3 mRNA	3e-92	123255	HOMEODOMAIN PROTEIN HOXB7 (HOX-2C)	9e-23
1469	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	5e-94	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	7e-34
1470	X74504	M.musculus T10 mRNA	7e-97	1711658	SER/THR-RICH PROTEIN T10 IN DGCR REGION >gi 480900 pir S37488 gene T10 protein - mouse	3e-59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1471	U13175	Rattus norvegicus clone ubc10a ubiquitin conjugating enzyme (E217kB) mRNA, complete cds.	3e-98	1351345	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 3) >gi 1085588 pir S53358 ubiquitin conjugating enzyme (E217kB) - rat >gi 595666 (U13175) ubiquitin conjugating enzyme [Rattus norvegicus] >gi 1145691 (U39318) UbcH5C [Homo sapiens]	5e-05
1472	S79873	h-lamp-2=lysosome-associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	e-119	<NONE>	<NONE>	<NONE>
1473	D13623	Rat mRNA for p34 protein, complete cds	e-112	480379	ribosome-binding protein p34 - rat sp.]	2e-05
1474	AB013357	Mus musculus mRNA for 49 kDa zinc finger protein, complete cds	e-136	4153886	(AB013357) 49 kDa zinc finger protein	5e-08
1475	AB016930	Cricetulus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	e-117	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	4e-32
1476	U38253	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	e-103	2494312	TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) subunit [Rattus norvegicus]	3e-42

468

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1477	X73683	R.norvegicus mRNA for histone H3.3	e-117	122075	(H3.3Q) histone H3.3 - fruit fly (Drosophila melanogaster) histone H3.3B - chicken >gi 2119023 pir S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136 [Oryctolagus cuniculus] >gi 8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi 51198 gallus] >gi 161190 (M17876) histone H3 [Spisula solidissima] >gi 211853 (M11393) histone 3.3 [Gallus gallus] >gi 306848 (M11354) H3.3 histone [Homo sapiens] melanogaster] >gi 963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus]	1e-45
1478	U32498	Rattus norvegicus rsec8 mRNA, partial cds	e-108	2143962	rsec8 - rat (fragment) >gi 1019441 (U32498) rsec8 [Rattus norvegicus]	7e-48
1479	U41736	Mus musculus ancient ubiquitous 46 kDa protein AUP1 precursor (Aup1) mRNA, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	5e-49
1480	AF041338	Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds	e-119	2895578	(AF041338) vacuolar proton pump subunit SFD alpha isoform [Bos taurus]	3e-49
1481	AF064553	Mus musculus NSD1 protein mRNA, complete cds	e-121	3329465	(AF064553) NSD1 protein [Mus musculus]	2e-50
1482	AB000517	Rattus sp. mRNA for CDP-diacylglycerol synthase, complete cds	e-146	1517822	(U41736) ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus]	2e-51
1483	D38517	Mouse mRNA for Dhml protein, complete cds	e-118	2137562	mouse Dhml protein - mouse musculus]	6e-54

469

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1484	X54352	M.domesticus MD6 mRNA	e-139	1085499	CDC4 repeat unit-containing protein - mouse	1e-55
1485	U57692	Mus musculus N-terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-118	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) >gi 1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	5e-57
1486	X80169	M.musculus mRNA for 200 kD protein	e-119	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	9e-58
1487	U57692	Mus musculus N-terminal asparagine amidohydrolase (Ntan1) mRNA, complete cds	e-120	2498797	PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) >gi 1373365 (U57691) N-terminal asparagine amidohydrolase [Mus musculus] amidohydrolase [Mus musculus]	8e-58
1488	U08215	Mus musculus Hsp70-related NST-1 (hsr.1) mRNA, complete cds.	e-109	473407	(U08215) NST-1 [Mus musculus]	7e-58
1489	D85926	Mouse mRNA for Ray, complete cds	e-110	1944389	(D85926) Ray [Mus musculus]	2e-58
1490	L20427	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	e-123	457372	(L20427) dihydroxypolyprenylbenzoate methyltransferase dihydroxypolyprenylbenzoate methyltransferase [Rattus norvegicus]	4e-59
1491	X56044	M.musculus mRNA for protein Htf9C	e-121	3183977	(X56044) protein Htf9C [Mus musculus]	1e-60

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					PROTO-ONCOGENE	
1492	S74774	p59fyn(T)=OKT3-induced calcium influx regulator	e-163	729896	TYROSINE-PROTEIN KINASE FYN (P59-FYN) >gi 420217 pir A44991 protein-tyrosine kinase (EC 2.7.1.112) fyn - mouse	8e-63
1493	U88873	Mus musculus BUB2-like protein 1 (HBLP1) mRNA, complete cds	e-123	4099611	(U88873) BUB2-like protein 1 [Mus musculus]	1e-63
1494	U48852	Cricetulus griseus HT protein mRNA, complete cds.	e-117	1216486	(U48852) HT protein [Cricetulus griseus]	7e-64
1495	AF032667	Rattus norvegicus rexo70 mRNA, complete cds	e-142	2827160	(AF032667) rexo70 [Rattus norvegicus]	5e-66
1496	M62722	Chinese hamster phosphatidylserine decarboxylase mRNA, 3' end.	e-114	118910	PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME >gi 109423 pir A38732 phosphatidylserine decarboxylase (EC 4.1.1.65) - Chinese hamster (fragment)	2e-67
1497	AF072758	Mus musculus fatty acid transport protein 3 mRNA, partial cds	e-130	3335567	(AF072758) fatty acid transport protein 3; FATP3 [Mus musculus]	1e-67
1498	AB005549	Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds	e-113	3868778	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	2e-69
1499	U57344	Mus musculus homeobox protein Meis3 mRNA, complete cds	e-143	3024124	HOMEBOX PROTEIN MEIS3	6e-72
1500	U09874	Mus musculus SKD3 mRNA, complete cds.	e-142	2493735	SKD3 PROTEIN SKD3 [Mus musculus]	1e-72
1501	U72194	Mus musculus muskelin mRNA, complete cds	e-148	3493462	(U72194) muskelin [Mus musculus]	2e-74
1502	X80169	M.musculus mRNA for 200 kD protein	e-155	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	3e-77

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1503	U72194	muskelin mRNA, complete cds	e-154	3493462	(U72194) muskelin [Mus musculus]	2e-78
1504	Y12836	Cricetulus griseus mRNA for Zn finger factor	e-146	3150148	(Y12836) Zn finger factor [Cricetulus griseus]	3e-83

H72

Table 5

SEQ ID	Start	Stop	Score	Direction	Description
29	295	421	5872	For	mkk like kinases
30	31	182	3943	For	Basic region plus leucine zipper transcription factors
31	298	397	5625	For	mkk like kinases
186	175	395	7660	For	SH2 Domain
187	358	432	4320	For	Ank repeat
196	37	322	6049	For	mkk like kinases
234	23	121	4607	For	SH3 Domain
308	110	172	4150	For	Zinc finger, C2H2 type
410	42	191	4036	For	Basic region plus leucine zipper transcription factors
431	71	428	5538	Rev	ATPases Associated with Various Cellular Activities
552	116	288	3930	Rev	Basic region plus leucine zipper transcription factors
639	157	561	5797	For	ATPases Associated with Various Cellular Activities
746	209	427	5379	For	Fibronectin type III domain
768	116	288	3930	For	Basic region plus leucine zipper transcription factors
807	339	392	3620	For	Zinc finger, C2H2 type
820	341	406	2930	Rev	EF-hand
822	108	262	4179	For	Basic region plus leucine zipper transcription factors
836	158	353	4430	For	Basic region plus leucine zipper transcription factors
1157	41	444	5279	Rev	protein kinase
1192	186	416	5469	For	Fibronectin type III domain
1268	238	315	3540	For	Ank repeat
1269	79	240	11640	For	LIM domain containing proteins
1288	73	234	3953	For	Basic region plus leucine zipper transcription factors

SEQ ID	Start	Stop	Score	Direction	Description
1309	248	404	8226	for	LIM domain containing proteins
1324	294	356	4690	for	Zinc finger, C2H2 type
1325	1	234	8981	for	C2 domain (prot. kinase C like)
1336	66	164	6390	for	WD domain, G-beta repeats
1360	222	377	8686	for	LIM domain containing proteins
1365	69	257	5221	for	Basic region plus leucine zipper transcription factors
1380	42	140	7130	for	WD domain, G-beta repeats
1386	243	398	8736	for	LIM domain containing proteins
1410	222	350	10553	for	Trypsin
1417	8	354	6073	for	Protein Tyrosine Phosphatase
1454	49	209	3996	for	Basic region plus leucine zipper transcription factors
1464	4	180	4978	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1478	54	437	5176	for	protein kinase
1496	241	520	3929	for	Helicases conserved C-terminal domain
1496	40	612	5187	for	protein kinase
1503	154	216	4870	for	Zinc finger, C2H2 type
1514	2	252	4662	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1527	156	212	3520	for	Zinc finger, C2H2 type
1538	9	635	11087	for	wnt family of developmental signaling proteins
1540	289	471	4107	for	Basic region plus leucine zipper transcription factors
1549	200	391	4118	for	Basic region plus leucine zipper transcription factors
1556	163	354	3958	for	Basic region plus leucine zipper transcription factors
1557	207	398	4038	for	Basic region plus leucine zipper transcription factors
1563	107	298	3978	for	Basic region plus leucine zipper transcription factors

SEQ ID	Start	Stop	Score	Direction	Description
1622	180	365	4022	for	Basic region plus leucine zipper transcription factors
1630	100	291	3998	for	Basic region plus leucine zipper transcription factors
1674	196	258	4880	for	Zinc finger, C2H2 type
1676	9	86	6610	for	Homeobox Domain
1677	316	369	5780	rev	Thioredoxins
1688	109	410	17414	for	Ras family
1704	184	372	3977	for	Basic region plus leucine zipper transcription factors
1707	92	439	24100	rev	Phosphatidylinositol-specific phospholipase C, Y domain
1711	263	361	6400	for	WD domain, G-beta repeats
1744	238	433	10572	rev	Serine carboxypeptidases
1755	281	367	2580	for	EF-hand
1762	236	334	5880	for	WD domain, G-beta repeats
1779	64	126	4790	for	Zinc finger, C2H2 type
1801	295	351	4030	for	Zinc finger, C2H2 type
1804	301	378	3460	for	Ank repeat
1808	36	161	4170	for	Basic region plus leucine zipper transcription factors
1811	184	315	8390	for	N-terminal homology in Ets domain
1814	127	294	10770	for	Bromodomain (conserved sequence found in human, Drosophila and yeast proteins.)
1818	9	146	4741	for	Double-stranded RNA binding motif
1819	278	355	3460	for	Ank repeat
1820	123	299	12150	for	Homeobox Domain
1821	127	303	12180	for	Homeobox Domain
1830	184	267	4270	for	Ank repeat
1832	18	173	8987	for	SH3 Domain
1835	51	206	8987	for	SH3 Domain
1839	224	307	4270	for	Ank repeat
1846	12	398	36700	for	G-protein alpha subunit

SEQ ID	Start	Stop	Score	Direction	Description
1909	160	258	6370	for	WD domain, G-beta repeats
1911	35	151	9335	for	Zinc finger, C3HC4 type (RING finger)
1980	60	197	7917	for	Zinc finger, C3HC4 type (RING finger)
2065	253	306	5410	for	Zinc finger, CCHC class
2135	2	401	10596	for	ATPases Associated with Various Cellular Activities
2216	90	179	5380	for	WW/rsp5/WWP domain containing proteins
2218	127	225	5500	for	WD domain, G-beta repeats
2281	20	387	6044	for	Protein Tyrosine Phosphatase
2282	183	353	5136	for	C2 domain (prot. kinase C like)
2286	12	382	5228	for	protein kinase
2310	20	371	5962	for	Protein Tyrosine Phosphatase
2363	48	211	4132	for	Basic region plus leucine zipper transcription factors
2424	43	194	3996	for	Basic region plus leucine zipper transcription factors
2428	25	350	4675	for	Dual specificity phosphatase, catalytic domain
2562	18	101	4560	for	Ank repeat
2577	0	311	10295	for	4 transmembrane segments integral membrane proteins
2591	60	165	4560	for	SH2 Domain
2684	9	461	5759	for	ATPases Associated with Various Cellular Activities
2826	116	400	16107	for	DEAD and DEAH box helicases
2859	100	320	5550	rev	ATPases Associated with Various Cellular Activities
2871	198	392	9384	for	DEAD and DEAH box helicases
2944	18	281	10480	for	Calpain large subunit, domain III
2969	5	387	5976	rev	protein kinase
3015	131	214	3600	for	Ank repeat
3047	191	292	5295	for	WD domain, G-beta repeats
3081	190	252	4360	for	Zinc finger, C2H2 type
3108	275	367	5791	for	WD domain, G-beta repeats
3147	190	369	4022	for	Basic region plus leucine zipper transcription factors
3152	129	320	3947	for	Basic region plus leucine zipper transcription factors
3158	167	334	4180	for	Basic region plus leucine zipper transcription factors
3175	14	164	5951	for	mkk like kinases

SEQ ID	Start	Stop	Score	Direction	Description
3175	8	112	5968	for	protein kinase
3178	45	386	19398	for	ATPases Associated with Various Cellular Activities
3183	14	215	9133	for	4 transmembrane segments integral membrane proteins
3190	229	390	6089	for	mkk like kinases
3190	118	390	8063	for	protein kinase
3193	293	355	3570	for	Zinc finger, C2H2 type
3195	0	215	10146	for	4 transmembrane segments integral membrane proteins
3197	281	343	4490	for	Zinc finger, C2H2 type
3208	34	256	4190	for	Basic region plus leucine zipper transcription factors
3258	138	394	9877	for	Ras family
3266	8	139	9328	for	ATPases Associated with Various Cellular Activities
3267	97	180	3820	for	Ank repeat
3274	11	187	15442	for	Fork head domain, eukaryotic transcription factors
3281	15	182	9681	for	mkk like kinases
3285	16	102	4680	for	EF-hand
3292	208	300	5585	for	WD domain, G-beta repeats
3297	7	153	6100	for	Helicases conserved C-terminal domain
3306	161	223	4900	for	Zinc finger, C2H2 type
3307	43	321	8740	for	SH2 Domain
3339	94	342	14970	for	SH2 Domain
3345	65	271	12512	for	PDZ domain
3351	124	270	6068	for	Phorbol esters/diacylglycerol binding

Example 4

DIFFERENTIAL EXPRESSION OF POLYNUCLEOTIDES OF THE INVENTION:
DESCRIPTION OF LIBRARIES AND DETECTION OF DIFFERENTIAL EXPRESSION

5 The relative expression levels of the polynucleotides of the invention
was assessed in several libraries prepared from various sources, including cell lines and
patient tissue samples. Table 6 provides a summary of these libraries, including the
shortened library name (used hereafter), the mRNA source used to prepare the cDNA
library, the abbreviated name of the library that is used in the tables below (in quotes),
10 and the approximate number of clones in the library.

Table 6
Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in this Clustering
1	Km12 L4 Human Colon Cell Line, High Metastatic Potential (derived from Km12C) "High Colon"	307133
2	Km12C Human Colon Cell Line, Low Metastatic Potential "Low Colon"	284755
3	MDA-MB-231 Human Breast Cancer Cell Line, High Metastatic Potential; micro-metastases in lung "High Breast"	326937
4	MCF7 Human Breast Cancer Cell, Non Metastatic "Low Breast"	318979
8	MV-522 Human Lung Cancer Cell Line, High Metastatic Potential "High Lung"	223620
9	UCP-3 Human Lung Cancer Cell Line, Low Metastatic Potential "Low Lung"	312503

Library (lib #)	Description	Number of Clones in this Clustering
12	Human microvascular endothelial cells (HMEC) – Untreated PCR (OligodT) cDNA library	41938
13	Human microvascular endothelial cells (HMEC) – Basic fibroblast growth factor (bFGF) treated PCR (OligodT) cDNA library	42100
14	Human microvascular endothelial cells (HMEC) – Vascular endothelial growth factor (VEGF) treated PCR (OligodT) cDNA library	42825
15	Normal Colon – UC#2 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	34285
16	Colon Tumor – UC#2 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	35625
17	Liver Metastasis from Colon Tumor of UC#2 Patient PCR (OligodT) cDNA library “High Colon Metastasis Tissue”	36984
18	Normal Colon – UC#3 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	36216
19	Colon Tumor – UC#3 Patient PCR (OligodT) cDNA library “High Colon Tumor Tissue”	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient PCR (OligodT) cDNA library “High Colon Metastasis Tissue”	30956
21	G RRpz Human Prostate Cell Line	164801
22	WOca Human Prostate Cancer Cell Line	162088

The KM12L4 and KM12C cell lines are described in Example 1 above.
The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly
5 differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma.

479

The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran et al., *Cancer Res.* (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar et al., *J Med Chem* (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson et al., *Br J Cancer* (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang et al., *Nucleic Acids Res* (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki et al., *Int J Cancer* (1987) 40:46 (UCP-3); Varki et al., *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki et al., *Anticancer Res.* (1990) 10:637; (MV-522); Kelner et al., *Anticancer Res* (1995) 15:867 (MV-522); and Zhang et al., *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz cell line refers to low passage (3 passages or fewer) human prostate cells, and the WOca cell line refers to low passage (3 passages or fewer) human prostate cancer cells.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac et al., *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may

occur in computational clustering just as artifacts can occur in “wet-lab” screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones
5 can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones
10 corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a “ratio” of percent expression between the two libraries. In general, the “ratio” is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in
15 the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the
20 second library. If the “number of clones” corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the “depth” of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially
25 expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5 , where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, “Differences between Proportions,” pp 296-298 (1974)).

EXAMPLE 5

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
BREAST CANCER CELLS VERSUS LOW METASTATIC BREAST CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential breast
cancer tissue and low metastatic breast cancer cells. Expression of these sequences in
breast cancer can be valuable in determining diagnostic, prognostic and/or treatment
information. For example, sequences that are highly expressed in the high metastatic
10 potential cells can be indicative of increased expression of genes or regulatory
sequences involved in the metastatic process. A patient sample displaying an increased
level of one or more of these polynucleotides may thus warrant more aggressive
treatment. In another example, sequences that display higher expression in the low
metastatic potential cells can be associated with genes or regulatory sequences that
15 inhibit metastasis, and thus the expression of these polynucleotides in a sample may
warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially
expressed between high metastatic potential breast cancer cells and low metastatic
potential breast cancer cells.

Table 7

25 Differentially expressed polynucleotides: Higher expression in
high metastatic potential breast cancer (lib3) relative to low metastatic
breast cancer cells (lib4)

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
472	64	0	62
1851	6	0	6
1856	8	0	8
1867	6	0	6
1872	6	0	6
1875	12	3	4
1923	89	22	4

482

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
2118	7	0	7
2119	7	0	7
2135	37	13	3
2190	19	0	19
2193	16	5	3
2232	12	2	6
2239	6	0	6
2338	21	2	10
2378	16	4	4
2394	6	0	6
2395	6	0	6
2490	13	3	4
2505	16	2	8
2540	8	1	8
2542	11	1	11
2607	11	2	5
2640	22	5	4
2674	8	0	8
2679	19	0	19
2684	14	4	3
2707	8	0	8
2724	9	0	9
2757	6	0	6
2776	10	0	10
2804	13	2	6
2818	6	0	6
2906	14	0	14
2959	26	8	3
2964	17	4	4
2968	6	0	6
2977	22	3	7
2980	13	1	13
3010	6	0	6
3043	10	1	10
3071	33	12	3
3072	9	1	9
3095	19	3	6
3097	11	2	5
3173	12	2	6
3203	8	1	8
3210	27	8	3

483

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
3212	13	1	13
3284	8	0	8
3288	6	0	6
3331	14	3	5
3335	13	1	13

Table 8

Differentially expressed polynucleotides: Higher expression in low metastatic breast cancer cells (lib4) relative to high metastatic potential breast cancer (lib3)

5

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
402	0	6	6
614	3	21	7
624	0	6	6
626	0	8	8
712	0	9	9
744	0	7	7
1325	2	29	15
1452	2	13	7
1880	0	9	9
1915	0	7	7
1951	0	6	6
1955	8	32	4
2015	0	7	7
2046	0	7	7
2076	1	22	23
2087	0	6	6
2124	0	9	9
2145	0	8	8
2162	0	6	6
2163	0	12	12
2164	5	19	4
2172	2	15	8
2192	5	16	3
2244	20	43	2
2266	3	18	6
2313	24	56	2
2346	1	13	13

484

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
2355	0	10	10
2371	0	6	6
2393	1	17	17
2404	1	21	22
2443	0	6	6
2460	0	11	11
2523	0	6	6
2575	1	10	10
2578	0	6	6
2584	1	17	17
2590	0	6	6
2609	1	9	9
2632	5	24	5
2714	5	24	5
2728	0	6	6
2752	1	14	14
2794	4	15	4
2826	0	7	7
2987	5	15	3
3005	1	14	14
3009	20	58	3
3047	4	17	4
3057	2	17	9
3075	2	11	6
3076	0	6	6
3102	0	6	6
3128	15	52	4
3132	15	52	4
3142	0	6	6
3187	22	49	2
3253	23	96	4
3282	19	46	2
3285	20	40	2
3346	0	9	9

485

EXAMPLE 6

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL LUNG
CANCER CELLS VERSUS LOW METASTATIC LUNG CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential lung
cancer cells and low metastatic lung cancer cells. Expression of these sequences in lung
cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment
information. For example, sequences that are highly expressed in the high metastatic
10 potential cells can be indicative of increased expression of genes or regulatory
sequences involved in the metastatic process. A patient sample displaying an increased
level of one or more of these polynucleotides may thus warrant more aggressive
treatment. In another example, sequences that display higher expression in the low
metastatic potential cells can be associated with genes or regulatory sequences that
15 inhibit metastasis, and thus the expression of these polynucleotides in a sample may
warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially
expressed between high metastatic potential lung cancer cells and low metastatic
potential lung cancer cells:

Table 9

Differentially expressed polynucleotides: Higher expression in high metastatic potential lung cancer cells (lib8) relative to low metastatic lung cancer cells (lib9)

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
14	10	0	10
137	5	0	5
151	5	0	7
152	9	0	13
171	6	0	8
200	10	0	14
254	5	0	7
262	5	0	7
271	5	0	7
348	6	1	8
412	5	0	7
507	5	0	7
520	6	0	8
530	5	0	7
588	5	0	7
623	7	0	10
637	7	0	10
660	5	0	7
678	8	0	11
680	5	0	7
700	9	2	6
714	28	13	3
774	11	0	15
812	5	0	7
834	8	2	6
901	11	2	8
1168	5	0	7
1333	6	0	8
1352	5	0	7
1524	11	1	15
1706	5	0	7
1752	17	9	3
1768	20	4	7
1769	5	0	7
1780	6	0	8

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
1781	40	3	19
1799	6	1	8
1803	6	1	8
1811	16	9	2
1884	6	0	8
1919	8	1	11
1939	6	0	8
1975	43	9	7
2024	12	1	17
2045	8	1	11
2060	20	13	2
2071	16	4	6
2128	5	0	7
2177	10	2	7
2181	44	13	5
2184	11	1	15
2185	10	4	3
2283	7	0	10
2311	10	4	3
2314	10	0	14
2393	14	6	3
2398	6	1	8
2460	10	4	3
2514	6	0	8
2597	5	0	7
2657	8	2	6
2669	6	1	8
2670	6	1	8
3047	21	3	10
3050	16	5	4
3092	7	1	10
3140	181	119	2
3157	5	0	7
3187	16	5	4
3210	5	0	7
3220	28	4	10
3236	7	1	10
3249	16	0	22
3264	8	2	6
3305	7	0	10
3309	20	0	28

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
3318	24	4	8
3330	5	0	7
3331	5	0	7

Table 10

Differentially expressed polynucleotides: Higher expression in low metastatic lung cancer cells (lib 9) relative to high metastatic potential lung cancer cells (lib 8)

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
24	3	20	5
53	0	18	13
64	0	8	6
70	0	11	8
105	10	66	5
129	0	16	11
214	1	14	10
233	4	35	6
237	0	13	9
264	0	29	21
329	2	17	6
368	1	37	26
370	0	11	8
418	0	8	6
450	0	9	6
461	0	9	6
484	0	26	19
494	0	41	29
517	1	12	9
522	1	11	8
581	1	17	12
614	3	23	5
706	0	11	8
726	5	23	3
806	0	14	10
824	0	9	6
836	1	14	10
874	0	12	9
900	5	21	3
1017	2	14	5

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
1144	0	8	6
1154	0	12	9
1166	2	45	16
1170	1	13	9
1302	2	13	5
1326	1	13	9
1327	1	13	9
1367	0	12	9
1377	0	12	9
1437	2	18	6
1442	1	14	10
1466	0	13	9
1476	0	13	9
1495	0	8	6
1496	1	13	9
1664	38	253	5
1682	1	17	12
1687	0	9	6
1758	0	8	6
1817	4	18	3
1837	3	16	4
1845	3	23	5
1856	2	17	6
1910	1	18	13
2146	2	16	9
2156	0	9	6
2463	0	12	9
2724	10	38	3
2749	403	2000	4
2801	6	25	3
2993	3	18	4
3080	0	10	7
3107	3	23	5
3292	0	20	14
3324	110	548	4

EXAMPLE 7

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
COLON CANCER CELLS VERSUS LOW METASTATIC COLON CANCER CELLS

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high metastatic potential colon
cancer cells and low metastatic colon cancer cells. Expression of these sequences in
colon cancer tissue can provide diagnostic, prognostic and/or treatment information.
For example, sequences that are highly expressed in the high metastatic potential cells
10 can be indicative of increased expression of genes or regulatory sequences involved in
the metastatic process. A patient sample displaying an increased level of one or more of
these polynucleotides may thus warrant more aggressive treatment. In another example,
sequences that display higher expression in the low metastatic potential cells can be
associated with genes or regulatory sequences that inhibit metastasis, and thus the
15 expression of these polynucleotides in a sample may warrant a more positive prognosis
than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a
diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the
like. These polynucleotide sequences can also be used in combination with other
20 known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with
differential expression between high metastatic potential colon cancer cells and low
metastatic potential colon cancer cells:

Table 11

25 Differentially expressed polynucleotides: Higher expression in low metastatic colon
cancer cells (lib 2) relative to high metastatic potential colon cancer cells (lib 1)

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
429	0	9	10
1494	0	8	9
1923	34	114	4
1986	3	12	4
2018	0	9	10
2036	2	10	5
2049	8	25	3
2135	24	87	4

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
2146	2	16	9
2208	6	27	5
2215	2	11	6
2239	1	10	11
2307	2	12	6
2313	28	62	2
2357	5	14	3
2360	3	21	8
2362	0	6	6
2378	3	12	4
2569	3	20	7
2571	0	6	6
2588	54	172	3
2592	15	41	3
2611	0	6	6
2636	0	9	10
2641	7	20	3
2650	0	9	10
2662	0	9	10
2674	4	13	4
2682	0	6	6
2702	9	25	3
2704	8	23	3
2715	2	12	6
2804	9	22	3
2821	13	29	2
2840	1	8	9
2846	2	15	8
2866	0	6	6
2906	0	6	6
2915	44	109	3
2933	0	6	6
2935	5	16	3
2957	1	11	12
2959	3	27	10
2977	16	30	2
2980	12	27	2
3000	2	13	7
3009	12	29	3
3115	0	7	8
3156	502	2170	5

492

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
3210	2	21	11
3211	0	9	10
3213	0	7	8
3235	2	12	6
3251	2	12	6
3296	3	12	4
3335	1	8	9

EXAMPLE 8

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

5

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

10

15

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

20

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer tissue and normal colon tissue:

493

Table 12

Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3 and) : Lower expression in high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20) vs. normal colon tissue (patient 2:lib 15; patient 3:lib 18)

5

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
69	19	7	3
123	6	0	6
140	24	8	3
197	6	0	6
198	113	0	121
254	28	9	3
412	28	9	3
512	11	1	12
641	17	7	3
642	7	0	8
954	12	3	4
1011	209	16	14
1024	8	0	9
1040	12	3	4
1055	26	7	4
1106	31	15	2
1125	17	0	18
1129	17	0	18
1138	109	0	117
1244	14	1	15
1253	73	0	78
1283	34	7	5
1285	34	7	5
1339	13	4	3
1474	73	0	78
1505	18	3	6
1553	68	6	12
1554	2542	14	195
1605	2542	14	195
1628	6	0	6
1643	142	4	38
1753	12	0	10
1764	13	0	14

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
SEQ ID NO:	Lib18 Clones	Lib20 Clones	lib18/lib20
105	28	11	2
198	21	0	18
254	9	0	8
412	9	0	8
1011	11	1	9
1138	14	0	12
1253	23	0	20
1643	18	0	15
1764	12	0	10
3156	140	43	3

Table 13

Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3): Lower expression in normal colon tissue (patient 2:lib 15; patient 3:lib 18)vs. high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20).

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
321	3	23	7
363	1	9	8
836	21	99	4
859	6	20	3
885	13	28	2
916	13	28	2
981	2	11	5
1226	8	70	8
1308	0	8	7
1317	29	84	3
1429	27	127	4
1442	0	9	8
1534	1	12	11
1540	12	43	3
1552	0	7	7
1556	1	9	8
1557	1	9	8
1569	2189	5122	2
1571	6	18	3
1576	3	25	8

495

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
1581	4	22	5
1601	25	157	6
1613	9	48	5
1616	15	61	4
1620	2	17	8
1622	4	99	23
1626	6	35	5
1647	4	22	5
1664	4	28	7
1683	2	18	8
1704	3	15	5
1800	0	7	7
2749	23	60	2
2784	4	14	3
2805	1	9	8
2976	3	14	4
3128	18	57	3
3129	26	124	4
3146	64	210	3
3150	940	2267	2
3151	2	15	7
SEQ ID NO:	lib 18 clones	lib 20 clones	lib 20/lib 18
865	0	5	6
1569	1	7	8
1580	1	7	8
1590	1	7	8
2790	0	5	6

EXAMPLE 9

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH COLON TUMOR POTENTIAL
PATIENT TISSUE VERSUS METASTASIZED COLON CANCER PATIENT TISSUE

5 A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from colon cancer tissue and cells derived from colon cancer tissue metastases to liver. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the transformation of precancerous tissue to malignant tissue. This information

496

can be useful in the prevention of achieving the advanced malignant state in these tissues, and can be important in risk assessment for a patient.

The following table summarizes identified polynucleotides with differential expression between high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells:

Table 14

Differentially expressed polynucleotides:

Greater expression in metastatic colon tumor tissue (lib 20) vs.
colon tumor tissue (lib 19)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 20/lib 19
937	0	6	8
976	0	5	7
1520	1	8	11
1546	1	11	15
1550	1	11	15
1574	1	8	11
1580	0	7	9
1590	0	7	9
1599	8	21	4
1607	158	632	5
1622	1	7	9

Table 15

Greater expression in colon tumor tissue (lib 19) than metastatic colon tissue (lib 20)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 19/lib 20
105	64	11	4
1011	53	1	40
1226	18	4	3
1571	8	0	6
1726	15	3	4
1811	17	2	6
2749	47	6	6
3146	19	2	7
3324	20	1	15

467

EXAMPLE 10

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH TUMOR POTENTIAL
COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

5 A number of polynucleotide sequences have been identified that are
differentially expressed between cells derived from high tumor potential colon cancer
tissue and normal tissue. Expression of these sequences in colon cancer tissue can
provide diagnostic, prognostic and/or treatment information associated with the
prevention of the malignant state in these tissues, and can be important in risk
10 assessment for a patient. For example, sequences that are highly expressed in the
potential colon cancer cells are associated with or can be indicative of increased
expression of genes or regulatory sequences involved in early tumor progression. A
patient sample displaying an increased level of one or more of these polynucleotides
may thus warrant closer attention or more frequent screening procedures to catch the
15 malignant state as early as possible.

The following tables summarize polynucleotides that are differentially
expressed between high metastatic potential colon cancer cells and normal colon cells:

Table 16

Differentially expressed polynucleotides detected in samples from patient (patient 2)

20 Higher expression in normal colon tissue (patient 2, lib 15)
vs. tumor potential colon tissue (patient 2:lib16)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
69	19	7	3
105	116	54	2
140	24	4	6
197	6	0	6
198	113	3	40
254	28	6	5
412	28	6	5
642	7	0	7
830	10	2	5
938	31	13	3
1011	209	37	6
1095	12	3	4
1125	17	0	18

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
1129	17	0	18
1138	109	1	115
1253	73	1	77
1283	34	13	3
1285	34	13	3
1339	13	3	5
1453	11	3	4
1474	73	1	77
1505	18	6	3
1554	2542	448	6
1605	2542	448	6
1614	36	14	3
1630	24	9	3
1643	142	2	75
1646	39	14	3
1649	24	8	3
1677	19	6	3
1753	13	0	14
1764	13	0	14
1766	177	65	3
1772	24	8	3

Table 17

Differentially expressed polypeptides detected in samples from patient. Lower expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
3146	3	19	6
3150	21	228	10
3324	3	20	6